

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 27, 2002, 20:25:35 ; Search time 3172 Seconds  
(without alignments)  
5994.168 Million cell updates/sec

Title: US-09-837-961-8  
Perfect score: 6244  
Sequence: 1 MNNIQQCVPYCNLNPEV.....IGETGTFIVDSVELLMEE 1174

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlp  
-O=/cgn2.1/USPNC.spool/US09837961/runat\_25112002.142416.5933/app\_query.fasta\_1.1351  
-DB=EST -QFWT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -List=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09837961 -CGN\_1.1.2735 -runat\_25112002.142416.5933 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	122	2.0	1192	12	BG425459
2	115	1.8	1457	11	AK009951
3	111	1.8	993	12	BG164308
4	111	1.8	1438	12	BE896304
5	110.5	1.8	638	12	BG641200
6	109.5	1.8	1699	12	BE971314
7	108.5	1.7	1284	11	AK011138
8	108	1.7	3750	11	AK019545
9	107.5	1.7	616	13	BI637532
10	107.5	1.7	629	13	BI635059
11	107.5	1.7	649	13	BI639112
12	107.5	1.7	699	13	BI372337
13	107.5	1.7	970	10	BE561336
14	107.5	1.7	1382	10	BE541010
15	106	1.7	580	12	BG385276
16	106	1.7	2914	11	BC022105
17	104.5	1.7	671	13	BI234068
18	104.5	1.7	1309	12	BG491756
19	104.5	1.7	1615	11	BC020373
20	104	1.7	1130	12	BG331892
21	104	1.7	2282	11	AK012926
22	104	1.7	2874	11	BC020549
23	103	1.6	2685	11	AK016554
24	102.5	1.6	575	9	AA596165
25	102.5	1.6	1214	14	BQ926267
26	102	1.6	917	14	BQ924785
27	101.5	1.6	772	12	BF968812
28	101.5	1.6	999	10	BE542913
29	101.5	1.6	1097	17	CNS06LC5
30	101.5	1.6	2072	11	AK005502
31	101	1.6	854	17	CNS0729V
32	101	1.6	1170	12	BF568423
33	101	1.6	1576	14	BM906297
34	100.5	1.6	543	13	BI343429
35	100.5	1.6	612	9	AI405242
36	100.5	1.6	651	17	BH390224
37	100.5	1.6	682	13	BI228162
38	100.5	1.6	689	9	AI777237
39	100.5	1.6	689	13	BI486958
40	100.5	1.6	935	14	BQ215157
41	100.5	1.6	2361	11	BC014239
42	100.5	1.6	2944	11	AK004769
43	100	1.6	1137	17	CNS06QJF
44	100	1.6	1383	12	BG615889
45	99.5	1.6	688	9	AV086490

ALIGNMENTS

RESULT 1  
BG425459

LOCUS

DEFINITION

602447303F1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4585728 5',

mrna sequence.

ACCESSION

BG425459

VERSION

BG425459.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1192)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DPF  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Place: LLM1313 row: f column: 01  
High quality sequence stop: 626.  
Location/Qualifiers  
1. .1192  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4585728"  
/tissue\_lib="NH\_MGC\_14"  
/lab\_host="DH10B (phage-resistant)"  
/note="organ: kidney; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(S). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 248 a 407 c 310 g 227 t

FEATURES  
source

## Alignment Scores:

Pred. No.: 0.0069 Length: 1192  
Score: 122.00 Matches: 75  
Percent Similarity: 33.77% Conservative: 28  
Best Local Similarity: 24.59% Mismatches: 104  
Query Match: 1.95% Indels: 15  
DB: 12 Gaps: 15

US-09-837-961-8 (1-1174) x BG425459 (1-1192)

Qy 358 ThrLeuSerAspProValPheVal-----Arg 366  
Db 127 ACGCCTCCGAGCCCTGTCTCCATCGTCGGCTGCCCCAGACACCGAGCGGTCAAT 186  
Qy 367 GlyGlyPheGlyAsnProHisThrValLeuGlyLeuArgGly----- 380  
Db 187 GGTGGCATGGCCAGAGAGCTCTCTGCGGCGACGAGGCGCCAGAGCAATGCGTGCA 246  
Qy 381 -----ValAlaPheGlnGlnThrGlyThrAsnHisThr 391  
Db 247 TCCTGACCTGAAGTACCCATTGAGCATGCGTACCAACATGGGACG----- 297  
Qy 392 ArgThrPheArgAsnSerGlyThrIleAspSer----- 402  
Db 298 ---ACATGGAGAGATCTGGCACCAACACACTTCTACACGAGCTGGCGCGGAGGA 354  
Qy 403 -----LeuAspGluIleProGlnAspAsnSerGlyAlaProThrAsnAsp 418  
Db 355 GCACCATGCTGCTGACCGAGTCCCTGAACCCCAAGGCCAACAGAGAGAGATGAC 414  
Qy 419 TyrSerHisVal-----LeuAsnHisValThrPheValArg---TrpProGlyGluIle 435  
Db 415 TCAGATTATGCTGAGACCTTCAACACCCCGCCATGTACGTGGCCATCCAGCGCTGCT 474  
Qy 436 SerGlySerAspSerTrpAlaProMet---PheSerTrpThrHisArgSerAlaThr 454  
Db 475 GTTCTCTACGCCTCTGGCGCGCACCACTGGCATGTCTGATGACCTCTGGAGACGGGTCA 534  
Qy 455 ProThrAsnThrIleAspProGluArgIleThrGlnIleProLeuValIleAlaHisThr 474  
Db 535 CCC-----ACACGGTCCCATCTACAGGGCT---ACG 564

Qy 475 LeuGlnSerGlyThrThrValValArgGlyProGlyPheThrGlyGlyAspIleLeuArg 494  
Db 565 CTCCTCCCCACGCACAAATCCTGCTGTGACCTGGTGGACGGGACCTGAC-----CGA 618  
Qy 495 ArgThrSerGlyGlyProPheAlaThrThrIleValAsnIleAsnGlyGlnLeuProGln 514  
Db 619 CTAACCTATGCAGATCCTCAGTGGCCGAGGTTTACAGCTTCACCCACACACTGGCGGAG 678  
Qy 515 ArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsnLeuArgIleThrValThrVal 534  
Db 679 CGGGGACAATCCGTGGCGGA----- 699  
Qy 535 AlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeu 554  
Db 700 -----CAATTACAGAGAGAGCTGTGCTTACACGCTGCCTCTG 735  
Qy 555 ThrPhe-----GlnSerPheSerTyrAlaThrIleAsnThrAla 567  
Db 736 ACTTTCGACCTGGACATGTGCCACGCCCATCCCTCTACTCGAGAAACAAAC----- 789  
Qy 568 PheThrPheProMetSerGlnSerSerPheThrValGly----- 580  
Db 790 TAGACCTAGCCAGATGCCAGTTCTCACTCACCTTGGCCACTGACAGATCCGAGTGGCC 849  
Qy 581 AlaAspThr-----PheSerSerGlyAsnGluValTyrIle 592  
Db 850 CGAGACACTGTTCCAGGCGTTTCATACGTGCGACTTGTTCATCATTTGCGGCCATCAGACGA 909  
Qy 593 AspArgPheGluLeu 597  
Db 910 CCACGCTTCTCAGTA 924  
RESULT 2  
AK009951  
LOCUS  
DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310057B22:homolog to DNA DOUBLE-STRAND BREAK REPAIR AND V(D)J RECOMBINATION PROTEIN XRCC4, full insert sequence.  
ACCESSION AK009951.1 GI:12845062  
VERSION AK009951  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone:lib-RIKEN full-length enriched mouse cDNA library clone:2310057B22.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagao,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913



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Db 478 -----GAAATGAAGGCTCTCAGAGACTGG----- 504
Qy 700 ThrileGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPhe 719
Db 505 -----AATGATGTT-----CAAGCGCGATTT 525
Qy 720 AspGluCysTyrProThrTyr-----LeuTyrGlnLys----- 730
Db 526 GAGAAATCTGTGAGTCCCAAGAACCTTGAGGCTGATTTCATCAAGATTATCTCTG 585
Qy 731 ---lleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyrleGlu 749
Db 586 GTGTCGAATGAGAAACAAAGATCGGAGCTTCATAAATTG-----CTAAAT 636
Qy 750 AspSerGlnAspLeuGlu 755
Db 637 GAAGTCCAGAGCTGGAG 654

RESULT 3
LOCUS BGI164308 993 bp mRNA linear EST 06-FEB-2001
DEFINITION 602341347F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4449226 5',
mRNA sequence.
ACCESSION BGI164308
VERSION BGI164308.1 GI:12671011
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 993)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10232 row: n column: 11
High quality sequence start: 24
High quality sequence stop: 589.
FEATURES
Location/Qualifiers
1..993
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/db_xref="taxon:9606"
/clone="IMAGE:4449226"
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/lab_host="DH10B (phage-resistant)"
/notes="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dt primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 231 a 308 c 305 g 149 t
ORIGIN

Alignment Scores:
Pred. No.: 0.105 Length: 993
Score: 111.00 Matches: 60
Percent Similarity: 33.73% Conservative: 25
Best Local Similarity: 23.81% Mismatches: 78
Query Match: 1.78% Indels: 90
DB: 12 Gaps: 11

US-09-837-961-8 (1-1174) x BGI164308 (1-993)
Qy 316 TrpGlyGly-HisLeuValSerArgAsnThrAlaGlyAsnArgIleAsnPheProSe 335

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Db 346 TCGGGAGGATCATTTAGGATCTCTCAAGGAAACGAGGACCAAGGTGCTTCTGTGTA 405
Qy 335 rTyrGlyValPheAsn-ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProp 355
Db 406 ACACCTCTCTCTCTCTCTCCATCC-----CCAT 432
Qy 355 heTyrArgThrLeuSerAspProValPheValArgGlyGlyPheGlyAsnProHisTyrV 375
Db 433 CTACAGATGATTAAAG-----AAGCCTCAGATGA 462
Qy 375 alLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly----- 387
Db 463 GCATGCGCGCGCTGTGTGAGCGCAAGGCACAGGATTGACATGATGGCAGGCC 522
Qy 388 -----ThrAsnHisThr- 391
Db 523 CATTGACTTTGTGCTCTCAATGCCGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 582
Qy 392 -----ArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluLeuProGlnA 410
Db 583 GCATCGCACCTCGCAGTACGTAGCGGATGATGATCGGCGGATGATGATGATGATGAT 640
Qy 410 spAsnSerGlyAlaProTyrAsnAspTyrSerHisValLeuAsnHisValThrPheVal 430
Db 641 -----GCCACCGCTGAACAT----- 658
Qy 430 rGTrpProGlyGluLeuSerGlySerAspSerTyrArgAlaProMetPheSerTyr--T 449
Db 659 -----TCGGGGAACGAGGCTGTGAAGAAACCCCACTGGACTGGGCC 701
Qy 449 hrHisArgSerAlaThrProThrAsnThrIleAspProGluArg--lleThrGlnleP 468
Db 702 CCCACCGGCGGAGCGGACCATGACCGGCGGCGGCGGCGGCTGTGAGACCCCTTC 761
Qy 468 roLeuValLysAlaHisThrLeuGlnSerGlyThrValValArgGlyProGlyPheT 488
Db 762 CACAATCCGTCACCATACA-----C 782
Qy 488 hrGlyGlyAspLeuLeuArgThrSerGlyGlyProPheAlaTyrThrIleValAsnI 508
Db 783 CCAGCAGACATCTACTACTACTAACGAAACGGGAGCACCC---CGGGGAGGCGGCGCACAG 839
Qy 508 leAsnGlyGlnLeuProGlnArg-----TyrArgAlaArgIleArgTyrA 523
Db 840 TCGGAGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 899
Qy 523 laSerThrThrAsnLeuArgIleTyrValThr 533
Db 900 CCCAAACCCAGGAGCTACGACACACACAGCACA 931

RESULT 4
LOCUS BE896304 1438 bp mRNA linear EST 20-OCT-2000
DEFINITION 601439143F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924083 5',
mRNA sequence.
ACCESSION BE896304
VERSION BE896304.1 GI:10360572
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1438)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

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Clone distribution: WGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9761 row: e column: 12
High quality sequence stop: 299.
Location/Qualifiers
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by life

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FEATURES  
SOURCE

	Technologies.		
BASE COUNT	429 a	477 c	311 g
ORIGIN			221 t

Alignment Scores:

Pred. No.:	0.197	Length:	1438
Score:	111.00	Matches:	103
Percent Similarity:	32.21%	Conservative:	31
Best Local Similarity:	24.76%	Mismatches:	123
Query Match:	1.78%	Indels:	159
DB:	12	Gaps:	23

US-09-837-961-8 (1-1174) x BE896304 (1-1438)

[illegible]

QY	324	gAsnThrAlaGlyAsnArgIleAsnProSer-TyrGlyValPheAsnProGlyGlyA	344	
Db	774	CACCTGTGGCACTGGGAAGATCAATACATACAGGAGTGGACCTCGGAGCCACACGCG	833	
QY	344	laIleTTPileAlaAspGluAspProArgProPheTyrArgThrLeuSerAspProValp	364	
Db	834	CA-----AGCAGCGGATCAGCTCAACAGCTCAATACAGTCCCAATAAGT	878	
QY	364	heValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGlyValAlaPheG	384	
Db	879	TCGCAAGG-----CTACCGCAC-----CCTGGGGATCACCTCA	911	
QY	384	lnGlnThrGlyThrAsnHisThrArg-----	392	
Db	912	CACAAGCGACACACACACACCGGCGCGCGACGAGCACACATGAGAGTAACCT	971	
QY	393	-----ThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIleP	407	
Db	972	CCATCCAGAGGGCACACATACACCAACGAGGGAAC-----ACCACGACAACTCGA	1025	
QY	407	roProGlnAspAsnSerGlyAlaProTrpAsn-----AspTyrSerHisValLeuAsnH	425	
Db	1026	CGCCACAA-----AAGCGCGCCGCCAAATAGAGAGACAGCAGCAACCCACAAACC	1079	
QY	425	isValThrPheValArgTrp-ProGlyGluIleSerGlySerAspSerTrpArgAlaPro	444	
Db	1080	AC-----GACAGACAGCGCTCGCGAACTA-----	1103	
QY	445	MetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIle	464	
Db	1104	-----CGACACCGCTAAGCGGACCGCGGCAACCGGGCCACACAGCGG---	1148	
QY	465	ThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrValValArgGly	484	
Db	1149	-----ACCCCGAGGCGGCACG	1163	
QY	485	ProGlyPheThrGlyGlyAspIleLeuArgArgThrSergly	498	
Db	1164	CCACGCTCACCGCGGC-----AGACGCGATCGCGC	1196	
RESULT 5	BG641200	638 bp	linear	EST 23-APR-2001
LOCUS	SD12481.5	prime SD	Drosophila melanogaster	Schneider L2 cell culture
DEFINITION	PO72	Drosophila melanogaster	cDNA clone	SD12481 5, mRNA sequence.
ACCESSION	BG641200			
VERSION	BG641200.1	GI:13773126		
KEYWORDS	EST.			
SOURCE	fruit fly.			
ORGANISM	Drosophila melanogaster			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
AUTHORS	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
	Ephyroidae; Drosophilidae; Drosophila.			
	1 (bases 1 to 638)			
	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,			
	Lewis, S. and Rubin, G.M.			
TITLE	BDGP/HMT Drosophila EST Project			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Stapleton, M.			
	BDGP			
	Lawrence Berkeley National Lab			
	One Cyclotron Rd, Berkeley, CA 94720, USA			
	Fax: 510 486 6798			
	Email: <a href="http://www.fruitfly.org/EST_estefruitfly.berkeley.edu">http://www.fruitfly.org/EST_estefruitfly.berkeley.edu</a>			
	hit genomic AB003553: arm:3L1882534,9109551]			
	estimated-cyto:66B3-67A1: 04/13/2001			
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	High quality sequence stop: 587.			
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	/db_xref="taxon:7227"			

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/clone="SD12481"
/clone.lib="SD Drosophila melanogaster Schneider L2 cell
culture pot2"
/lab_host="DH5-alpha"
/notes=vector: pot2; Site_1: EcoRI; Site_2: XhoI; Sized
fractionated cDNAs were directly ligated into pot2.
Plasmid cDNA library."
BASE COUNT 168 a 161 c 157 g 152 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0566 Length: 638
Score: 110.50 Matches: 50
Percent Similarity: 34.27% Conservative: 35
Best Local Similarity: 20.16% Mismatches: 96
Query Match: 1.77% Indels: 67
DB: 12 Gaps: 11

US-09-837-961-8 (1-1174) x BG641200 (1-638)
Qy 930 HisArgIleAtrGluAlaTyrLeuProGluLeuSerValIleProGlyValAsnValasp 949
Db 28 TATCGGTAGAAGACAGACAGCATTTCCGAGATGTTATCAAAATCCTTGACATACGTTGCG 87
Qy 950 IlePhe-----GluGluLeuLysGlyA-GillePheThrAlaPhePheLeuTyr 965
Db 88 ATCTTTGGCCITTTTGGGGCTCAATTGCGGAAGTGTAGTGTGATGATGATGATATAT 147
Qy 966 AspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnVal 985
Db 148 GGTGTTTACCGGATTACCACACGAGGAGTAAATGCGGAGTTCGCTGCATGAACATC 207
Qy 986 -----LysGlyHisValAspValGluGluAsnAsnHisArgSerValLeuValVal 1003
Db 208 ATCCCGAGAACTCGGTGGACTGGAGCAGAG----- 240
Qy 1004 ProGluTrpGluAlaGluValserGlnGluValArgValCysProGlyArgGlyTyrIle 1023
Db 241 -----ATGGGACTCTGGTACGGC 258
Qy 1024 LeuArgValThrAlaTyrLysGluGlyTyrGly-----GluGlyCysVal 1038
Db 259 AGCAGGATTATGTCACAGGACAGATTTCCGGGCACCTACGAGTACGACATCATGTGTC 318
Qy 1039 ThrIleHisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnAsnValGluGlu 1058
Db 319 ATCATTCAT---CTGACCGATCCCGGATCAGATCCGTTTGAGCCAGCAAAATCGCGGC 375
Qy 1059 GluValTyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyr 1078
Db 376 TATGGCTATGGAAT-----CAGGACTACACCGTAACCAAGATTAACATAT 420
Qy 1079 GlyGlyAlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSer 1098
Db 421 GGAGCACACACACACACTCAATCC-----TCCATCCGGATACGATGAG 465
Qy 1099 ValProAlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAsp-----Gly 1115
Db 466 TACCG-----TTCAGATTCGATTCAGCCAGCAGAGTACCTACGTTTGATCTGGAGT 519
Qy 1116 ArgArgAspAsnProCysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAla 1135
Db 520 GAGCGTGATAACAATCTGGAG-----TATACC----- 546
Qy 1136 GlyTyrValThrLysGluLeuGluTyrPheProGluThrAspLysValTrpIleGluIle 1155
Db 547 -----TTCAACTATACCAACAGTGCACCTGGTCACTGGTGGTCCCAACATC 588
Qy 1156 GlyGluThrGluGlyThrPheIle 1163
Db 589 GCGGATACGCGGGGATCCTTGGTC 612

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RESULT 6

BE971314  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

BE971314  
601651647F1 NIH\_MGC\_81 Homo sapiens cDNA clone IMAGE:3935051 5',  
mRNA sequence.  
BE971314  
BE971314.1 GI:10584650  
EST.  
human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1699)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: CLONETECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
CDNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM776 row: n column: 12  
High quality sequence stop: 66.  
Location/Qualifiers  
1..1699

FEATURES

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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3935051"  
/clone.lib="NIH\_MGC\_81"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: muscle (skeletal); Vector: pDNR-LIB  
(Clontech); Site\_1: SfiI (ggccgctcgcc); Site\_2: SfiI  
(ggccattatggcc); 5' and 3' adaptors were used in cloning  
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'  
and 3' adaptor sequence:  
5'-ATTCTAGGCGGAGGCGCGGACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size  
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained  
inserts by PCR. This library was enriched for full-length  
clones and was constructed by Clontech Laboratories (Palo  
Alto, CA)."  
BASE COUNT 556 a 516 c 273 g 353 t 1 others  
ORIGIN

Alignment Scores:

Pred. No.: 0.395 Length: 1699  
Score: 109.50 Matches: 86  
Percent Similarity: 33.01% Conservative: 50  
Best Local Similarity: 20.87% Mismatches: 178  
Query Match: 1.75% Indels: 100  
DB: 12 Gaps: 16

US-09-837-961-8 (1-1174) x BE971314 (1-1699)

Qy 166 HisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrpGlyLeuAspIleAla 185  
Db 95 CATATTGCAACACCTCAAGATACATCATCATGTTATGGCCAAAGGCTCTTCATTCCA 154  
Qy 186 ThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArgTyrThrLysHisCys 205  
Db 155 ATCATTCACCATCATCATCATCATCATGTC---ATCATTCACCAAGCACACATCATCAGT 211  
Qy 206 LeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsnThrArgGlnTrpAla 225  
Db 212 TTCTCTTATATGTCGCGACATTCCTTCA-----TCCATCCACTCCAAAGCTGGTCT 265  
Qy 226 ArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAspIle---ValAlaLeu 244  
Db 266 CGTTATGTCAAATTCAAGCCCAATACTATCTTCACACACATCAAGCCACATCTCAAGT 325

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Qy 245 PheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGlnLeuThrArgGlu 264
    ||| ||| ||| ||| ||| |||
Db 326 CTCACAGA-----TGTTCAACGGCTTCACAC-ACACCAGT 363
Qy 265 IleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIleProAsnGlyPhe 284
    ||| ||| ||| ||| ||| |||
Db 364 GCTTGTAATATAAGCGGTGTGAGCCCATCTCCCAT----- 399
Qy 285 AsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMetAsnSerLeuPhe 304
    : : : ||||| |||
Db 400 -----ATTGGCGGCACAT-----TTT 417
Qy 305 ValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeuValSerSerArg 324
    ||| ||| ||||| ||||| |||||
Db 418 TTCACACTACCAAGGTCGTTATACGACGATGGGA-----TCTCGC 462
Qy 325 AsnThrAlaGlyAsn-ArgIleAsnProSerTyrGlyValPhe----- 339
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Db 463 TCGCGCGGTTCAACACAGGTCACCTTCCAGGGTTGAGCGTTACACACCCCACTGTTAC 522
Qy 340 -----AsnProGlyGlyAlaIleTr 346
    : : : ||||| |||||
Db 523 ACCGCCAACACACACATAGTCGCCCAACCCACGACGAGAACCCCATATCCCGTTGTG 582
Qy 346 PileAlaAspGluAspProArgProPheTyrArgThrLeuSerAspProValPheValArg 366
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    : ||| ||| ||| ||| |||
Db 619 AAACACCTCTGTATACACCCATATACACAGCAGTGGGGCAATATATTTCCACAACA 678
Qy 386 rGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIl 406
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Db 679 AACATGTACTCTATATACAGATCCGACACAGAGACGACGATACACGCCCAAGAGAT 738
Qy 406 eProGlnAspAsnSerGlyAlaProTrp-----AsnAspTyrSerHisValIle 423
    ||| ||| ||| ||| |||
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Qy 423 uAsnHisValThrPheValArgTrpPro-----G1 433
    : ||| ||| ||| ||| |||
Db 799 CGACCACACTACTATTCCCATATCAAGATAAAAGGAACATACGCCACCTCATACGG 858
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    |||| ||| ||| ||| ||| ||| |||
Db 859 AGAGCTCATTCACCCGCACTACACTTCACAGACGAGGAGGACTACACACACAGGGCGCG 918
Qy 453 aThrProThrAsnThrIleAspProGluArgIle-----ThrGlnIleProLeuValIly 471
    ||| ||| ||| ||| ||| |||
Db 919 CACACAAATTCACAGTCGCACACACACGCTTACCACCCACACAGTGTGACATCTTCCA 978
Qy 471 sAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPheThrGlyGlyAs 491
    : : : ||||| ||| ||| ||| |||
Db 979 AATTGACAAATCGAAAGCGGTAGCAACTTCTTGAT-----ACCTGGGCAGA 1026
Qy 491 pIleLeuArgArgThrSerGlyGlyProPheAlaThrThrIleValAsnIleAsnGlyG1 511
    : : : ||||| ||| ||| ||| |||
Db 1027 CGGCATCTACGCTACATAGTACATTTCTGTC-----GTCAA-AACAA 1070
Qy 511 nLeuProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsnLeuArgIleTyr 531
    ||||| ||| ||| ||| ||| |||
Db 1071 CACACCACACAGTATCATTCG-----GGACACACAGACAATGTGAGG----- 1113
Qy 531 rValThrValAlaGlyGluArgIlePheAlaGly 542
    ||| ||| ||| ||| |||
Db 1114 -----GCAAACTCACTTATATTCACACGGA 1137
RESULT 7
LOCUS AK011138 1284 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2600001J17:homolog to ARSENITE RELATED GENE

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1. full insert sequence.
AK011138
AK011138-1 GI:12847071
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA,
clone.lib:RIKEN full-length enriched mouse cDNA library
clone:2600001J17.
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci,P., and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsumai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Stauble,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
5 (bases 1 to 1284)
Arachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Adakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hangaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,K., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,

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REFERENCE 1 (bases 1 to 649)
AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
          Lewis,S. and Rubin,G.M.
TITLE     BDGP/HMMI Drosophila EST Project
JOURNAL   Unpublished (2001)
COMMENT   Contact: Stapleton, M.
          BDGP
          Lawrence Berkeley National Lab
          One Cyclotron Rd, Berkeley, CA 94720, USA
          Fax: 510 486 6798
          Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
          hit genomic AE003553: arm:3L [8822534,9109551]
          estimated-cyto:66E3-67A1: 05/19/2001
          Plate: SD.215 row: F column: 3
          High quality sequence stop: 587.
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            /db_xref="taxon:7227"
            /clone="SD21563"
            /clone_lib="SD Drosophila melanogaster Schneider L2 cell
            culture pOT2"
            /lab_host="DH5-alpha"
            /note="Vector: pOT2; Site_1: EcoRI; Site_2: XhoI; Sized
            fractionated cDNAs were directly ligated into pOT2.
            Plasmid cDNA library."
BASE COUNT 171 a 164 c 159 g 155 t
ORIGIN
Alignment Scores:
Pred. No.: 0.133 Length: 649
Score: 107.50 Matches: 54
Percent Similarity: 36.73% Conservative: 36
Best Local Similarity: 22.04% Mismatches: 94
Query Match: 1.72% Indels: 61
DB: 13 Gaps: 14

US-09-837-961-8 (1-1174) x BI639112 (1-649)
QY 930 HisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValAsnValAsp 949
Db 39 TATCGGTAGAAACAGCAGCAGCTTTCCGACAGATGCTCAAAATCCTTGACATGCTGCG 98
QY 950 IlePhe-----GluGluLeuLysGlyArgIlePheThrAlaPheLeuTyr 965
Db 99 ATCTTTGGCCCTTTTGGGGCTCAATTCGGGAACCTAGTGTGATCATTTGGATATAT 158
QY 966 AspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnVal 985
Db 159 GGTGGTTCACCGATTACCAACACGGAAGAGTAATGCGGAGTTGCGCTGCATGAACATC 218
QY 986 -----LysGlyHisValAspValGluGluAsnAsn-----HisArgSerValLeu 1001
Db 219 AATCCGAGAACCTCGGGGACTTGGACGACATGATGGACTCTGGTACGCGAGAGATT 278
QY 1002 ValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArgGly 1021
Db 279 ATCGTGCAC-----AGCCAGATTTT-----CCGGC----- 305
QY 1022 TyrIleLeuArgValThrAlaTyrLysGluGlyTyrGluGluGlyCysValThrIleHis 1041
Db 306 -----ACCTACGAGTAC-----GACTCATGTGTCATCATTTTCAT 338
QY 1042 GluIleGluAsnAsnThrAspGluLeuLysPheSerAsnGlyValGluGluValTyr 1061
Db 339 ---CTGACCAGTCCAGCATGATCCGTTGTGACCAAGCAATCCGCGCTATGGCTAT 395
QY 1062 ProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGlyAla 1081
Db 396 GGAAT-----CAGGACTACACCGTAAACCAAGATACTATGACGCGACC 440
QY 1082 TyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValProAla 1101
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Db 441 ACCACCACCTCAATCC-----TCCTATCCGGATAGCGATAGTACCG--- 482
QY 1102 AspTyrAlaSerValTyrGluLysSerTyrThrAsp-----GlyArgAsp 1118
Db 483 ---TTGAGATCGATTCAAAGCCAGCAAGTACCTAGCTTTGATCTGGAGTGCAGTGTAT 539
QY 1119 AsnProCysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrVal 1138
Db 540 AACAACTCTGGAG-----TATACC----- 557
QY 1139 ThrLysGluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThr 1158
Db 558 -----TTCAACTATACCAACCAAGTGCACCTGCTCAGTGGTCCAAACATCGGGGATCAG 608
QY 1159 GluGlyThrPheIle 1163
Db 609 CGGGGATCCTTGGTC 623
RESULT 12
BI372337
LOCUS      BI372337                699 bp      mRNA      linear      EST 01-AUG-2001
DEFINITION Drosophila melanogaster cDNA clone RE59277 5, mRNA sequence.
ACCESSION  BI372337
VERSION     BI372337.1  GI:15068365
KEYWORDS   EST.
SOURCE     fruit fly.
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 699)
AUTHORS   Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson
            J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
            R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S.,
            Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
            Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
            G.M.
TITLE      BDGP/HMMI RE Drosophila EST Project
JOURNAL    Unpublished (2001)
COMMENT    Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic AE003553: arm:3L [8822534,9109551]
            estimated-cyto:66E3-67A1: 05/16/2001
            Plate: RE.592 row: G column: 5
            High quality sequence stop: 630.
FEATURES   Location/Qualifiers
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           /sex="male and female"
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           /lab_host="DH5-alpha Tona"
           /note="Organ: embryo; Vector: pPIC1; Site_1: XhoI; Site_2:
           BamHI. Library was kindly generated by Piero Carninci at
           the RIKEN. The library was normalized and excised using
           Cre recombinase. Plasmid cDNA library."
BASE COUNT 182 a 171 c 179 g 167 t
ORIGIN
Alignment Scores:
Pred. No.: 0.151 Length: 699
Score: 107.50 Matches: 54
Percent Similarity: 36.73% Conservative: 36
Best Local Similarity: 22.04% Mismatches: 94
Query Match: 1.72% Indels: 61

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Db 616 CATTGAACCTAGAGAGAAATTCATCTCCTACCAGAGGAGCAATCCAGGGAATGAGACCC 675
QY 392 rGthrPheArgAsnSerGlyThrIleAspSerLeuAspGluIleProProGlnAspAsns 412
Db 676 CTTTCGTACAGGGTTCGAGGT-----CARACATCTT 705
QY 412 erGlyAlaProTrpAsnAspTyrSerHisValLeuAsn-----HisV 426
Db 706 CCGCGCTTCCCTATGTCACAGTTCAGTGTGCGAGGTACCGGTGGCTTCCTGGCATC 765
QY 426 alThrPheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProMetp 446
Db 766 TTTCAGAGCCCGCTGCGCGGTTCCTCTCCGCACTGGAACG-----CCCGCA 816
QY 446 heSerTrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleHrG 466
Db 817 TTTCCTGGTGGCACCTGTGGGCGACGCCATTTCG-----GGCCGGGATATGGCCC 870
QY 466 lntleProLeuValLysAlaHisThrLeuGlnSerGlyThrValValArgly 484
Db 871 AATGGCCCTGGGTGCGGCGGTCCGCGAGAGAGTGTCTACGCTGGCAACGGGG 926

RESULT 14
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LOCUS BE541010 1382 bp mRNA linear EST 09-AUG-2000
DEFINITION 601064356F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450877 5',
mRNA sequence.
ACCESSION BE541010
VERSION BE541010.1 GI:9769754
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1382)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLAM8429 row: p column: 14
High quality sequence stop: 210.
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Location/Qualifiers
1..1382
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Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
BASE COUNT 353 a 387 c 387 g 255 t
ORIGIN

Alignment Scores:
Pred. No.: 0.482 Length: 1382
Score: 107.50 Matches: 103
Percent Similarity: 30.67% Conservative: 39
Best Local Similarity: 22.25% Mismatches: 128
Query Match: 1.72% Indels: 193
DB: 10 Gaps: 25

US-09-837-961-8 (1-1174) x BE541010 (1-1382)

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QY 180 TrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsn----- 192
Db 128 TGGGGAAACCCACGTGCGGGGTGCGTACCACCTGGCAGCACCATCCCGTCTTGAAGAAG 187
QY 193 ---ArgLeuIleAsnLeuIleHisArgTyrThrLysHisCysLeuAspThrTyrAsnGln 211
Db 188 GAACGGGTACTGGGAGTCCGACCGA-----CACTGCTGCTGTACGGGGCCCC 238
QY 212 GlyLeuGlnAsnLeuArgGlyThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArg 231
Db 239 GGG-----TCTAAGCGCGGTACGGGAGCAAGTCCAGTCTCGCGGAGAACACTGGCGG 292
QY 232 ArgAspLeuThrLeuThrValLeuAspIleValAlaLeuPhePro-AsnTyrAspValar 251
Db 293 CAAGGCTTACCA-----CGCGAGGGGCCAGGATTACGAGGTCT 331
QY 251 gThrTyrProIleGlnThrSer-----SerGlnLeuThrArgGluIleTyrTh 267
Db 332 CCGGTTCCCGCTTACGGGCTGTAAACGCCCGTGGGGGCTTCCCGCTTAAAGCTTT-- 389
QY 267 rSerSerValIleGluAspSerProValSerAlaAsnIlePro-----AsnGl 283
Db 390 -----CCAGAGGTGTCTCCACCCCGCGCGCGGTGGAGAGG 427
QY 283 yPhe---AsnArgAlaGluPheGly-----Valar 292
Db 428 ATTCCCAACAGGGCAGCAGCGGCGCAGACACTTTATACGGATGGCGTTAAAGCGTTAG 487
QY 292 gProProHisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSe 312
Db 488 GCGGCGCGCAA----- 497
QY 312 rGlnThrValTrpGlyGlyHisLeuValSerSerArgAsnThrAlaGlyAsnArgIleAs 332
Db 498 -----TGGGGGCCCAACGCGCCAGCGGCAAGAAAGAACCCACAGACGAG 547
QY 332 nPheProSerTyrGly----- 337
Db 548 CCGGCCCAACAGAGGGGAGGGAATATCCAGTTACTCCAGACGACTGGTGAGAAAGC 607
QY 338 -----ValPheAsnProGlyGlyAlaI 345
Db 608 GCAAAATGTCCTATTTAAAGCCCTAACAGCTCAGACGATTCATCCGGCGGACAAAT 667
QY 345 eTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSerAspPro----- 362
Db 668 TACCAAAAACGATGTGGACCT-----CTGGTTTCGGAGGTATACAGCA 712
QY 363 -----ValPheValArgGlyGly-----PheGl 370
Db 713 AGTGCAACACGGCGGCACACACCTAGTGTATACAGAGCGGGCCACCATACATCTTGG 772
QY 370 yAsnProHisTyrValLeuGly---LeuArgGlyValAlaPheGln-----GlnThrGl 387
Db 773 GCGATTAAACCATATCTTAGCGAGCTTTATGGGAGAGACTGCGGCATTACAGCTGCGG 832
QY 387 yThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIle-P 407
Db 833 CGAGCAACATACCCGCAACA-----AACAAATATTATTCAGAAAGCGTTTTCATACCTTACC 886
QY 407 roProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValT 427
Db 887 CACCACAGGACCATGGAGAGCCCCA-----CCACAT----- 918
QY 427 hrPheValArgTrpProGlyGluIleSerGlySerAspSerTrpArg----- 442
Db 919 -----TCATCCCAACAGTTGGCGCCCTTTTGGCAGC 952
QY 443 -----AlaProMetPheSerTrpThrHisArg-SerAlaThr 454
Db 953 AGCCACGGGAAAAAATCTTCCCGCCCGCGGATTTGTCTGGCGGCAGACATAGCCACACC 1012

```



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 27, 2002, 18:30:04 ; Search time 93 seconds

(without alignments)  
2601.068 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MNNIQOCVPYCNLNPNVE.....IGTEGTFIVDSVELLMEE 1174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp.archaea.\*
- 2: sp.bacteria.\*
- 3: sp.fungi.\*
- 4: sp.human.\*
- 5: sp.invertebrate.\*
- 6: sp.mammal.\*
- 7: sp.mhc.\*
- 8: sp.organelle.\*
- 9: sp.phage.\*
- 10: sp.plant.\*
- 11: sp.podent.\*
- 12: sp.virus.\*
- 13: sp.vertebrate.\*
- 14: sp.unclassified.\*
- 15: sp.rvirus.\*
- 16: sp.bacteriaph.\*
- 17: sp.archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5406	86.6	1174	2	Q45749
2	4373	70.0	1180	2	Q9S5V8
3	4328	69.3	1176	2	Q45736
4	4312	69.1	1176	2	Q9RC30
5	4209.5	67.4	1189	2	Q9L877
6	4192.5	67.1	1155	2	Q9F296
7	4186.5	67.0	1155	2	Q93721
8	4184	67.0	1176	2	Q9S514
9	4169	66.8	1171	2	Q06894
10	4151.5	66.5	1177	2	Q45735
11	4145.5	66.4	1177	2	Q03743
12	4144	66.4	1178	2	Q9R826
13	4142	66.3	1178	2	Q45768
14	4136	66.2	1160	2	Q93TF9
15	3624.5	58.0	1118	2	Q9AM83
16	3545.5	56.8	1118	2	Q9AM82

Q93T75 bacillus th  
Q93NM5 bacillus th  
Q9AM81 bacillus th  
Q9AM80 bacillus th  
Q45745 bacillus th  
Q9S4B5 bacillus th  
Q9FDC0 bacillus th  
Q8VUK9 bacillus th  
Q8VUK9 bacillus th  
Q939T3 bacillus th  
Q8VUL0 bacillus th  
Q45720 bacillus th  
Q32306 bacillus th  
Q45737 bacillus th  
Q93NJ5 bacillus th  
Q93NJ5 bacillus th  
Q85796 bacillus th  
Q9F0P8 bacillus th  
Q8VUL1 bacillus th  
Q45721 bacillus th  
Q45789 bacillus th  
Q87654 bacillus th  
Q32308 bacillus th  
Q9S6N9 bacillus th  
Q8VW63 bacillus th  
Q9S603 bacillus th  
Q8VW61 bacillus th  
Q93NJ3 bacillus th  
Q8RQJ6 bacillus th  
Q93NJ4 bacillus th  
Q45740 bacillus th

## ALIGNMENTS

### RESULT 1

Q45749 PRELIMINARY; PRT; 1174 AA.  
AC Q45749;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Crystal protein.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BTS00349A;  
RA Lambert B.;  
RT "NO INFORMATION";  
RL Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; Z22512; CAA80235.1; -.  
DR HSP; P02965; ICIY.  
DR InterPro; IPR001178; Endotoxin.  
DR Pfam; PF00555; endotoxin; 1.  
SQ SEQUENCE 1174 AA; 133350 MW; 8C7F122F9446F15C CRC64;

Query Match 86.6%; Score 5406; DB 2; Length 1174;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 1017; Conservative 60; Mismatches 95; Indels 4; Gaps 3;  
QY 1 MNNIQOCVPYCNLNPNVEILNEERSTGRLPLDLSLTRLFLSEVPVGVGAVGLFD 60  
Db 1 MNNIQOCVPYCNLNPNVEILNEERSTGRLPLDLSLTRLFLSEVPVGVGAVGLFD 60  
QY 61 LIWGFTPSDWSLFLQEQLEQRIETFLNRATTLURGLADSVYIEALREWEANPN 120  
Db 61 LIWGFTPSDWSLFLQEQLEQRIETFLNRATTLURGLADSVYIEALREWEANPN 120  
QY 121 NAQLREDVRIRFANTDDALITAINNFTLSTPEIPLLSYVQAANHLISLLRDVAFSGOGW 180  
Db 121 NAQLREDVRIRFANTDDALITAINNFTLSTPEIPLLSYVQAANHLISLLRDVAFSGOGW 180

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QY 181 GLDIATVNNHYNRLNLHRYTHKCHLDYNOGLENLRCNTNRQARPNQFRDLTLTVID 240
Db 181 GLDIATVNNHYNRLNLHRYTHKCHLDYNOGLENLRCNTNRQARPNQFRDLTLTVID 240
QY 241 IVALFPNDVRYPIQTSQSLTREYTSVIEDSPVSNIPNGFNRAEFGVRRPPLMDFM 300
Db 241 IVALFPNDVRYPIQTSQSLTREYTSVIEDSPVSNIPNGFNRAEFGVRRPPLMDFM 300
QY 301 NSLFTVATVRSQVWGHLVSSRNAGNRINFPYGVNPGGAJWIADDEPRPFYRLS 360
Db 301 NSLFTVATVRSQVWGHLVSSRNAGNRINFPYGVNPGGAJWIADDEPRPFYRLS 360
QY 361 DPVVRGFGNPHYVGLRGVAFQGTGNHRTFRNSGTIDSLDEIPQDNGAPNDYS 420
Db 361 DPVVRGFGNPHYVGLRGVAFQGTGNHRTFRNSGTIDSLDEIPQDNGAPNDYS 420
QY 421 HVLNHTVVRWPGELSGDSNRAPMFSWTHRSATPTNTIDPERITQIPVKAHTLQSGTT 480
Db 421 HVLNHTVVRWPGELSGDSNRAPMFSWTHRSADRTNIINPNIITQIPVKAHTLQSGTT 480
QY 481 VVRGPGTGGDILRTSGGPAYTIVNINCOLPQYRARIYASTNRIYVTVAGERIF 540
Db 481 VVRGPGTGGDILRTSGGPAYTIVNINCOLPQYRARIYASTNRIYVTVAGERIF 540
QY 541 AGQFNKMTDGDPLTFQSFYSVATINTAFTFPMSSQSFVAGADTFSSGNEVYIDRFELPV 600
Db 541 QGNFQRTMNRGNLSEGNFRTAGSTFSPFSNAQSTFTLGTQAFSN-QEVIIDRIEFVPA 599
QY 601 TATPEAYDLERAKAVNALPSTINQIGIKPDVTDYHIDQVSNLVDCLSEDFCLDEREL 660
Db 600 EVTFEASDLERAKAVNALPSTISQLGLTNVTGYHIDQVSNLVACLSEDFCLDEREL 659
QY 661 SEKVKAHRLSDERNLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVILPGTFD 720
Db 660 SEKVKAHRLSDERNLQDPNFKGINQLDRGWRGSTDITIQGGDDVFKENYVILPGTFD 719
QY 721 ECYPTYLYQKIDSKLPYTRYQLRGVIEDSQDLLEIYLIRYNAKHETVNLGTGSLMPLS 780
Db 720 ECYPTYLYQKIDSKLPYTRYQLRGVIEDSQDLLEIYLIRYNSHHEIVNPGTGLMPLS 779
QY 781 VQSPIRKCGPNRCAPHLNPNLDLSCRDGKCAHSHHPSLDIDYDCTDLNEDLDVWV 840
Db 780 VENQIGPCGPNRCAPHLNPNLDLSCRDGKCAHSHHPSLDIDYDCTDLNEDLDVWV 839
QY 841 IFKIKTODGHARLGNLEFLEKPLVGEALARYKAERKWRDKREKLEINIVYKEAKES 900
Db 840 IFKIKTODGHARLGNLEFLEKPLVGEALARYKAERKWRDKREKLEINIVYKEAKES 899
QY 901 VDALFVNSQYDOLQADNTIAMIHAADKRVHRIREAYLPELSVPGVNVVDIPEELKGRIFT 960
Db 900 VDALFVNSQYDOLQADNTIAMIHAADKRVHRIREAYLPELSVPGVNVNAIPEELKGRIFT 959
QY 961 AFPLYDARNVTKNGDFNNGLSCHWNKGVHDVDEQNNHRSVLVPEWEAEVSVQVRVCPGR 1020
Db 960 AISLYDARNVTKNGDFNNGLSCHWNKGVHDVDEQNNHRSVLVPEWEAEVSVQVRVCPGR 1019
QY 1021 GYLIRVTAKEGEGCVTITHEFNNTDELKFSNCVVEEYVPNNVTVCNDYTANO--EY 1078
Db 1020 GYLIRVTAKEGEGCVTITHEFNNTDELKFSNCVVEEYVPNNVTVCNNTMNOGVEG 1078
QY 1079 GGAYTSNRNRYDETYGSSNVSPADYASVYEKSYTGDRDNPCNESRGYDGYTLPAGYV 1138
Db 1079 TDACNVNRNGYDAYGNPSTPVHYTTPYEETVYDERRNPCEANKGYNYTLPYGVY 1138
QY 1139 TKELEYFPETDVTWIEIGETEGTFIVDSVLELLMEE 1174
Db 1139 TKELEYFPETDVTWIEIGETEGTFIVDSVLELLMEE 1174

RESULT 2
Q9S5V8 PRELIMINARY; PRT; 1180 AA.
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Q9S5V8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BtT84A1 crystal protein.
GN BtT84A1.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
[1]
SEQUENCE FROM N.A.
RC STRAIN-T84A1;
RA Nagamatsu Y.;
RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
[2]
SEQUENCE FROM N.A.
RC STRAIN-T84A1;
RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
RT "Nucleotide Sequence of the lepidoptera-toxic Protein Gene of Bacillus
thuringiensis subsp. dendrolimus T84A1.";
RL J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
[3]
SEQUENCE FROM N.A.
RC STRAIN-T84A1;
RA Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
RT "A Toxic Fragment from the Entomocidal Crystal Protein of Bacillus
thuringiensis.";
RL Agric. Biol. Chem. 48:611-619(1984).
DR EMBL; AB026261; BAA77213.1;
DR HSSP; P02965; ICIY
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DCE62D CRC64;

Query Match 70.0%; Score 4373; DB 2; Length 1180;
Best Local Similarity 71.9%; Pred. No. 2.6e-288;
Matches 856; Conservative 85; Mismatches 222; Indels 28; Gaps 11;

QY 1 MENNIIQ-NQCVYPNCLNNEVEILNEER-STGRPLPLDISLTLSEFLSEFVPGVGVAFGL 58
Db 1 MDNNPNINECIYPNCLSNPEVEVLGGERIETGYTPIDISLTLQTLSEFVPGVGVAFGL 60
QY 59 FDLIWTGITSQWSLFLQIQLQIEQLIEQLERNAITTLRLGLADSYEITYEALREWEAN 118
Db 61 VDIITWIGFSGSQWDAFLVQIEQLINQIEEFARNOAISRLGLESLNLYQIYAESFEWEAD 120
QY 119 PNAQLREDYRIRFANTDDALITAINNFTLTSPEIPLLSVVVOAANLHLSLRDAVSFGQ 178
Db 121 PTNPALREEMRIQPNMNSALTALPLFAYQYQVPLLSVVOAANLHLSLRDVSFVGQ 180
QY 179 GWGLDIATVNNHYNRLNLHRYTHKCHLDYNOGLENLRCNTNRQARPNQFRDLTLTV 238
Db 181 RWGFDAAATISNRXNDLRLIGNTDYAVRYNTGLRWGDPDSRDWVRYNQFRDLTLTV 240
QY 239 LDIVALPNYDVRYPIQTSQSLTREYTSVIEDSPVSNIPNGF----NRAEFGVRRP 294
Db 241 LDIVALFNSDSSRIPRTVTSQTLREIYTNFVLE-----NFDGSGFRGMAQRIEQNRQP 294
QY 295 HLMDFMNSLFTVATVRSQVWGHLVSSR--NTAGNRINFPSPVGVNPGGAI--WIADE 350
Db 295 HLMDLNRIIYTDVHRGFYNSWHSQITASPVGSGFEFAFPLFG--NAGNAAPVVLVSL 352
QY 351 DRRPFVRLSDPVFVR-----GGFGNPHYVGLRGVAFQGTGNHRT-FRNSGTIDSLD 404
Db 353 TGLGIFRTLSSPLRYRIILGSGPNNOLEFVLDTGTEFASLTNLPTIYRQRTVDSLD 412
QY 405 EIPPQDNGAPNDYSVHLNHTVVRWPGELSGDSNRAPMFSWTHRSATPTNTIDPER 463
Db 413 VIPQDNSVPPRAGFSHRLSHVTML---SQAGAVYTLRPTFSWQHSRAEFNNIIPSSQ 469
QY 464 ITQIPLVKAHTLQSGTIVVRGPGTGGDILRTSGGPAYTIVNINCOLPQYRARIYA 523
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Db 470 ITQPLTKSTNLGSGTSVVGKPGFTGDDILRRTPSGQISTLRVNITAPLSQRYVRIRYA 529
QY 524 STTNLRIVYVAGERIFAGQFNKMTDGDPLTQSFYAVINTAFTFPMQSSFTVGADT 583
Db 530 STTNLOFHTSIDGRPINQGNFSAATMSSGSLQSGSFRTVGTTFPNSGSSVFTLSAHV 589
QY 584 FSSGNEVYIDRFELIPVTATFEAYDLERAKAVNALFTSINQIGIKTDVTDYHIDQVSN 643
Db 590 FNSGNEVYIDRIEVPVAFVFEAYDLERAKAVNELFTSSNQIGLKTVDYDIDQVSN 649
QY 644 LVCLSDPEFLDDEKREUSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQ 703
Db 650 LVECLSDPEFLDDEKREUSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQ 709
QY 704 GDDVFKENYVTLPGTFDECPYTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYA 763
Db 710 GDDVFKENYVTLGTFDECPYTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYA 769
QY 764 KHETVNVLGTGSLWPLSVQSPIRKCGEPNRCAPHEWNPDLDCSCRDGCKCAHSHHFS 823
Db 770 KHETVNVLGTGSLWPLSVQSPIRKCGEPNRCAPHEWNPDLDCSCRDGCKCAHSHHFS 829
QY 824 DIDVGCDDLNEEDLVWVIFIKITQDGHARLGNLEFLBEKPLVGEALARKVRAEKKWRDK 883
Db 830 DIDVGCDDLNEEDLVWVIFIKITQDGHARLGNLEFLBEKPLVGEALARKVRAEKKWRDK 889
QY 884 EKLELETFNIVYKAKESVDALFVNSQYDQLOADTNIAHAAKRVHIREAYLPESLVI 943
Db 890 EKLEWETNIVYKAKESVDALFVNSQYDQLOADTNIAHAAKRVHIREAYLPESLVI 949
QY 944 PGVNVDFEELKGRIFTAFFLYDARNVKNKGDFNGLSCNVKGVHVEEONNHRSLVW 1003
Db 950 PGVNAALFEELGRIFTAFSLYDARNVKNKGDFNGLSCNVKGVHVEEONNHRSLVW 1009
QY 1004 PEWEAEVSQEVRCVPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYVP 1063
Db 1010 PEWEAEVSQEVRCVPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYVP 1069
QY 1064 NTVTCNDYTANOQEEYGAYSRNREGYDETGSNSVPAADYASVYEEKSYTDGRDNPCES 1123
Db 1070 NTVTCNDYTANOQEEYGAYSRNREGYDETGSNSVPAADYASVYEEKSYTDGRDNPCES 1129
QY 1124 NRGYGDYPLPAGVYKVELEFPDVKVTEIGTEGTFIVDSVELLME 1174
Db 1130 NRGYGDYPLPAGVYKVELEFPDVKVTEIGTEGTFIVDSVELLME 1180

RESULT 3
ID Q45736 PRELIMINARY; PRT; 1176 AA.
AC Q45736;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Insecticidal crystal protein.
GN CryIA(A).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FU-2-7;
RA Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
RT "Cloning and nucleotide sequencing of two insecticidal delta-endotoxin
RL genes from Bacillus thuringiensis var. kurstaki HD-1 DNA.";
RL Agric. Biol. Chem. 51:455-463(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FU-2-7;
RX MEDLINE=94289859; PubMed=7764972;
RA Udayasuriyan V., Nakamura A., Mori H., Masaki H., Uozumi T.;
RT "Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain
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RT FU-2-7 and analysis of chimaeric CryIA(a) proteins for toxicity.";
RL Biosci. Biotechnol. Biochem. 58:830-835(1994).
DR EMBL; D17518; BAA04468.1; -.
DR HSSP; P02963; ICIV.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
FT CONFLICT 77 77 L -> P (IN REF. 1).
FT CONFLICT 965 965 S -> F (IN REF. 1).
SQ SEQUENCE 1176 AA; 133075 MW; AA4135B4A289F85 CRC64;
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Query Match 69.3%; Score 4328; DB 2; Length 1176;

Best Local Similarity 71.4%; Pred. No. 2.9e-285;

Matches 850; Conservative 86; Mismatches 223; Indels 32; Gaps 12;

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QY 1 MENNIO-NQCVYPNCLANPEVEILNEER-STGRPLDLSISLTLRFLSEFVPGVGFAGL 58
Db 1 MDNPNNECIPNCLSNPEVEILGERIETGYTPDISLTOFLSEFVPGVGFAGL 60
QY 59 FDLTWGFTTSDWSLFLQLEOLLEQRIETLERNAITTLNGLADSYEITYEALREWEAN 118
Db 61 VDIITWIFGFSQWDAFLVQLEQLNQRIEERFARQAISRLEGLSNLIQIYAESREWEAD 120
QY 119 PNNAQLREDVRIRFANTDDALITAINNFTLTTFEIPLLSVYQAANLHLSLLRDVAFSG 178
Db 121 PTNPALREEMRIQFDMNSALTATPILAVQNYQVPLSVYQAANLHLSVLRDVSFVGQ 180
QY 179 GWGLDIATVNNHYNRLNLHRYTKHCLDIYNOGLENRGTNTQWAFNQFRDLILTV 238
Db 181 RWGPDATINSRYNDLTRLIGNYTDYAVRWYNTGLERWGPDSRDWVRYNQFRELTIV 240
QY 239 LDIVALPNVDVRYPIOTSSQLTREIYTSVIEDSPVSANIPNGF---NRAEFGVRRP 294
Db 241 LDIVALSNDSDRYPIRTVSQLTREIYTNVLE-----NFDGSRGMAQRIQNIRQP 294
QY 295 HLMDFMNSLFTABTVRSQTVWGHLYSSR--NTAGNRINFPYSYGVNPGGAI--WIADE 350
Db 295 HLMDLNSITITVDHVRGYNVSGHQITASPVGSGPEFAFLFG--NAGNAAPVLVSL 352
QY 351 DPRFYFTLSDPVVR-----GGFGNPHYVLGLRGVAPQQTGTHRT--FRNSGTIDSLD 404
Db 353 TGLGIFRTLSPLYRRILGSGPNQNELFVLDGTETFSASLTTLNPLSTIYRQGRDVSLD 412
QY 405 EIPQDQSGAPWNDYSHVLNHTVFRWPGETSG--DSWRAPMFSWTHESATPTIDPER 463
Db 413 VIPQDQNSVPPRAGFSRLSHVWML---SQAGAVYVLRATFSWQHSRAEFNIIIPSSQ 469
QY 464 ITQIPLVKAHTLQSGTTVVRGPGTGGDILRRISGPGFAYTIVNINGQLPORYRARIYA 523
Db 470 ITQIPLTKSTNLGSGTSVVGKPGFTGDDILRRTPSGQISTLRVNITAPLSQRYVRIRYA 529
QY 524 STTNLRIVYVAGERIFAGQFNKMTDGDPLTQSFYAVINTAFTFPMQSSFTVGADT 583
Db 530 STTNLOFHTSIDGRPINQGNFSAATMSSGSLQSGSFRTVGTTFPNSGSSVFTLSAHV 589
QY 584 FSSGNEVYIDRFELIPVTATFEAYDLERAKAVNALFTSINQIGIKTDVTDYHIDQVSN 643
Db 590 FNSGNEVYIDRIEVPVAFVFEAYDLERAKAVNELFTSSNQIGLKTVDYDIDQVSN 649
QY 644 LVCLSDPEFLDDEKREUSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQ 703
Db 650 LVECLSDPEFLDDEKREUSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQ 709
QY 704 GDDVFKENYVTLPGTFDECPYTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYA 763
Db 710 GDDVFKENYVTLGTFDECPYTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYA 769
QY 764 KHETVNVLGTGSLWPLSVQSPIRKCGEPNRCAPHEWNPDLDCSCRDGCKCAHSHHFS 823
Db 770 KHETVNVLGTGSLWPLSVQSPIRKCGEPNRCAPHEWNPDLDCSCRDGCKCAHSHHFS 829
QY 824 DIDVGCDDLNEEDLVWVIFIKITQDGHARLGNLEFLBEKPLVGEALARKVRAEKKWRDK 883
Db 830 DIDVGCDDLNEEDLVWVIFIKITQDGHARLGNLEFLBEKPLVGEALARKVRAEKKWRDK 889
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QY 884 EKLEETNIVYKEAKESVDALFVNSQYDQADNTAMTHAADKRVHRIRREAYLELSVI 943
DB 890 EKLEETNIVYKEAKESVDALFVNSQYDQADNTAMTHAADKRVHRIRREAYLELSVI 949
QY 944 PGVNVDFEELKGRIFTAFFLYDARNVKNNGSLSCWNVKGVHVDVEEQNNHRSVLV 1003
DB 950 PGVNAAFEELEGRISTAFSLYDARNVKNNGSLSCWNVKGVHVDVEEQNNHRSVLV 1009
QY 1004 PEWEAEVSQEVKCPGCGYILVATYKGEYGGCVTHIEIENNTDELKESCVSEVEEYVN 1063
DB 1010 PEWEAEVSQEVKCPGCGYILVATYKGEYGGCVTHIEIENNTDELKESCVSEVEEYVN 1069
QY 1064 NTVTCNDYTAQOEYGGAYTSRNRGDEYGSNSVPADYASVYEKSYTDGRRDNPCES 1123
DB 1070 NTVTCNDYTAQOEYGGAYTSRNRGDEYGSNSVPADYASVYEKSYTDGRRDNPCES 1125
QY 1124 NRGYDYTPLPAGYVTKLEYFPPETDKWIEIGETGTFIVDSVELLMEE 1174
DB 1126 NRGYDYTPLPAGYVTKLEYFPPETDKWIEIGETGTFIVDSVELLMEE 1176

RESULT 4
Q9RC30 PRELIMINARY; PRT: 1176 AA.
AC Q9RC30;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE 135 kDa insecticidal protein.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-1-02;
RA Hou B.K., Chen Z.H.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF154676; AAD5382.1; -
DR HSSP: P02965; 1CIY.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
DR SEQUENCE 1176 AA; 133010 MW; FCEE069D0B81D8C4 CRC64;

Query Match 69.1%; Score 4312; DB 2; Length 1176;
Best Local Similarity 71.2%; Pred. No. 3.6e-284;
Matches 848; Conservative 85; Mismatches 226; Indels 32; Gaps 12;

QY 1 MERNIO-NOCVPVNCNNPEVEILNEER-STGRPLDIDSLSLRFLLSFVPGVGVAFGL 58
DB 1 MDNPNINEGIPYCNLSNPVEVLGGRIETGTPPIDISLQFLLSFVPGVGVAFGL 60
QY 59 FDLWIGFTPSDMSFLQIQEIQRIETPLRNRAITTLRGLADSYEYIEALREWEAN 118
DB 61 VDIWIGFGPSQWDTFLVQIEQLINRIERFARNQALSLEGLSNLYQIYAFREWEAD 120
QY 119 PNAQLREDYRISEANTDDALITAINFTLTSPEILSLVYVOAANHLHLRLDVAVSFG 178
DB 121 PTPALREEMKRIOFNDMSNLSALTAPILLAVQNYOVLPSVVOAANHLHLSVLSDVSFG 180
QY 179 GWGLDIATVNNHNLRLNHRHTKCHOLDYTNQGLENTLRGTNRQWAFENQFRDLTLTV 238
DB 181 RWGFDATINSRYNDLFLIGNYTDYAVRYNTGLERVWGPSRSDVRYNQFRDLTLTV 240
QY 239 LDIVALPENVDRYPTIOTSQTLREYTSVIEDSPVSANINPGF----NRAEFGVRPP 294
DB 241 LDIVALFSNDSRRYPRTVTSQTLREYTSVIEDSPVSANINPGF----NFDGSPGMAQRIQRP 294
QY 295 HLMDFMNSLFVATVFSQTVWGHLVSSR--NTAGNRINPSPGVFNPGGAI--WIAE 350
DB 295 HLMDFMNSLFVATVFSQTVWGHLVSSR--NTAGNRINPSPGVFNPGGAI--WIAE 352

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QY 351 DPRPFYTLSDPVEVR-----GQFNPHYYVLGRGVAFOQTGTHNHT-PRNSETIDSLD 404
DB 353 TGLGIFRTLSPLVRRILGSGPNQBELFVLDGTETEFASLTITNLPSTIYRQRTVDSLD 412
QY 405 EIPQDNGSPWPDYSHVNLHVFVRKPGELSGS-OSWRAPMESWTHRSATPNTIDPER 463
DB 413 VIPQDNGSPVPRAGFSHRLGHVTML---SOAGAVYFLRAPTFESQWHRSAEFNNIIPSSQ 469
QY 464 ITQIPLVKAHTLQSGTWRVPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYA 523
DB 470 ITQIPLVKAHTLQSGTWRVPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIRYA 529
QY 524 STTNLRIYVTVBRIIPAGOFNMTQDPLTFQSPYATINATFPPMQSQSFTVGADT 593
DB 530 STTNLQFHTSIDGRPINQGNFSATMSSGSLNQSSEFTVGTFFPFNFSGSSVFTLSAHV 589
QY 584 FSSGNEVYIDREFELIPYATFATFAEYDLERAKAVNALFTSINOIGIKTDTVDYHDOVSN 643
DB 590 FNSGNEVYIDREFELIPYATFATFAEYDLERAKAVNALFTSINOIGIKTDTVDYHDOVSN 649
QY 644 LVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGINRQLDRGWRGSTDITQIR 703
DB 650 LVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGINRQLDRGWRGSTDITQIR 709
QY 704 GDDVFKENYVTLPGTFDECYPTLYXQIDSKLKPTRYQYQLRGVIEDSQDLEYLIRYNA 763
DB 710 GDDVFKENYVTLPGTFDECYPTLYXQIDSKLKPTRYQYQLRGVIEDSQDLEYLIRYNA 769
QY 764 KHEVNVLTGSLWPLSVQSPIRKCGEPNRCAPHLNPNLDCSCRDGKCAHSHHFSL 823
DB 770 KHEVNVLTGSLWPLSVQSPIRKCGEPNRCAPHLNPNLDCSCRDGKCAHSHHFSL 829
QY 824 DIDVGTDLNEDLDVWVIFKIKTODGHARLGNLEFLKPLVGEALARKVKAQKWKDKR 883
DB 830 DIDVGTDLNEDLDVWVIFKIKTODGHARLGNLEFLKPLVGEALARKVKAQKWKDKR 889
QY 884 EKLEETNIVYKEAKESVDALFVNSQYDQADNTAMTHAADKRVHRIRREAYLELSVI 943
DB 890 EKLEETNIVYKEAKESVDALFVNSQYDQADNTAMTHAADKRVHRIRREAYLELSVI 949
QY 944 PGVNVDFEELKGRIFTAFFLYDARNVKNNGSLSCWNVKGVHVDVEEQNNHRSVLV 1003
DB 950 PGVNAAFEELEGRIFTAFSLYDARNVKNNGSLSCWNVKGVHVDVEEQNNHRSVLV 1009
QY 1004 PEWEAEVSQEVKCPGCGYILVATYKGEYGGCVTHIEIENNTDELKESCVSEVEEYVN 1063
DB 1010 PEWEAEVSQEVKCPGCGYILVATYKGEYGGCVTHIEIENNTDELKESCVSEVEEYVN 1069
QY 1064 NTVTCNDYTAQOEYGGAYTSRNRGDEYGSNSVPADYASVYEKSYTDGRRDNPCES 1123
DB 1070 NTVTCNDYTAQOEYGGAYTSRNRGDEYGSNSVPADYASVYEKSYTDGRRDNPCES 1125
QY 1124 NRGYDYTPLPAGYVTKLEYFPPETDKWIEIGETGTFIVDSVELLMEE 1174
DB 1126 NRGYDYTPLPAGYVTKLEYFPPETDKWIEIGETGTFIVDSVELLMEE 1176

RESULT 5
Q9L877 PRELIMINARY; PRT: 1189 AA.
AC Q9L877;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Toxin CryIcA6.
GN CRIC6.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2-F;

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RA Yu J., Pang Y., Li J.;  
RT "Cloning and sequence analysis of the cryIcA6 gene from *Bacillus*  
RT thuringiensis, strain A2-P";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF215647; AAF37224.1;  
DR HSSP: P02965; ICIV.  
DR InterPro: IPR001178; Endotoxin.1.  
DR Pfam: PF00555; endotoxin.1.  
SQ SEQUENCE 1189 AA; 134685 MW; 98F8C1D978DF9451 CRC64;

Query Match 67.4%; Score 4209.5; DB 2; Length 1189;  
Best Local Similarity 68.6%; Pred. No. 3.4e-277;  
Matches 830; Conservative 99; Mismatches 224; Indels 57; Gaps 17;

QY 1 MENNIOQCVPYNCLNNPEVEILNEER-STGRLLPDLTSLTRELLEFVPGVAGFLF 59  
Db 1 MEENNOQCIPYNCLNPEVEILLGERISTGSSIDLSLVQLVSNFVPGGFLVGLI 60  
QY 60 DLWGFITPDSWLSFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIALREWEANP 119  
Db 61 DFVWGIQVPSQWDAFLQIEQLINERAEFARNAAIANLEGUNFNLIYVEAFKEWEDP 120  
QY 120 NNAQLREDVIRFANTDALTAINNETLTSTFEPLSLSVYVQAAHLSSLRDVSGQG 179  
Db 121 NNPAIRTRVIRDFRILDGLRDIPIRISGFVEPLLSVYAAQAANHLAIIRDSVIFGER 180  
QY 180 WGLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLGTNTROWARENOPRRDLTLVL 239  
Db 181 WGVTTINVENYRLRHIDYADHCANTYNRGLNLPKSYQDWITTYNRRLDLTLVL 240  
QY 240 DIVALFNIDYRTPIQTSSTLREIYTSVIEDSP---VSANIPGNFNRAE-FCVRPPH 295  
Db 241 DIAAFPNYDNRRYPIQVPGQLTREVTDPDLINFPQLSVAQLPT-PNVMESSAIRNPH 299  
QY 296 LMDPNSLFTAE--TVRSQTWGHVLSRNTAGRNINFPESYGVNPGGAIWADEDP- 352  
Db 300 LFDILNLTITFDVSGRNFYWGHRVYSSILIGGNITSPYI-----REANQPP 351  
QY 353 -----RPEVRLSDPV--FVRGFGFNPHYVL-GLRGVAFQGTGTHHPTFRNSGTDSL 403  
Db 352 RSFTFNGVFTLNNPRLRLQQWPAPPFNLRGVEGVEF-STPTN-SFTIRGRTVDLSL 409  
QY 404 DEIPPQNGSAPWNDYSHLVNHTVFRWPGISGSDSWRAP-----MFSWTHRSATPTN 457  
Db 410 TELPEDNSVPPREGYSHRCHAFVQRSG-----TPFLITGVVFSWTHRSATLTN 460  
QY 458 TIDPERITQPLVKAHLOSCTTVVRGPGFTGGILLRTSGGPAYTIVNGLQPQYR 517  
Db 461 TIDPERINQPLVGRFVWGGTSVITGPGFTGGDILRNTFGDFVSLQVNSIPITQYR 520  
QY 518 ARIRYASTNLRIRYV-TVAGERIEFAGQ-----FNKMTMDTGDTLQFSFSYATINTAFTF 570  
Db 521 LRFRYASSRQARVILVTCASSTGVGGQVSVNMPKQKMEIGENLTSRTFRYTDFSNPFSP 580  
QY 571 PMSOSSTV-----GADTFSSGNEVIDRELIPVTAFAEYDLERAQKAVNALFTSI 624  
Db 581 RANPDITIGISRRPLFGAGSISG-ELYIDKTEIILADATFAESDLERAQKAVNALFTSS 639  
QY 625 NOIGIKTDVTDYHIDQVSNLVDCLSDERCLDEKSELSEKVKHAKLSLDERNLQDPNFKG 684  
Db 640 NOIGLKTVDVTDYHIDQVSNLVDCLSDERCLDEKSELSEKVKHAKLSLDERNLQDPNFKG 699  
QY 685 INRQDRGWRGSTDITIQRGDDVFNENVTLPGLTFDECYPTLYLQKIDESKLKPYRYOL 744  
Db 700 INRQDRGWRGSTDITIOGGDDVFNENVTLPGLTFDECYPTLYLQKIDESKLKPYRYOL 759  
QY 745 RGYIEDSODLEIYLIRYNAKHETVNVLTGSLWPLSVQSPKRCGCEPNRCAPHLEWNPDL 804  
Db 760 RGYIEDSODLEIYLIRYNAKHETVNVLTGSLWPLSVQSPKRCGCEPNRCAPHLEWNPDL 819  
QY 805 DCSRDGEKCAHSHHFLSDIDVGCSTDLNEDLDVWVIFKIKTQGHARLGNLEFLKPL 864  
Db 820 DCSRDGEKCAHSHHFLSDIDVGCSTDLNEDLDVWVIFKIKTQGHARLGNLEFLKPL 879

QY 865 VGEALARVKRAEKKWRDKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHA 924  
Db 880 LGEALARVKRAEKKWRDKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHA 939  
QY 925 ADKRVHRIREAYLPESLVPGVNVDIIFEEELGRIFTAFFLYDARNVTKNGDPNGLSCWN 984  
Db 940 ADKRVHRIREAYLPESLVPGVNAAIPEELEGRIFTAYSLYDARNVTKNGDFNGLLSCWN 999  
QY 985 VKGHVDYEEQNHNHRSVLVWPEWEAEVSOEVRVCPGRGVILRVATYKKGCGCYTHIEIE 1044  
Db 1000 VKGHVDYEEQNHNHRSVLVWPEWEAEVSOEVRVCPGRGVILRVATYKKGCGCYTHIEIE 1059  
QY 1045 NNTDELAFSCNVEEVPNNVTCTNCTANOEYGGAYTSNRGVDYETYSNSVPADYA 1104  
Db 1060 DNTDELAFSCNVEEVPNNVTCTNCTANOEYGGAYTSNRGVDYETYSNSVPADYA 1119  
QY 1105 SVYEKSYTDGRRDNPCESNRGYGDTPLPAGYVTKLEYEPETDKVWIEIGETEGTIV 1164  
Db 1120 SVYEKSYTDGRRDNPCESNRGYGDTPLPAGYVTKLEYEPETDKVWIEIGETEGTIV 1179  
QY 1165 DSVELLMLLEE 1174  
Db 1180 DSVELVLMEE 1189  
RESULT 6  
Q9F296 PRELIMINARY; PRT: 1155 AA.  
ID Q9F296 AC Q9F296;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Delta endotoxin.  
OS *Bacillus thuringiensis*.  
OC Bacteria; Firmicutes; *Bacillus*/Clostridium group; Bacillales;  
OC Bacillaceae; *Bacillus*.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Meza-Basso L.A., Theoduloz C.;  
RT "Cloning and expression of a delta endotoxin gene from a Chilean  
RT native *Bacillus thuringiensis* strain";  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U94191; AAG16877.1;  
DR HSSP: P02965; ICIV.  
DR InterPro: IPR001178; Endotoxin.  
DR Pfam: PF00555; endotoxin.1.  
SQ SEQUENCE 1155 AA; 130557 MW; 5D69E3E2F527749D CRC64;

Query Match 67.1%; Score 4192.5; DB 2; Length 1155;  
Best Local Similarity 69.7%; Pred. No. 4.7e-276;  
Matches 827; Conservative 85; Mismatches 230; Indels 45; Gaps 9;

QY 1 MENNIO-QCVPYNCLNNPEVEILNEER-STGRLLPDLTSLTRELLEFVPGVAGFL 58  
Db 1 MDNPNNECIPYNCLNPEVEILGGERIETGYTPIDISLITQFLSEFVPGAGFLGL 60  
QY 59 FDLWGFITPDSWLSFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIALREWEAN 118  
Db 61 VDIWGFIPGSQWDAFLVQIEQLINQRIEFAFNQAIARLEGLNLIYQIYAESFREWAD 120  
QY 119 PNNALQREDVIRFANTDALTAINNETLTSTFEPLSLSVYVQAAHLSSLRDVSGFG 178  
Db 121 PTNPALEEMRIQFNDMNSALTALPLFAVONYQVPLSLSVYVQAAHLSSLRDVSGFG 180  
QY 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLGTNTROWARENOPRRDLTLVL 238  
Db 181 RWGFDAAATINSRYNDLRELIGNYTDHVRWYNTGLERWGPDSRDWIRYNGFRRELITV 240  
QY 239 LDIVALFPNVDRYPIQTSQSLTREIYTSVIEDSPVSANIPGNFNA-----RFGVRPP 294  
Db 241 LDIVSLFPNYSRTYPIRTVSQLTREIYTNVLE-----NFDGSRGSAQGIERSIRP 294

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QY 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINFPISYGVF--NPGGAIWIADED 351
DB 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINFPISYGVF--NPGGAIWIADED 351
QY 352 PRPFYTLSDPVEVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTTSDLSDEIP 407
DB 352 PRPFYTLSDPVEVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTTSDLSDEIP 407
QY 355 GCGVYRTLSSTLYRRPFGNIGNQQLSVLDGTFAFYAGTSNLPSSAVYRKSGTVDLSDEIP 414
DB 355 GCGVYRTLSSTLYRRPFGNIGNQQLSVLDGTFAFYAGTSNLPSSAVYRKSGTVDLSDEIP 414
QY 408 PQDNGAPWNDYSHVNLNHYTVFVRWPGCEISGDSWRAPMSWTHRSATPTNTIDPERITQI 467
DB 408 PQDNGAPWNDYSHVNLNHYTVFVRWPGCEISGDSWRAPMSWTHRSATPTNTIDPERITQI 467
QY 415 PQNNVPPRQGSFHRSLSHVSMFSGFSNVSIIIRAPMSWTHRSATPTNTIDPERITQI 474
DB 415 PQNNVPPRQGSFHRSLSHVSMFSGFSNVSIIIRAPMSWTHRSATPTNTIDPERITQI 474
QY 468 PLVKAHTLQSGTTVVRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 527
DB 468 PLVKAHTLQSGTTVVRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 527
QY 475 PLTKSTNLGSGTSVVGKPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 534
DB 475 PLTKSTNLGSGTSVVGKPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 534
QY 528 LRIYVTVAGERIFAGQFNKTMGTGDLPTFQSPSYATINTAFTFPMSSQSTFVGADTFSSG 587
DB 528 LRIYVTVAGERIFAGQFNKTMGTGDLPTFQSPSYATINTAFTFPMSSQSTFVGADTFSSG 587
QY 535 LQFHTSIDGRINQGNFSAITSSGNSLQSGFTVGTTPFNFSGSVFTLSAHVFNSSG 594
DB 535 LQFHTSIDGRINQGNFSAITSSGNSLQSGFTVGTTPFNFSGSVFTLSAHVFNSSG 594
QY 588 NEVYIDRFELIPVTATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 647
DB 588 NEVYIDRFELIPVTATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 647
QY 595 NEVYIDRFELIPVTATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 654
DB 595 NEVYIDRFELIPVTATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 654
QY 648 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 707
DB 648 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 707
QY 655 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 714
DB 655 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 714
QY 708 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 767
DB 708 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 767
QY 715 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 774
DB 715 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 774
QY 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHSLDIDV 827
DB 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHSLDIDV 827
QY 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHSLDIDV 808
DB 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHSLDIDV 808
QY 828 GCTDNLNEDLVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAEKKWRDKREKLE 887
DB 828 GCTDNLNEDLVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAEKKWRDKREKLE 887
QY 809 GCTDNLNEDLVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAEKKWRDKREKLE 868
DB 809 GCTDNLNEDLVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAEKKWRDKREKLE 868
QY 888 LETNIVYKEAKESVDALFVNSOYDQADNTIAMHAADKRVHRIEAYLPELSVIPGVN 947
DB 888 LETNIVYKEAKESVDALFVNSOYDQADNTIAMHAADKRVHRIEAYLPELSVIPGVN 947
QY 869 WETNIVYKEAKESVDALFVNSOYDQADNTIAMHAADKRVHRIEAYLPELSVIPGVN 928
DB 869 WETNIVYKEAKESVDALFVNSOYDQADNTIAMHAADKRVHRIEAYLPELSVIPGVN 928
QY 948 VDIPELAKGRIFTAFPLDYDARVNIKNGFNGLSCWNVKGVHVDSEONNHRSLVVPWE 1007
DB 948 VDIPELAKGRIFTAFPLDYDARVNIKNGFNGLSCWNVKGVHVDSEONNHRSLVVPWE 1007
QY 929 AAIFEELEGRISTAFSLDYDARVNIKNGFNGLSCWNVKGVHVDSEONNHRSLVVPWE 988
DB 929 AAIFEELEGRISTAFSLDYDARVNIKNGFNGLSCWNVKGVHVDSEONNHRSLVVPWE 988
QY 1008 AEVSQEVRCVGRGVLRTAYKEGEGCVTIHEIENNTDELKFSNCVEEYVYNNVT 1067
DB 1008 AEVSQEVRCVGRGVLRTAYKEGEGCVTIHEIENNTDELKFSNCVEEYVYNNVT 1067
QY 989 AEVSQEVRCVGRGVLRTAYKEGEGCVTIHEIENNTDELKFSNCVEEYVYNNVT 1048
DB 989 AEVSQEVRCVGRGVLRTAYKEGEGCVTIHEIENNTDELKFSNCVEEYVYNNVT 1048
QY 1068 CNDYTANOEYGGATSNRNGYDETYGSSNVPADYASYVEEKSYTDGRRDNPCCSNRGY 1127
DB 1068 CNDYTANOEYGGATSNRNGYDETYGSSNVPADYASYVEEKSYTDGRRDNPCCSNRGY 1127
QY 1049 CNDYTANOEYGGATSNRNGYDETYGSSNVPADYASYVEEKSYTDGRRDNPCCSNRGY 1108
DB 1049 CNDYTANOEYGGATSNRNGYDETYGSSNVPADYASYVEEKSYTDGRRDNPCCSNRGY 1108
QY 1128 GDTPLPAGYVTKELYEPETDKWIEGTGEGTGTIVDSVLELLMEE 1174
DB 1128 GDTPLPAGYVTKELYEPETDKWIEGTGEGTGTIVDSVLELLMEE 1174
QY 1109 GDTPLPAGYVTKELYEPETDKWIEGTGEGTGTIVDSVLELLMEE 1155
DB 1109 GDTPLPAGYVTKELYEPETDKWIEGTGEGTGTIVDSVLELLMEE 1155

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RESULT 7

Q93T21

ID Q93T21

AC Q93T21

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Crystall protein Crylab16

GN Crystall protein Crylab16

OS Bacillus thuringiensis (subsp. israelensis).

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI\_TaxID=1430;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=407;

RA Yu J., Tan L., Wu D., Pang Y.;

RT "Molecular characterization of a silent gene encoding a 130-kilodalton

crystal protein from *Bacillus thuringiensis* subsp. *israelensis*."

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF375608; AAK55546.1; -

DR InterPro; IPR001178; Endotoxin.

DR Pfam; PF00555; endotoxin; 1.

SQ SEQUENCE 1155 AA; 130747 MW; 7F0C98E0100C7698 CRC64;

Query Match

Best Local Similarity 67.0%; Score 4186.5; DB 2; Length 1155;

Matches 826; Conservative 85; Mismatches 231; Indels 45; Gaps 9;

QY 1 MENNIO--NOCVPYCNLNNPEVEILNEER--STGRLPLDLSLTLRFLLSFVPGVGAFL 58

DB 1 MENNIO--NOCVPYCNLNNPEVEILNEER--STGRLPLDLSLTLRFLLSFVPGVGAFL 58

QY 59 FDLWGFITPDSWLSFLQLIEQRIETLERNRAITTLRGLADSYEIVIALREWEAN 118

DB 59 FDLWGFITPDSWLSFLQLIEQRIETLERNRAITTLRGLADSYEIVIALREWEAN 118

QY 61 VDIWIGIFGSPQWDAFLVQIEQLINQRIEFAFNQAISRLGSLNLYQIYAFSFEWEAD 120

DB 61 VDIWIGIFGSPQWDAFLVQIEQLINQRIEFAFNQAISRLGSLNLYQIYAFSFEWEAD 120

QY 119 PNNALREDVRIRFANTDDALTAINNFTLTSPFELSVYVQAAHLHLRLDAYVFGQ 178

DB 119 PNNALREDVRIRFANTDDALTAINNFTLTSPFELSVYVQAAHLHLRLDAYVFGQ 178

QY 121 PTPNALREEMRIQFNDMSALTAIPFAVQNVRYVPLLSVYVQAVNLHLVLRDLVFGQ 180

DB 121 PTPNALREEMRIQFNDMSALTAIPFAVQNVRYVPLLSVYVQAVNLHLVLRDLVFGQ 180

QY 179 GWGLDIATVNNHYNLNLHRYTKHCLDLYNOGLNLRGTNTROWARENQPRDLTIV 238

DB 179 GWGLDIATVNNHYNLNLHRYTKHCLDLYNOGLNLRGTNTROWARENQPRDLTIV 238

QY 181 RKGFAATATNSYNDLTRIGNYTDHAWRYNTGLERWVGPDSDROWIRYNQFRRLTLV 240

DB 181 RKGFAATATNSYNDLTRIGNYTDHAWRYNTGLERWVGPDSDROWIRYNQFRRLTLV 240

QY 239 LDVALFPNDYRTPIQTSOLTRISLTREIYTSVIEDSPVSANIPNGFNRA---EFQVRPP 294

DB 239 LDVALFPNDYRTPIQTSOLTRISLTREIYTSVIEDSPVSANIPNGFNRA---EFQVRPP 294

QY 241 LDVLSLFPNDYRTPIQTSOLTRISLTREIYTSVIEDSPVSANIPNGFNRA---EFQVRPP 294

DB 241 LDVLSLFPNDYRTPIQTSOLTRISLTREIYTSVIEDSPVSANIPNGFNRA---EFQVRPP 294

QY 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINFPISYGVF--NPGGAIWIADED 351

DB 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINFPISYGVF--NPGGAIWIADED 351

QY 352 PRPFYTLSDPVEVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTTSDLSDEIP 407

DB 352 PRPFYTLSDPVEVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTTSDLSDEIP 407

QY 355 GCGVYRTLSSTLYRRPFGNIGNQQLSVLDGTFAFYAGTSNLPSSAVYRKSGTVDLSDEIP 414

DB 355 GCGVYRTLSSTLYRRPFGNIGNQQLSVLDGTFAFYAGTSNLPSSAVYRKSGTVDLSDEIP 414

QY 408 PQDNGAPWNDYSHVNLNHYTVFVRWPGCEISGDSWRAPMSWTHRSATPTNTIDPERITQI 467

DB 408 PQDNGAPWNDYSHVNLNHYTVFVRWPGCEISGDSWRAPMSWTHRSATPTNTIDPERITQI 467

QY 415 PQNNVPPRQGSFHRSLSHVSMFSGFSNVSIIIRAPMSWTHRSATPTNTIDPERITQI 474

DB 415 PQNNVPPRQGSFHRSLSHVSMFSGFSNVSIIIRAPMSWTHRSATPTNTIDPERITQI 474

QY 468 PLVKAHTLQSGTTVVRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 527

DB 468 PLVKAHTLQSGTTVVRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 527

QY 475 PLTKSTNLGSGTSVVGKPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 534

DB 475 PLTKSTNLGSGTSVVGKPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 534

QY 528 LRIYVTVAGERIFAGQFNKTMGTGDLPTFQSPSYATINTAFTFPMSSQSTFVGADTFSSG 587

DB 528 LRIYVTVAGERIFAGQFNKTMGTGDLPTFQSPSYATINTAFTFPMSSQSTFVGADTFSSG 587

QY 535 LQFHTSIDGRINQGNFSAITSSGNSLQSGFTVGTTPFNFSGSVFTLSAHVFNSSG 594

DB 535 LQFHTSIDGRINQGNFSAITSSGNSLQSGFTVGTTPFNFSGSVFTLSAHVFNSSG 594

QY 588 NEVYIDRFELIPVTATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 647

DB 588 NEVYIDRFELIPVTATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 647

QY 595 NEVYIDRFELIPVTATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 654

DB 595 NEVYIDRFELIPVTATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 654

QY 648 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 707

DB 648 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 707

QY 655 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 714

DB 655 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 714

QY 708 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 767

DB 708 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 767

QY 715 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 774

DB 715 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 774

QY 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHSLDIDV 827

DB 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHSLDIDV 827

QY 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHSLDIDV 808

DB 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHSLDIDV 808

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QY 828 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKEPLVGEALARKKRWDRKREKLE 887
Db 809 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKEPLVGEALARKKRWDRKREKLE 868
QY 888 LETNIVYKAKESVDALFVNSQYDQLOADNTAMIAHAADKRVHRIEAYLPESLVPGVN 947
Db 869 WETNIVYKAKESVDVAVFVNSQYDQLOADNTAMIAHAADKRVHRIEAYLPESLVPGVN 928
QY 948 VDFEELKGRIFTAFPLXDARNVKNKGDFNGLSCWNVKGVHVDVEQNHRSLVVPWE 1007
Db 929 AIFELEGRIFTAFSLYDARNVKNKGDFNGLSCWNVKGVHVDVEQNHRSLVVPWE 988
QY 1008 AEVSQVRVPCRGYILRVYAYKEGEGCVTHIEIENNTDELKFSNCVEEYVPPNVT 1067
Db 989 AEVSQVRVPCRGYILRVYAYKEEYEGCVTHIEIENNTDELKFSNCVEEYVPPNVT 1048
QY 1068 CNDYANQOEYGGATSRNRGDEYTGSSNPADYASVYEKSYTDGRDNCESNRGY 1127
Db 1049 CNDYATQOEYEGYTSNRGDEYTGSSNPADYASVYEKSYTDGRDNCESNRGY 1108
QY 1128 GGYTLPAGYVTKLEYFPETDKVWIEIGETEGTFTIVDSVELLME 1174
Db 1109 GGYTLPAGYVTKLEYFPETDKVWIEIGETEGTFTIVDSVELLME 1155

RESULT 8
Q9S514
ID Q9S514 PRELIMINARY; PRT: 1176 AA.
AC Q9S514;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE Insecticidal crystal protein.
GN CRY1
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C12;
RA Osman Y.A., Ibrahim M.A., Ashour S.A., Bulla L.A. Jr.;
RT "Nucleotide sequence and expression of a cry gene from Bacillus
RT thuringiensis strain C12.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081790; RAD46139.1;
DR HSP; P02965; 1C1Y
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1176 AA; 133038 MW; 280654B3EDBF8C8 CRC64;

Query Match 67.0%; Score 4184; DB 2; Length 1176;
Best Local Similarity 69.6%; Pred. No. 1.8e-275;
Matches 829; Conservative 88; Mismatches 242; Indels 32; Gaps 12;

QY 1 MENNIQ-NOCVPYNCLNPEVEILNEER-STGRPLDIDLSLTFLLSEFPVGVAFGL 58
Db 1 MDNPNINCEIPNCLSNPEVEVLGERIETGYPTDLSLTQFLSSEFPVGAFLGL 60
QY 59 FDLINGFTPSWSLLEQIOLEIQRITLERNAITLRLGLADSYEYIEALREWEAN 118
Db 61 VDIINGIFGFSQMDAFVQTEQLINRIIEFARNQAIISLEGSLNLYQIYAESFREWEAD 120
QY 119 PNAQLREDVRIRFANTDALITAINNFLTSEIFLLSVYQAAHLHLSDAYSPGQ 178
Db 121 PTPNALREMRQFNQDMSALTAIFLLAVQNVQVPLLSVYQAAHLHLSDVSVFGQ 180
QY 179 GWGLDIATVNNHYNLINLIHRYTKCLDTYNOGLENLKTNTROWARENOFERDLTLTV 238
Db 181 RWGFDATINSRYNDLTRILIGNYTDYAVRWNTGLSRVWGPDSRWRYNQFRELTLTV 240
QY 239 LDIVALFPNDYVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGF---NRAEFGVRPP 294

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Db 241 LDIVALFVNSDSSRYPIRTVSQLTRIYNPVL-----NEDGSFRGMAQRIETPEYRQP 294
QY 295 HLMDFNLSLVFAETVRSQTVGCHLVSSR--NTAGNRINFPSPSYGVNPGGAI--WIADE 350
Db 295 HLMDIILSIITVDVHURGFNYSGHQITTSVPGFSGPEFAFPLFG--NAGNAAPPVLVSL 352
QY 351 DRRPFYRTSLSDPVEFV-----GGFGNPHVYVGLRGVAFQQTGNHRT-PRNSTGTDISLD 404
Db 353 TGLGIFRTLSPPYIRKLIILGSGPNNQELFVLDGTETESFASLTNLNSTIYRQRTGVDLSLD 412
QY 405 ETPPDQNSGAPWMDYGHVNLNHVTFVWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPER 463
Db 413 VIPPDQNSVPPRAGPSHRLSHVPEML--SQAGAVVTLRASLFLRLDPSAEFNIIPSFT 469
QY 464 IQQIPLVKAHTLOSQTVVYRGPGFTGGDILRLRTSGGFFAYTVININGQLPQRTARIRYA 523
Db 470 NYQIPLTKTSLGSGTSVVKGPFTGGDILRLRTSPGLISTLRVNIITAPLSQRYRIRYA 529
QY 524 STTNLIYVTVAGERTFAGQFNKMTDGTPLTFQSFYSATINTAFTPMQSSQFTVGADT 583
Db 530 STTNLFHISIDGRPINQGNFYATMSGNLSQSGSFTVGTPTFPNFSNGSSVFTLSAHV 589
QY 584 FSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSN 643
Db 590 FNSGNEVYIDRIEFVPAEYTFEAEYDLERAQNGVNOFLTSSNOIGLTKDGTDYHIDQVSN 649
QY 644 LVDCLSDFCLEKRELSEKVKHAKLSDERNLLQDPNPKGINRQLDGRWGRTDITIQ 703
Db 650 LVECLSDFCLEKRELSEKVKHAKLSDERNLLQDPNPKGINRQLDGRWGRTDITIQ 709
QY 704 GDDVFKENVTVLPGTDECYPTLYOKIDESKLPKTRYOLRGYIEDSODLEYLLRYNA 763
Db 710 GDDVFKENVTVLPGTDECYPTLYOKIDQSKLKATSTQLRGYIEDSODLEYLLRYNA 769
QY 764 KHETVNLGTSLWPLSVQSPKRCGEPNRCAPHLBNPDLDCSDRGEKCAHSHHFSL 823
Db 770 KOOTVNVPGTSLWPVSAPKPIGKCGEPNRCAPHLBNPDLDCSDRGEKCAHSHHFSL 829
QY 824 DIDVGTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKEPLVGEALARKKRWDRK 883
Db 830 DIDVGTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKEPLVGEALARKKRWDRK 889
QY 884 EKLEETNIVYKAKESVDALFVNSQYDQLOADNTAMIAHAADKRVHRIEAYLPESLVI 943
Db 890 EKLEETNIVYKAKESVDALFVNSQYDQLOADNTAMIAHAADKRVHRIEAYLPESLVI 949
QY 944 PGVNVDFIPEELKGRIFTAFPLXDARNVKNKGDFNGLSCWNVKGVHVDVEQNHRSLV 1003
Db 950 PGVNAAFIPEELKGRIFTAFPLXDARNVKNKGDFNGLSCWNVKGVHVDVEQNHRSLV 1009
QY 1004 PEKEAEVSQVRVPCRGYILRVYAYKEGEGCVTHIEIENNTDELKFSNCVEEYV 1063
Db 1010 PEKEAEVSQVRVPCRGYILRVYAYKEGEGCVTHIEIENNTDELKFSNCVEEYV 1069
QY 1064 NTVTCNDYITANOEYGGATSRNRGDEYTGSSNPADYASVYEKSYTDGRDNCES 1123
Db 1070 NTVTCNDYITANOEYGGATSRNRGDEYTGSSNPADYASVYEKSYTDGRDNCES 1125
QY 1124 NRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFTIVDSVELLME 1174
Db 1126 NRGYRDYTLPGVYVTKLEYFPETDKVWIEIGETEGTFTIVDSVELLME 1176

RESULT 9
O06894
ID O06894 PRELIMINARY; PRT: 1171 AA.
AC O06894;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE CryIeA4.
GN CRY1E4.

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QY 463 RITQIPLVKAHTLQSGTAVVRGPGTGGDILKRTSGGPFATVIVNING-----OLP----- 513
DB 469 SITQIPAVKGNFLNG-SVISPGETGDLVNLSSGN-----NIQNRGIEVPIHPFS 521
QY 514 --QRYARIRYASTNLRIYVTVAGERIPAGOFNKMTDGTPLTFQSFYATINTAFITFP 571
DB 522 TSTRVVRVYASVPIHLNVNMGSSIFSNTPATATSLDNQSSDFGYESANAFIT-- 579
QY 572 MSQSFTVGADTFSSGNEVYIDRFELIPVATFAEYDLERAQKAVNALFTSINOIGIKT 631
DB 580 --SSLGNIVGVRNFSGTAGVIIDRFEFIPVATLEAEYNLERAKAVNALFTSTNQLGLK 638
QY 632 DVTDHIDQVSNLVDCLSDPECLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDR 691
DB 639 NYTDHIDQVSNLVDCLSDPECLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDR 698
QY 692 GWRGSDITIQGDDVFKENYVTLPGTDECYPTLYOKIDESKLPKRYTQLRGYIEDS 751
DB 699 GNGSGTITIQGDDVFKENYVTLPGTDECYPTLYOKIDESKLPKRYTQLRGYIEDS 758
QY 752 QLEIYILIRYNAKHETVNLVGTSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSRDG 811
DB 759 QLEIYILIRYNAKHETVNLVGTSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSRDG 818
QY 812 EKCAHSHHFLSDIDVGCTDLNEDLVWIFKIKTQDGHARLGNLEFLEEKPLVGEALAR 871
DB 819 EKCAHSHHFLSDIDVGCTDLNEDLVWIFKIKTQDGHARLGNLEFLEEKPLVGEALAR 878
QY 872 VKRAEKWKDKREKLELEFNIVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRVHR 931
DB 879 VKRAEKWKDKREKLELEFNIVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRVHR 938
QY 932 IREAYLPELSVPGVNVMDIFEELKGRIFTAFPLDARNVKNKNGDNGLSCWNVKGVHDV 991
DB 939 IREAYLPELSVPGVNVMDIFEELKGRIFTAFPLDARNVKNKNGDNGLSCWNVKGVHDV 998
QY 992 EQGNHRSVLVPEWAEVSVQVRVCPGRGYILRTVATYKEGEGECVTIHEIENNTDELK 1051
DB 999 EQGNHRSVLVPEWAEVSVQVRVCPGRGYILRTVATYKEGEGECVTIHEIENNTDELK 1058
QY 1052 FNSCVEEYVYNNVTCNDYTANQBEYGGAYTSRREGYDETYSNSSVPADYASYEKS 1111
DB 1059 FNSCVEEYVYNNVTCNDYTANQBEYGGAYTSRREGYDETYSNSSVPADYASYEKS 1114
QY 1112 YTDGRDNCESNRGSDYTPPLPAGVYTKRELYFPDTRKWIEIGETGTFIVDSVELLL 1171
DB 1115 YTDGRDNCESNRGSDYTPPLPAGVYTKRELYFPDTRKWIEIGETGTFIVDSVELLL 1174
QY 1172 MEE 1174
DB 1175 MEE 1177

RESULT 12
QY 9826 ID QY 9826 PRELIMINARY; PRT: 1178 AA.
AC QY 9826;
DT 01-MAY-2000 (trEMBLrel. 13, Created)
DT 01-MAY-2000 (trEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (trEMBLrel. 17, Last annotation update)
DE Crystal toxin protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Makhdoum R., Riazuddin S.;
RT "Sequence of a novel gene from a variant of Bacillus thuringiensis.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBS databases.
DR EMBL; AJ130970; CAAL0270.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.

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DR Pfam; PF00555; endotoxin; 1.
-SQ SEQUENCE 1178 AA: 133270 MW: B6C016781EB3F0F4 CRC64;

Query Match 66.4%; Score 4144; DB 2: Length 1178;
Best Local Similarity 69.2%; Pred. No. 9.6e-273;
Matches 830; Conservative 83; Mismatches 240; Indels 46; Gaps 16;

QY 1 MENNIQ--NOCVPYNCLNNEPEVEILNEER--STGRPLDLSLSTFRLLSEFVPGVAGVL 58
DB 1 MDNPNINECIPNCLSNPEVEVLGGERIETGTPIDISLSLTFQLLSLSEFVPGVAGVL 60
QY 59 FDLIWLGPITSDSLSLELLOLEOIEORIEFLERNALITLRLGLADSYEIVIEALREWEAN 118
DB 61 VDIIWIGFSGQDAFLVQIEQLINORIEEFARNQAIKSLLEGSLNLYQIYAEFRWEAD 120
QY 119 PNAQLREDYRIKIFANTDDALITAINNFTLTSFEIPLSVYQAAHLHLSLLRDAYSFGQ 178
DB 121 PTNPALREEMRIQFNDMNSALTITAPLLAVONYQVPLSVYQAAHLHLSLSDVSVFGQ 180
QY 179 GWGLDIATVNNHNLINLHRYTKHCLDLYNOGLENLKGTNTROWARENOFRDLTLTV 238
DB 181 RWGFDAATINSRYNDLTRLIGNYTDYAVRYNTGLERKVGPDSDRWVYNQFRRETLTV 240
QY 239 LDIIVALEPNYDVRYPIQTSQSLTREIYTSVIEDSPSANIPNGFNRA----EFGVRRP 294
DB 241 LDIIVALEPNYDSRYPRTVTSQTLREIYTNPVL-----NFDGSRGSAQGIERSIRP 294
QY 295 HLMDPMSLSFVTAETVRSQVWGGH--LVSSRNTAGNRINFPYSYGVF--NPGGAIWADED 351
DB 295 HLMDILMSITITDAHRYGIYWSGHQIMASPVGSGPEFTFPLYGTGMNAAPOORIVAGL 354
QY 352 PRPYRTLSDPVFRVGFG---NPHYVLGRGVAFQ--TGTN--HTRFRNSGTIDSLDEI 406
DB 355 GQGYRILSS--TFYRPFENGINNOQLSVLDGTEFAFGTSSNLPSSAVYKRSIGVDSIDEI 413
QY 407 PPQNSGAPNDYSHLVNHTVFWPGEISGDSWRAPMSFWHRSATPTNTIDPRITQ 466
DB 414 PPQNNYPPRGQFSHRLSHVSMFRSGSSNSVSIIRAPMSFWHRSATPTNTIDPRITQ 473
QY 467 IPLVKAHTLQSGTAVVRGPGTGGDILKRTSGGPFATVIVNING-----OLP-----OR 515
DB 474 IPAVKGNFLNG-SVISPGETGDLVNLSSGN-----NIQNRGIEVPIHPFSITSTR 526
QY 516 YRARIRYASTNLRIYVTVAGERIPAGOFNKMTDGTPLTFQSFYATINTAFITFMSQS 575
DB 527 YRVVRYASVPIHLNVNMGSSIFSNTPATATSLDNQSSDFGYESANAFIT--SSL 583
QY 576 SFTVGADTFSSGNEVYIDRFELIPVATFAEYDLERAQKAVNALFTSINOIGIKTVD 635
DB 584 GNIVGVRNFSGTAGVIIDRFEFIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVD 643
QY 636 YHIDQVSNLVDCLSDPECLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRG 695
DB 644 YHIDQVSNLVDCLSDPECLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRG 703
QY 696 STDTIQRGDDVFKENYVTLPGTDECYPTLYOKIDESKLPKRYTQLRGYIEDSODLE 755
DB 704 STGITIQGDDVFKENYVTLPGTDECYPTLYOKIDESKLPKRYTQLRGYIEDSODLE 763
QY 756 IYLIRYNAKHETVNLVGTSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSRDGEKCA 815
DB 764 IYLIRYNAKHETVNLVGTSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSRDGEKCA 823
QY 816 HSHHFLSDIDVGCTDLNEDLVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARKRA 875
DB 824 HSHHFLSDIDVGCTDLNEDLVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARKRA 883
QY 876 EKKWRDKREKLELEFNIVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRVHIREA 935
DB 884 EKKWRDKREKLELEFNIVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRVHIREA 943
QY 936 YLPELSVPGVNVMDIFEELKGRIFTAFPLDARNVKNKNGDNGLSCWNVKGVHDVEEQN 995

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Db 944 YLPESLVIPGVNAAIFEELEGRIETAFSLYDARNVIKNGDFNGLSCWNKGVHVDVEQN 1003  
 Qy 996 NHRSLVVPWEAEVQSVRVCPRGYILRTAYKEGEGGCVTHIEINNTDELKFSNC 1055  
 Db 1004 NQSRSLVVPWEAEVQSVRVCPRGYILRTAYKEGEGGCVTHIEINNTDELKFSNC 1063  
 Qy 1056 VEEVYIPNNTVTCNDYTNQEEYGGAYTSRNGYDETYGNSVSPADYASVYEKSYTDG 1115  
 Db 1064 VEEVYIPNNTVTCNDYTNQEEYGGAYTSRNGYNEA---PSVPADYASVYEKSYTDG 1119  
 Qy 1116 RDNPCESNRGVDYTPLPAGYVTKELYFFETDKVWIEIGETEGTFIVDSVELLMEE 1174  
 Db 1120 RENPCEFNRGYRDYTPLPVGYVTKELYFFETDKVWIEIGETEGTFIVDSVELLMEE 1178

RESULT 13  
 Q45768  
 ID Q45768 PRELIMINARY; PRT: 1178 AA.  
 AC Q45768;  
 DT 01-NOV-1996 (TremBLrel. 01, Created)  
 DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
 DE Gene, complete cds.  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PS85A1;  
 RA Feltelson J.S.;  
 RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; M73249; AAA73077.1; -  
 DR HSP; P02965; ICIY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR Pfam; PF00555; endotoxin; 1.  
 SQ SEQUENCE 1178 AA; 133296 MW; 1336524F410E8863 CRC64;

Query Match 66.3%; Score 4142; DB 2; Length 1178;  
 Best Local Similarity 69.0%; Pred. No. 1.3e-272;  
 Matches 827; Conservative 85; Mismatches 242; Indels 44; Gaps 14;

Qy 1 MENNIQ-NOCYPYCNLPNPEVILNEER-STGRKLPDISLSTRLLSEFFVPGVGVAFGL 58  
 Db 1 MDNPNINECPYCNLPNPEVILGERIETGYTIDISLSTQTLSEFFVPGAGFVLGL 60  
 Qy 59 FDLWFTTPSDWSFLQIEOLISQRIETLERNRAITTLRGLADSYEYIIPALREWEAN 118  
 Db 61 VDIWIGFGPSQWDAFLVQIEOLINQRIEFAFARNOAISRLEGLSNLYIAESFREWEAD 120  
 Qy 119 PNAOLREDVIREANTDALTATNNTLTSTFEIPLLSVYVOAANLHLSLRDAVSFGQ 178  
 Db 121 PTNPALREEMRIQFNDMSALTATPLAVQNYQVPLSVYVOAANLHLSLRDVSFVGQ 180  
 Qy 179 GWGLDIATVNNHYNRLINLIHRYTHKCLDITYNOGLENLGTNTROWARFNQRRDILITY 238  
 Db 181 RWGFDAAINSYNDLTRIGNTYDAYRWYNTGLERWGPDSRDWRVYNQERRELTIV 240  
 Qy 239 LDIVALFPNDYVRTPIQTSOLTEITTSVIEDSPSANTPNGFNR----EFGVRPP 294  
 Db 241 LDIVALFPNDYVRTPIQTSOLTEITNPVLE-----NPDGFSRFGSAQIERISRP 294  
 Qy 295 HLMDFWNSLFTVAETVRSOTVWGGH--LVSSRNTAGRNINFPISYGVF-NPGGAIWADED 351  
 Db 295 HLMDFWNSLFTVAETVRSOTVWGGH--LVSSRNTAGRNINFPISYGVF-NPGGAIWADED 354  
 Qy 352 PRPFYRTLSDPFFVRG---GFGNPHY-VLGLRGVAFQOTGTNHTFRNSGTIDSLDEIP 407  
 Db 355 GGVVYRTLSLTYRPPNIGINNQLSLVDGTETAYGTSNLPASVYKSGVDSLDEIP 414  
 Qy 408 PODNSGAPWNDYSHLVNHVTFVRWPEIGSGSDSRAPMFSWTHRSATPTNTIDPRITQI 467  
 Db 415 PQNNVPPRQGSRLSHSVSMFRSGFSNSVSIIRAPMFSWTHRSAEFNIIASDSITQI 474

Qy 468 PLVKAHTLQSGTVVRGPGFTGGDILRRSTSGFPFAYTIVNING-----OLP-----QRY 516  
 Db 475 PAVKNFPLNG-SVISGPGFTGGDILVRNLSSGN-----NIQNRGYIEVPFIHPPSTSY 527  
 Qy 517 RARIRYASTTNIRIYTVVAGERIFAGQFNKMTMDTGPDLTFQSFYSATINTAFTFPMQSS 576  
 Db 528 RVRVRYASVTPIHLNVNMGNSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLG 584  
 Qy 577 FTVGADTFSSGNEVYIDREFELIPVATPEAEYDLERAKAVNALTSINQIGIKTDVTDY 636  
 Db 585 NIVGVNFSGTAVIDRPEFIPVATLEAEYNLERAKAVNALFTSNQLGLKTNVDY 644  
 Qy 637 HIDQVSNLVDCLSDREFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGNRDLDRGWS 696  
 Db 645 HIDQVSNLVTLSDEFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDINRPEKRWGS 704  
 Qy 697 TDITIQGGDDVFKENYVTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSDLEI 756  
 Db 705 TGITIQGGDDVFKENYVTLSGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSDLEI 764  
 Qy 757 YLIRYNAKHETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSRDGEKCAH 816  
 Db 765 YLIRYNAKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAH 824  
 Qy 817 HSHHFSLDIDVGCTDLNEDLVWVIFKIKTODGHARLGNLEFLSEKPLVGEALARKRAE 876  
 Db 825 HSHHFSLDIDVGCTDLNEDLVWVIFKIKTODGHARLGNLEFLSEKPLVGEALARKRAE 884  
 Qy 877 KWRDKREKLELETNIVYKEAESVDALFVNSQYDQLQADTNIAIHAADKRVHIREAY 936  
 Db 885 KWRDKREKLEWETNIVYKEAESVDALFVNSQYDQLQADTNIAIHAADKRVHIREAY 944  
 Qy 937 LPESLVIPGVNVDIFEELKGRIFTAFPLYDARNVIKNGDFNGLSCWNKGVHVDVEEQNN 996  
 Db 945 LPESLVIPGVNAAIFEELEGRIETAFSLYDARNVIKNGDFNGLSCWNKGVHVDVEEQNN 1004  
 Qy 997 HRSVLVPEWEAEVQSVRVCPRGYILRTAYKEGEGGCVTHIEINNTDELKFSNCV 1056  
 Db 1005 QRSVLVPEWEAEVQSVRVCPRGYILRTAYKEGEGGCVTHIEINNTDELKFSNCV 1064  
 Qy 1057 EBEVYIPNNTVTCNDYTNQEEYGGAYTSRNGYDETYGNSVSPADYASVYEKSYTDGR 1116  
 Db 1065 EBEVYIPNNTVTCNDYTNQEEYGGAYTSRNGYNEA---PSVPADYASVYEKSYTDGR 1120  
 Qy 1117 RDNPCESNRGVDYTPLPAGYVTKELYPPETDKVWIEIGETEGTFIVDSVELLMEE 1174  
 Db 1121 RENPCEFNRGYRDYTPLPVGYVTKELYPPETDKVWIEIGETEGTFIVDSVELLMEE 1178

RESULT 14  
 Q93TF9  
 ID Q93TF9 PRELIMINARY; PRT: 1160 AA.  
 AC Q93TF9;  
 DT 01-DEC-2001 (TremBLrel. 19, Created)  
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)  
 DE Insecticidal crystal protein.  
 GN CRYIDB.  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B-PR-88;  
 RA Li C., Zhang J., Huang D., Li G.;  
 RL "A crystal endotoxin from Bt strain B-Pr-88."  
 DR Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF358862; AAK48937.1; -  
 DR InterPro; IPR001178; Endotoxin.  
 DR Pfam; PF00555; endotoxin; 1.  
 SQ SEQUENCE 1160 AA; 130952 MW; B18B04193D87695E CRC64;



QY	1014	VRVCPGRGILRVYATKKEGCGGCVTHIENNTDELKFSNCVEEVYPNVTVCNDYTA	107
Db	1005	VRVCPGRGILRVYATKKEGCGGCVTHIENNTDELKFSNCVEEVYPNVTVCNDYTA	1062
QY	1074	NOEYGGATSRNRGVDYETGSGNSVPADYASVBEKSYTDGRRNPCESNRGYGDYTPL	1133
Db	1063	NKHGNAACSSRRNGVDESYENSSIPADYAPVBEAYTDGRRNPSEFNRG	1119
QY	1134	PAGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLLMEE	1174
Db	1120	PAGYVTALEYFPETDVWVEIGETGTFIVDSVELLLMEE	1160
RESULT 15			
Q9AM83			
ID	Q9AM83	PRELIMINARY;	PRT; 1118 AA.
AC	Q9AM83;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	Insecticidal crystal protein BPRX24.		
OS	Bacillus thuringiensis serovar kunthalarx24.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;		
OC	Bacillaceae; Bacillus.		
CN	NCBI_TaxID=147284;		
CC	[1]		
RP	SEQUENCE FROM P. A.		
RA	Nagarathinam P., Xavier R., Jayaraman K., Murugan V.;		
RT	"Characterization and full-length sequencing of insecticidal crystal		
RT	protein (cryI) of novel Bacillus thuringiensis subsp. kunthalarx24 and		
RT	its specific toxicity towards three economically important pests:		
RT	Spodoptera litura, Helicoverpa armigera and Plutella xylostella."		
RL	Submitted (DEC-2000) to the EMBL/Genbank/DDJB databases.		
DR	EMBL; AF237924; AAK14336.1; -		
DR	HSSP; P02965; IC1Y.		
DR	InterPro: IPR001178; Endotoxin.		
DR	Pfam: PF00555; endotoxin.1.		
SQ	SEQUENCE 1118 AA; 126617 MW; 33DA5B8C2CDF059D CRC64;		
Query Match			
Best Local Similarity 58.0%; Score 3624.5; DB 2; Length 1118;			
Matches 721; Conservative 88; Mismatches 227; Indels 45; Gaps			
QY	1	MENNIO-QCVPNCLNPNPVEILNER-STGRLPDISLITRFLLSFEVPGVGVARGL	58
Db	1	MDNNLNIECIPNCLSNPEVILGGERITGYTIDISLITQFLSFEVPGAGFVLGL	60
QY	59	FDLIWGPTSDSLFLQLEOLIEQRIITLENRAITTLRGLADSYEIVLEALREWAN	118
Db	61	VDIIWGTFGSQDAFLVQIEQLINQRIEEFARNQAISRLGLSNLYIVASFREWAD	120
QY	119	PNNALREDVRIIRFANTDDALITAINFTLSTPEILPLSVYQAAHLHLRLDAVSFGQ	178
Db	121	PTNPALEENRIQFNDMNSALTAIPLFAVQNYQVPLLSVYQAAHLHLVLRLDSVFEQ	180
QY	179	GWGLDIATVNNHYNRLNLHRYTKKCLDYNQGLNLRGTNTROWARENQERDLTLV	238
Db	181	RWGFDAATINSRNDLPRLIGNTDHAVRYNTGLERWGPDSRWIRYNQFRRELTIV	240
QY	239	LDIIVALEPNYDVRTYPIQTSSQLTREITYTSVVIDSPSANIPNGFNRA-----EFGVRPP	294
Db	241	LDIVSLFPNVDSTYPIRTYSQLTREIYNPVLE-----NFDGSGFRGSAQIGESIRSP	294
QY	295	HLMPFMSLFTVETVRSQTVGGH--LVSSRNTAGNRIINPFSYGVF-NPGGAIWIADED	351
Db	295	HLMDILNSITVTDHARGEYIWSGHQIMASPVGSGFPEFTFLYCTMGNAAPQOQRIVAQL	354
QY	352	PRPFYRLSDPVFVRG--GFGNPHY-VLGLRGVAFQQTGTNHTTRFRNSGTIDSLDELIP	407
Db	355	GGYIRLSSLTLYRRPNIGINNOQLSLVDGTEFAVGTGSSNLPASVYRKSGTVDSLDELIP	414
QY	408	PQDNGSAPWNDYSHLVNHVTVFRWPGIEGSDSWRAPMFSTWHRSTATPTNTIDPERITQ	467



Db 415 PQNNVPPROGSHRLSHVSMFSGFSNSVSITRAPMFSNIHRSAEFNNIIPSSQITOI 474  
QY 468 PLVKAHTLOSQTWVRGPGTGGDILIRTSGGPPAYTIVNINGOLPORVIRIYASTTN 527  
Db 475 PLTKSNLNGSGTSVVKGPFTGGDILIRTSFGQISLURVNITAPLSQRYRIRIYASTTN 534  
QY 528 LRIYTVAGERIFAGOFNKMTDGLTFQSFYAITNTAFTFPMSSQSFYVADTFSSG 587  
Db 535 LQHTSIDGRPIHQGNFSATMSGSLQCAEMTVGTTFFNFSGSSVFTLSAHVNSG 594  
QY 588 NEVYIDREFELIPYATFAEYDILERAQKAYNALFTSINOIGIKITDVTYHIDQVSNLVC 647  
Db 595 NEVYIDREFELIPYATFAEYDILERAQKAYNELFTSSNOIGIKITDVTYHIDQVSNLVC 654  
QY 648 LSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQOLDRGWRGSDITIQGGDV 707  
Db 655 LSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQOLDRGWRGSDITIQGGDV 714  
QY 708 FKENYVTLPGTFDECYPTIYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIYRNAKHET 767  
Db 715 FKENYVTLPGTFDECYPTIYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIYRNAKHET 774  
QY 768 VNYLGTSLWPLSVQSPDKRCGPNRCAPHELNPDLDSCROGCEKCAHSHHFSLDIDV 827  
Db 775 VNYLGTSLWPLSVQSPDKRCGPNRCAPHELNPDLDSCROGCEKCAHSHHFSLDIDV 808  
QY 828 GCTDLNEDLVWVIFKIKTODGHARLGNLEFLBEKPLVGEALARKVRAEKWKREKLE 887  
Db 809 GCTDLNEDLVWVIFKIKTODGHARLGNLEFLBEKPLVGEALARKVRAEKWKREKLE 868  
QY 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRVHRIREAYLPESLVIPGVN 947  
Db 869 WETNIVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRVHRIREAYLPESLVIPGVN 928  
QY 948 VDIFFELKGRIFTAFELYDARNVKNQDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWE 1007  
Db 929 AALFEELKGRIFTAFELYDARNVKNQDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWE 988  
QY 1008 AEVSQEVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYPPNNTVT 1067  
Db 989 AEVSQEVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYPPNNTVT 1048  
QY 1068 C 1068  
Db 1049 C 1049

Search completed: November 27, 2002, 20:24:22  
Job time : 98 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 17:21:14 ; Search time 37 seconds  
(without alignments)  
1316.033 Million cell updates/sec

Title: US-09-837-961-8  
Perfect score: 6244  
Sequence: 1 MENNIOQCVPYNNLNPEV.....IGETGTFIVDSVELLMEE 1174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6244	100.0	1174	1	C1FA_BACTA
2	5399.5	86.5	1169	1	C1FB_BACTM
3	4424.5	70.9	1181	1	C1AE_BACTL
4	4329	69.3	1176	1	C1AA_BACTK
5	4320	69.2	1179	1	C1AD_BACTA
6	4303	68.9	1166	1	C1GA_BACTU
7	4282.5	68.6	1185	1	C1DA_BACTA
8	4230.5	67.8	1172	1	C1HA_BACTU
9	4224.5	67.7	1169	1	C1GB_BACTZ
10	4223.5	67.6	1189	1	C1CA_BACTE
11	4211.5	67.4	1155	1	C1AB_BACTK
12	4173	66.8	1171	1	C1EA_BACTX
13	4148	66.4	1178	1	C1AC_BACTK
14	4146	66.4	1160	1	C1DB_BACTU
15	4134	66.2	1176	1	C1CB_BACTG
16	4127.5	66.1	1155	1	C1HB_BACTM
17	4098	65.6	1176	1	C1AG_BACTU
18	4025.5	64.5	1167	1	C1JA_BACTU
19	3874	62.0	1174	1	C1EB_BACTA
20	3788	60.7	1170	1	C1JB_BACTU
21	3690	59.1	1215	1	C1KA_BACTM
22	3552.5	56.9	1229	1	C1BB_BACTU
23	3465	55.5	1228	1	C1BA_BACTK
24	3437.5	55.1	1233	1	C1BC_BACTM
25	3411	54.6	1231	1	C1BD_BACTZ
26	3376	54.1	1227	1	C1BE_BACTU
27	2633	42.2	911	1	C1AF_BACTU
28	2138.5	34.2	1138	1	C7AB_BACUK
29	2129.5	34.1	1138	1	C7AA_BACTU
30	2126.5	34.1	1138	1	C7AB_BACUA
31	2006.5	32.1	1157	1	C8AA_BACUK
32	1947.5	31.2	1157	1	C9CA_BACTO
33	1922.5	30.8	1169	1	C8BA_BACUK

34	1838	29.4	1150	1	C9EA_BACTA	Q92nl9	Bacillus th
35	1825.5	29.2	1169	1	C9DA_BACTP	O06014	Bacillus th
36	1713.5	27.4	1163	1	C9AA_BACTF	Q9x597	Bacillus th
37	1685.5	27.0	1160	1	C8CA_BACTG	Q45706	Bacillus th
38	1630.5	26.1	1156	1	C9AA_BACTG	Q99031	Bacillus th
39	1597.5	25.6	1109	1	CSAA_BACTF	Q9x682	Bacillus th
40	1519	24.3	1136	1	C4BA_BACTI	P05519	Bacillus th
41	1495.5	24.0	1180	1	C4AA_BACTI	P16480	Bacillus th
42	1367	21.9	719	1	C1IB_BACTE	Q45709	Bacillus th
43	1360	21.8	719	1	C1IA_BACTU	Q45752	Bacillus th
44	1328.5	21.3	719	1	C1ID_BACTU	Q9xdl1	Bacillus th
45	1302	20.9	719	1	C1IC_BACTU	O87404	Bacillus th

## ALIGNMENTS

## RESULT 1

ID	C1FA_BACTA	STANDARD;	PRT;	1174 AA.
AC	Q03746:			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pesticidal crystal protein cryIIpa (Insecticidal delta-endotoxin			
DE	CRYIF(a)) (Crystalline entomocidal protoxin) (134 kDa crystal protein).			
GN	CX1FA OR CRYIF(A) OR CRYIF.			
OS	Bacillus thuringiensis (subsp. aizawai).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1433;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-EG6346;			
RX	MEDLINE=91286178; PubMed=2061280;			
RA	Chambers J.A., Jelen A., Gilbert M.P., Jany C.S., Johnson T.B.,			
RA	Gawron-Burke C.;			
RT	"Isolation and characterization of a novel insecticidal crystal			
RT	protein gene from Bacillus thuringiensis subsp. aizawai.";			
RL	J. Bacteriol. 173:3966-3976(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-NRRL B-18484 / PS811;			
RA	Payne J.M., Sick A.J.;			
RT	"Bacillus thuringiensis isolate active against lepidopteran pests, and			
RT	genes encoding novel lepidopteran-active toxins.";			
RL	Patent number US5188960, 23-FEB-1993.			
CC	-1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT			
CC	EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.			
CC	-1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING			
CC	SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART			
CC	OF THE SPORE COAT.			
CC	-1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE			
CC	N-TERMINUS.			
CC	-1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; M63897; AAA22348.1; -			
DR	EMBL; M73254; AAA22347.1; -			
DR	HSSP; P02965; IC1Y.			
DR	InterPro; IPR001178; Endotoxin.			
DR	Pfam; PF00555; endotoxin; 1.			
KW	Toxin; Sporulation.			
SQ	SEQUENCE 1174 AA; 133621 MW; B51E9751D7F91C61 CRC64;			

Query Match 100.0%; Score 6244; DB 1; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MENNIQNCQVPYCNLNPNPEVEIILNEERSTGRPLDLSLSTRFLJSEFVPGVGVAGFLD	60
Db	1	MENNIQNCQVPYCNLNPNPEVEIILNEERSTGRPLDLSLSTRFLJSEFVPGVGVAGFLD	60
QY	61	LINGFITPDSWSLFLQIEOLIEQRIETLERNRAITLRLGLADSVIETALREWEAPN	120
Db	61	LINGFITPDSWSLFLQIEOLIEQRIETLERNRAITLRLGLADSVIETALREWEAPN	120
QY	121	NAQUREDVRIRFANTDALLITANNFTLSFEIPLLSVYQAAHLHLSLRLDAVSFGGW	180
Db	121	NAQUREDVRIRFANTDALLITANNFTLSFEIPLLSVYQAAHLHLSLRLDAVSFGGW	180
QY	181	GLDIATVNNHYNRLINLIHRYTHKCLDITYNOGLENLGRNTTROWARFNQFRDLTLTVLD	240
Db	181	GLDIATVNNHYNRLINLIHRYTHKCLDITYNOGLENLGRNTTROWARFNQFRDLTLTVLD	240
QY	241	IVALFPNDVRYTPITQSSOLTREIYTSVIEDSPVSANIPNGFRAEGVPRPHLDM	300
Db	241	IVALFPNDVRYTPITQSSOLTREIYTSVIEDSPVSANIPNGFRAEGVPRPHLDM	300
QY	301	NSLFTVTAETVRSOTVWGGLVSRNTAGNINFPSPGVFNPGCAIWADEPRPYRTL	360
Db	301	NSLFTVTAETVRSOTVWGGLVSRNTAGNINFPSPGVFNPGCAIWADEPRPYRTL	360
QY	361	DPVFRGGFNGPHVYLGRLGVAFOQTGTHETFRNSGTIDSLDEIPPODMSGAPWNDYS	420
Db	361	DPVFRGGFNGPHVYLGRLGVAFOQTGTHETFRNSGTIDSLDEIPPODMSGAPWNDYS	420
QY	421	HVLNHVTFVRWPGCEISGDSWRAPFSWTHRSATNTNIDPRITQIPLVKAHLQSGTT	480
Db	421	HVLNHVTFVRWPGCEISGDSWRAPFSWTHRSATNTNIDPRITQIPLVKAHLQSGTT	480
QY	481	VWPGFTGSDILRRTSGGPFAYTVININGQLPQYRARIRYASTNLRIVTVVAGERIF	540
Db	481	VWPGFTGSDILRRTSGGPFAYTVININGQLPQYRARIRYASTNLRIVTVVAGERIF	540
QY	541	AGQFNKTMOTGDLPTQSFYSYATINTAFTFPMQSQSFVTGADTFSSGNEVYIDRFELIPV	600
Db	541	AGQFNKTMOTGDLPTQSFYSYATINTAFTFPMQSQSFVTGADTFSSGNEVYIDRFELIPV	600
QY	601	TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHDQVSNLVDCLSDFCFLDKREL	660
Db	601	TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHDQVSNLVDCLSDFCFLDKREL	660
QY	661	SEKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDITIQRGDDVFKENYVILPGTFD	720
Db	661	SEKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDITIQRGDDVFKENYVILPGTFD	720
QY	721	ECYPTLYQKIDBSKLPYTRYOLRGYIEDSODLEIYLIRYNAKHETYNVLGTSLMPLS	780
Db	721	ECYPTLYQKIDBSKLPYTRYOLRGYIEDSODLEIYLIRYNAKHETYNVLGTSLMPLS	780
QY	781	VOSPIRKCEPNRCAPHLEWNPDLCCSDCEKCAHSHHPSLDDIVGCTDLNEDLDVWV	840
Db	781	VOSPIRKCEPNRCAPHLEWNPDLCCSDCEKCAHSHHPSLDDIVGCTDLNEDLDVWV	840
QY	841	IFKIKTQDGHARLGNLEFLEKPLVGEALARVKRAEKWRDKREKLETNIVYKEAKES	900
Db	841	IFKIKTQDGHARLGNLEFLEKPLVGEALARVKRAEKWRDKREKLETNIVYKEAKES	900
QY	901	VDALFVNSOYDQLOADNTIAMHAADKRVHRIREAYLPESLIPGVNVDIPEELKGRIFT	960
Db	901	VDALFVNSOYDQLOADNTIAMHAADKRVHRIREAYLPESLIPGVNVDIPEELKGRIFT	960
QY	961	APFLYDARNVKNGDFNGLSCWNVKGHDVEEQNNHRSVLVPEWEAEYSQEVRCPCR	1020
Db	961	APFLYDARNVKNGDFNGLSCWNVKGHDVEEQNNHRSVLVPEWEAEYSQEVRCPCR	1020
QY	1021	GYLLRVATKESYGGECVTHIEIENNTDELFSNCVEEVPNTVTCNDYTAQOEYGG	1080
Db	1021	GYLLRVATKESYGGECVTHIEIENNTDELFSNCVEEVPNTVTCNDYTAQOEYGG	1080

QY	1081	AYTSRNRGXDYETGSSNSVPADYASVYIEKSYTDGRRNP	CESNRGYGDYTPLPAGYVTK	1140
DB	1081	AYTSRNRGXDYETGSSNSVPADYASVYIEKSYTDGRRNP	CESNRGYGDYTPLPAGYVTK	1140
QY	1141	ELEYFPTDKWIEIGETGTFIVDSVLELLMEE	1174	
DB	1141	ELEYFPTDKWIEIGETGTFIVDSVLELLMEE	1174	

## RESULT 2

CL1FE\_BACTM STANDARD; PRT; 1169 AA.

ID CL1FE\_BACTM AC 066377; Q9RC19;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Pesticidal crystal protein cryI**fb** (insecticidal delta-endotoxin

DE CryI**fb**(b)) (crystalline entomocidal protoxin) (132 kDa crystal protein).

GN CRY1FB OR CRY1F(B) OR CRY1NA67-1.

OS *Bacillus thuringiensis* (subsp. morrisoni).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

CC NCBI\_Taxid:1441;

RN [1]

RP SEQUENCE FROM N.A.

RA Song F.; Zhang J.; Ding Z.; Chen Z.; Li G.; Huang D.;

RL "A novel cryI**fb** gene from *Bacillus thuringiensis* subsp. morrisoni.";

RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA STRAIN-INA67;

RA Masuda K.; Asano S.;

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF INSECTS.

CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.

CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC N-TERMINUS.

CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

CC -----

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

Query Match 86.5%; Score 5399.5; DB 1; Length 1169;  
Best Local Similarity 86.6%; Pred. NO. 0;  
Matches 1018; Conservative 59; Mismatches 91; Indels 7; Gaps 4;

QY	1	MENNIOQVCVNCYNLNPNPEVLNEERSTGRPLDLSLSTRLLSEFYPGVGVAFLGD	60
		I-     :     :     :     :     :     :     :	
Db	1	MKNNIQOCVNCYNLNPNPEVLSEERSTGRPLDLSLSTRLLSEFYPGVGVAFLGD	60
QY	61	LWGIITSDSNLFLLQIEQLRIETLRNRAITTLRGADSYEITYEARWEANPN	12

Db 61 LTWGFITPSEWFLQIQEQIETLERNRAITTLRGLADSYEVYLEALREWEENP 120  
QY 121 NAOQREDVIRFANTDDALITAINNFTTSFEIPLSVVQAAHLHLRLDRAVSGQSW 180  
Db 121 NAOQREDVIRFANTDDALITAINNFTTSFEIPLSVVQAAHLHLRLDRAVSGQSW 180  
QY 181 GLDIATVNNHYNRLNLHRYTHKCLDYNQGLENLRTNTQWAFNPFRRDLTLTVD 240  
Db 181 GLDIATVNNHYNRLNLHRYTHKCLDYNQGLENLRTNTQWAFNPFRRDLTLTVD 240  
QY 241 IVALPNDVIRPTQTSQTLREIYTSVIEDSPSANIPNGFNRAEFGVPPHLMDFM 300  
Db 241 IVALPNDVIRPTQTSQTLREIYTSVIEDSPSANIPNGFNRAEFGVPPHLMDFM 300  
QY 301 NSLFTVATVRSQTVGGHLSVSSNTAGNRPSPSVGVNPGGAIWADEDPFPYRTLS 360  
Db 301 NSLFTVATVRSQTVGGHLSVSSNTAGNRPSPSVGVNPGGAIWADEDPFPYRTLS 360  
QY 361 DPVVRGGFGNPHYVLGRGVAFOQTGNTNTRFNSGTIDSLDETPQDMSGAPNDYS 420  
Db 361 DPVVRGGFGNPHYVLGRGVAFOQTGNTNTRFNSGTIDSLDETPQDMSGAPNDYS 420  
QY 421 HVLNHTVFRWPGEGISGDSWRAPFWSWTHRSATPNTTIDPERITQIPLVKAHTLQSGTT 480  
Db 421 HVLNHTVFRWPGEGISGDSWRAPFWSWTHRSATPNTTIDPERITQIPLVKAHTLQSGTT 480  
QY 481 VVRGPGFTGGDLRTSGGPEATVIVNINGOLPQRYRARIYASTNLRIYTVAGERIF 540  
Db 481 VVRGPGFTGGDLRTSGGPEATVIVNINGOLPQRYRARIYASTNLRIYTVAGERIF 540  
QY 541 AGQFNKMTDGTGDLTFQSFYSATINTAFTPMPSQSFVTGADTFSSGNEVYIDRFELIPV 600  
Db 541 OGNFORTWNRGNLSEGNFRTAGFSTPFSNAQSFITLGTQAFSN-QEYVIDRIEFVFA 599  
QY 601 TATFAEVDLERAQKAVNALFTSINOIGIKTDVTHIDQVNLVDCLDEFCLEKREL 660  
Db 601 TATFAEVDLERAQKAVNALFTSINOIGIKTDVTHIDQVNLVDCLDEFCLEKREL 660  
QY 661 SEKVHAKRLSDERNLQDPNFKGNQRLDRGRWGSTDITIORGDDVFNKENVYLPGLTFD 720  
Db 661 SEKVHAKRLSDERNLQDPNFKGNQRLDRGRWGSTDITIORGDDVFNKENVYLPGLTFD 720  
QY 721 ECPYLYXKIDESKLKPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNVGLTGSWLPLS 780  
Db 721 ECPYLYXKIDESKLKPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNVGLTGSWLPLS 780  
QY 781 VQSPIKCGEPNRCAPHLEWNPDLDCSDRGKCAHSHHFSLDIDVGCITDNLNEDLVWV 840  
Db 781 VQSPIKCGEPNRCAPHLEWNPDLDCSDRGKCAHSHHFSLDIDVGCITDNLNEDLVWV 840  
QY 841 IPKIXTQDGHARLGNLEFLEEXPLVGEALARYKRAEKKWRDKREKLELTINIVYKEAKS 900  
Db 841 IPKIXTQDGHARLGNLEFLEEXPLVGEALARYKRAEKKWRDKREKLELTINIVYKEAKS 900  
QY 901 VDALFVNSQYDQADNTAMIAHADKRVHIREAYLPESLVIPGVNVDIFELKGRIFT 960  
Db 901 VDALFVNSQYDQADNTAMIAHADKRVHIREAYLPESLVIPGVNVDIFELKGRIFT 960  
QY 961 AFPLDARVINKGNFENGLSCWNVKGVHVDVEQNNHRSVLVVPWEAEVQSVRVCPCR 1020  
Db 961 AFPLDARVINKGNFENGLSCWNVKGVHVDVEQNNHRSVLVVPWEAEVQSVRVCPCR 1020  
QY 1021 GYLIRVTAKEGEGCVTHIEIENNTDELKF-SNCEVEEYVNNVTCTNOCATANOEEYG 1079  
Db 1021 GYLIRVTAKEGEGCVTHIEIENNTDELKF-SNCEVEEYVNNVTCTNOCATANOEEYG 1079  
QY 1080 GAYTSNRGIDETYGSSNPADYASVYKEKSYTDGRONPCESNRGYDTPPLPAGYTT 1139  
Db 1080 GAYTSNRGIDETYGSSNPADYASVYKEKSYTDGRONPCESNRGYDTPPLPAGYTT 1139  
QY 1140 KELEYFPETDQVWIEIGETEGTFIVDSVELLMEE 1169  
Db 1140 KELEYFPETDQVWIEIGETEGTFIVDSVELLMEE 1169

Db 1135 ABLEYFPETDQVWIEIGETEGTFIVDSVELLMEE 1169  
RESULT 3  
CLAE\_BACTL STANDARD; PRT: 1181 AA.  
AC Q03748;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Pesticidal crystal protein cryIae (Insecticidal delta-endotoxin  
DE CRYIAE(e) (Crystalline entomocidal protoxin) (134 kDa crystal protein).  
GN CRYIAE OR CRYIA(E) OR ENDI.  
OS Bacillus thuringiensis (subsp. alesti).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1440;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92011442; PubMed=1655719;  
RA Lee C.S., Aronson A.I.;  
RT "Cloning and analysis of delta-endotoxin genes from Bacillus  
RL J. Bacteriol. 173:6635-6638(1991).  
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.  
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
CC SPOKULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
CC OF THE SPORE COAT.  
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE  
CC N-TERMINUS.  
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
CC  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC -----  
CC EMBL: M65252; AAA22410.1; -  
CC HSSP: P02965; ICIY.  
CC InterPro: IPR001178; Endotoxin.  
CC Pfam: PF00555; endotoxin; 1.  
CC Toxin: Sporulation.  
CC SEQUENCE 1181 AA; 133737 MW; FE86D2138C37D0FD CRC64;  
Query Match 70.9%; Score 4424.5; DB 1; Length 1181;  
Best Local Similarity 72.1%; Pred. No. 6.le-278;  
Matches 857; Conservative 93; Mismatches 216; Indels 23; Gaps 9;

QY 1 MENNIO-NOCVPYNCLNPEVEITNEER-STGRPLDIDSLSTRFLLSFVPQGVAFGL 58  
Db 1 MNNPKINCEIPYCNLSNPEVEVLGGERIETGYTPTDIDLSLTOFLLSFVPQGVAFGL 60  
QY 59 FDLINGFITPDSWFLQIQEQIETLERNRAITTLRGLADSYEVYLEALREWEAN 118  
Db 61 IDLINGFVGSQWDAFLVQIQEQIETLERNRAITTLRGLADSYEVYLEALREWEAN 120  
QY 119 PNAQLREDVIRFANTDDALITAINNFTTSFEIPLSVVQAAHLHLRLDRAVSGQ 178  
Db 121 PTPNALREEMRIQFNDMSALTAIFLFTVQNYQVLLSVYVQAVNLHLSVLDRVDFG 180  
QY 179 GWGLDIATVNNHYNRLNLHRYTHKCLDYNQGLENLRTNTQWAFNPFRRDLTLT 238  
Db 181 RWGLDVATINSYNDLTRIGITTYDFAVWYNTGLERWVGPSRQWVRYNQFRRETLTV 240  
QY 239 LDVALFPNDVIRPTQTSQTLREIYTSVIEDSPSANIPNGFNRAEFGVPPHLM 298  
Db 241 LDVLSLFPNDVIRPTQTSQTLREIYTSVIEDSPSANIPNGFNRAEFGVPPHLM 298  
QY 299 FMNSLFTVATVRSQTVGGH--LVSSRTNAGNRINFPSPYGVF-NPGGAIWADEDP 355  
Db 299 FMNSLFTVATVRSQTVGGH--LVSSRTNAGNRINFPSPYGVF-NPGGAIWADEDP 355

Db 299 ILNSITITDAHGYYWYSGHQIMASPVGSGPEFTFLYXTMGNAPOQRIVQAQLGGQV 358  
 QY 356 YRTLSDFEVRGGFGNGHYVLGRG-----VAFOQTGNGHTFNSGTTIDSLDE 405  
 Db 359 YRTLLS--TFYR---NP-FIIGINQRLSLVDGTFEYAGSSNLPASVYRKSGTVDSLDE 412  
 QY 406 IPPODNSGAPWNDYSHVLNHYTFVRWPEIGSGSDSWRAPFMSWTHRSATNTIDPERIT 465  
 Db 413 IPPODNNVPPRQGFSHRLSHVSMFRSGFNSSVSIIIRAPFMSWTHRSAEFNIIIPSSOIT 472  
 QY 466 QIPLVKAHTVLOSQTGTVRGGFTGGDILRTSGGPPFAITVINGQIPQYRARIYAST 525  
 Db 473 QIPLTKNTLNGSTVSVKPGFTGGDILRTSPGQISTLRVNTITAPLSQYRIRIYAST 532  
 QY 526 TNLRIYVTVAGERIFAGOFNKMTDGTPLDFOFSFYATINTAFFPMSQSFTVGADTF 585  
 Db 533 TNLQFHSIDGRPINQGNFNSATMSGGSLQSGSFRTGFTFPFNSGSSVFLSAHVFN 592  
 QY 586 SGNEVYIDRFLIPVATFAEYDLERAQKAVNALFTSINOIGIKTDTVDYHIDQVSNLV 645  
 Db 593 SGNEVYIDRIEFVPAEYTFEAYDLERAQKAVNALFTSPNQIGLKTDTVDYHIDQVSNLV 652  
 QY 646 DCLDFCLDEKRLSEKVKHAKLSDERNLLQDPNFKGINQLDRGWRGSTDITIOGD 705  
 Db 653 ECLDFCLDEKRLSEKVKHAKLSDERNLLQDPNFKGINQLDRGWRGSTDITIOGD 712  
 QY 706 DVFKENVYLPGTDECYPTLYKIDESKILKYTRYOLRGYIEDSDLEILYIRYNAKH 765  
 Db 713 DVFKENVYLPGTDECYPTLYKIDESKILKYTRYELRGYIEDSDLEILYIRYNAKH 772  
 QY 766 ETAVNLTGSLWPLSVOSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSHSLDI 825  
 Db 773 ETAVNLTGSLWPLSVFESSIGCKEPCNRCAPHLEWNPDLDCSCRDGKCAHSHHSHSLDI 832  
 QY 826 DVGCTDNLNEDLVVYFIKIKTQDGHARLGNLEFLKPLVGEALARYKRAKKWRDKREK 885  
 Db 833 DVGCTDNLNEDLVVYFIKIKTQDGHARLGNLEFLKPLVGEALARYKRAKKWRDKREK 892  
 QY 886 LELEFNIVYKEAKESVDALFVNSYDQLOADNTIAMHAKRVHREAYLPELSVIPG 945  
 Db 893 LOLEFNIVYKEAKESVDALFVNSYDQLOADNTIAMHAKRVHREAYLPELSVIPG 952  
 QY 946 VNVDFEELKGRIFTAFELYDARNVINKGNDFNGLSCWNVKGVHGVDEEONHRSVLVVE 1005  
 Db 953 VNAGIFEELGRIPTAYSLYDARNVINKGNDFNGLSCWNVKGVHGVDEEONHRSVLVVE 1012  
 QY 1006 WEAEVSQVRVCPGRGYILRVYATKEGEGCVTIHEIENNTDELKTSNCVEEYVYNN 1065  
 Db 1013 WEAEVSQVRVCPGRGYILRVYATKEGEGCVTIHEIENNTDELKTSNCVEEYVYNN 1072  
 QY 1066 VTCNDYTANQBEYGGAYTSRNRGYDETYGSSNVPADYASVYEKSYTDGRDNPCESNR 1125  
 Db 1073 VTCNDYTANQBEYGGAYTSRNRGYDETYGSSNVPADYASVYEKSYTDGRDNPCESNR 1132  
 QY 1126 YGVGYTPLPAGYVTKELYFPETDKVWIEIGETGTFIVDSVELLLMBE 1174  
 Db 1133 YGVGYTPLPAGYVTKELYFPETDKVWIEIGETGTFIVDSVELFLMBE 1181

## RESULT 4

C1AA\_BACTK STANDARD; PRT; 1176 AA.  
 ID C1AA\_BACTK AC P02965; P16478; P09664; Q09ED3; P09665;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin  
 DE CryIIa(a)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).  
 GN CRYIIA OR CRYIA(A) OR CRYIA(A) OR CRY-1-1 OR CRYA OR ICP OR CRYBNS3-1.  
 OS Bacillus thuringiensis (subsp. kurstaki),  
 OS Bacillus thuringiensis (subsp. aizawai),  
 OS Bacillus thuringiensis (subsp. entomocidus), and  
 OS Bacillus thuringiensis (subsp. sotto).

OG Plasmid 68 Kb.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=29339, 1433, 1436, 29340;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t.kurstaki; STRAIN=HD-1-Dippel;  
 RX MEDLINE=85207613; PubMed=2581950;  
 RA Schnepf H.E., Wong H.C., Whiteley H.R.;  
 RT "The amino acid sequence of a crystal protein from Bacillus  
 RT thuringiensis deduced from the DNA base sequence.";  
 RL J. Biol. Chem. 260:6264-6272(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t.kurstaki; STRAIN=BNS3;  
 RA Tounsi S., J'Mal A., Zouari N., Jaoua S.;  
 RT "Cloning and nucleotide sequence of a novel cryIIa-type gene from  
 RT Bacillus thuringiensis subsp.kurstaki.";  
 RL Biotechnol. Lett. 21:771-775(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t.kurstaki; STRAIN=IPL7;  
 RA Shimizu M., Oshie K., Nakamura K., Takada Y., Oeda K.;  
 RT "Cloning and expression in Escherichia coli of the 135-kDa  
 RT insecticidal protein gene from Bacillus thuringiensis subsp. aizawai  
 RT IPL7.";  
 RL Agric. Biol. Chem. 52:1565-1573(1988).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t.entomocidus;  
 RX MEDLINE=89098405; PubMed=2911478;  
 RA Masson L., Marcotte P., Prefontaine G., Brousseau R.;  
 RT "Nucleotide sequence of a gene cloned from Bacillus thuringiensis  
 RT subspecies entomocidus coding for an insecticidal protein toxic for  
 RT Bombyx mori.";  
 RL Nucleic Acids Res. 17:446-446(1989).  
 RN [5]  
 RP SEQUENCE OF 1-934 FROM N.A.  
 RC SPECIES=B.t.sotto;  
 RX MEDLINE=85332070; PubMed=2989108;  
 RA Shibano Y., Yamagata A., Nakamura N., Iizuka T., Sugisaki H.,  
 RA Takanami M.;  
 RT "Nucleotide sequence coding for the insecticidal fragment of the  
 RT Bacillus thuringiensis crystal protein.";  
 RL Gene 34:243-251(1985).  
 RN [6]  
 RP SEQUENCE OF 1-333 FROM N.A.  
 RC SPECIES=B.t.kurstaki; STRAIN=HD-1-Dippel;  
 RX MEDLINE=83109004; PubMed=6296116;  
 RA Wong H.C., Schnepf H.E., Whiteley H.R.;  
 RT "Transcriptional and translational start sites for the Bacillus  
 RT thuringiensis crystal protein gene.";  
 RL J. Biol. Chem. 258:1960-1967(1983).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 33-609.  
 RC SPECIES=B.t.kurstaki; STRAIN=HD-1-Dippel;  
 RX MEDLINE=96095803; PubMed=7490762;  
 RA Grochulski P., Masson L., Borisova S., Pusztai-Carey M.,  
 RA Schwartz J.L., Brousseau R., Cygler M.;  
 RT "Bacillus thuringiensis CryIIa(a) insecticidal toxin: crystal  
 RT structure and channel formation.";  
 RL J. Mol. Biol. 254:447-464(1995).  
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.  
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
 CC SPOREATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
 CC OF THE SPORE COAT.  
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE  
 CC N-TERMINUS.  
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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EMBL; J01554; ; NOT\_ANNOTATED\_CDS.

EMBL; Y09663; CAA70856.1; -.

EMBL; M1250; AAA22353.1; -.

EMBL; D00348; BAA00257.1; -.

EMBL; M10917; AAA22552.1; -.

EMBL; X13435; CAA31886.1; -.

PIR; A23962; USBSXH.

PIR; A22617; A22617.

PIR; JT0241; JT0241.

PIR; S02215; S02215.

PIR; A22798; A22798.

PDB; 1C1Y; 27-JAN-97.

InterPro; IP001178; Endotoxin.

Pfam; PF00555; endotoxin; 1.

Toxin; Sporulation; Plasmid; 3D-structure.

FT VARIANT 77 77 P -> L (IN STRAINS BNS3, IPL7 AND SOTTO).

FT VARIANT 148 148 L -> F (IN STRAINS IPL7 AND SOTTO).

FT VARIANT 302 302 S -> R (IN STRAIN SOTTO).

FT VARIANT 918 918 Q -> R (IN STRAIN SOTTO).

FT CONFLICT 1009 1009 V -> L (IN REF. 1).

SEQUENCE 1176 AA; 133119 MW; E2EE15AF12E5DD85 CRC64;

Query Match 69.3%; Score 4329; DB 1: Length 1176;

Best Local Similarity 71.4%; Pred. No. 9e-272;

Matches 850; Conservative 86; Mismatches 223; Indels 32; Gaps 12;

QY 1 MENNIO-NOCPYCNINPEVEILNEER-STGRPLDIDLSLTRLFLSEFPVCGVAFGL 58

DB 1 MDNPNINEICPYNCLNEPEVEILGERITETGTPIDISLTLQFLSEFPVCGVAFGL 60

QY 59 FOLLINGFIPDSKSLLEQIEIORTLERNRAITLRLGLADSYETIIEALREWEAN 118

DB 61 VDIWGIFGSDWAPVQIOLINORIEEFARNAQISRLGLSNLYQIYAESFREWEAD 120

QY 119 PNAQLREDVRIRFANTDALLTAINNFLTSPETPLLSVYQAAHLHLRLDAYSFGQ 178

DB 121 PNPALREEMRIQFNDMSALTTAIPLLAVQNYQVLLSVYQAAHLHLRLDAYSFGQ 180

QY 179 GWGLDITATNNHYNLILHRYTKHCLDTYNOGLNLRGTNRQWAFNRQFRLTLV 238

DB 181 RWGFAATINSRYNDLRLIGNYTDYAVRYNTGLRVGPGSDRWYRNQFRLTLV 240

QY 239 LDIVLFPNYDRTPIQTSOLTRIEYTSVIEDSPVSANIPNGF----NRAEFQVRPP 294

DB 241 LDIVLFSNYDSRRYPRTVSQTLREIYTPVLE-----NFDGSPRMAQRIEQNIQRP 294

QY 295 HLMDFMNSLFVRAETVRSQTVGGHVLVSR--NTAGNRINEPSPYVFNPGGAI--WIADE 350

DB 295 HLMDLINSLTIITDVRHGNYSNGHOITASPVGFSPEFAFLFG--NAGNAAPPVLSL 352

QY 351 DRRPYRTLSDFEVR-----GGFGNPHVVLGRVAFQQTGTNTHRT--FRNSGTIDSLD 404

DB 353 TGLGIFRTLSPLRYRIILGSPNNQLEFLVDGTETSPASLTNLPSTIYRQGTVDSLD 412

QY 405 EIPPDQNSGAPNDYSHVNHVTYVWQPEIGSG--DSWRAPMFSWTHRSATPTNTIDPR 463

DB 413 VTPPDQNSVPPRAGFGRHLSHTMTL---SQAAGAVYTLRAPTFSWGRSAEFNIIIPSSQ 469

QY 464 ITQIPLVKATLQSGTIVYVGGFTGGDILRLRTSGPGFAYTVININGQLPQRYRIRYA 523

DB 470 ITQIPLTKTSLNGSGSVVKGPGFTGGDILRLRTSPQISTLRVNTAPLSQRYRIRYA 529

QY 524 STTNLIYTVAGERIFAGQNKMTDGTPLTFQSPSYATINTAFTPMSSQSFTVGADT 583

DB 530 STTNLQFHTSIDGRPINQGNFSATMSGNLSQSGSFRTVGTTPPFNSGSSVFTLSAHV 589

QY 584 FSGNGEVYIDRELPVYATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSN 643

DB 584 FSGNGEVYIDRELPVYATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSN 643

DB 590 FNSGNEVYIDRELPVYATFAEYDLERAQKAVNELFTSSNQIGLKTDVTDYHIDQVSN 649

QY 644 LYDCLSDPECLDEKRELSKVHAKRLSDERNLQDPNFKGINRQDLDRGWRGSTDITIQ 703

DB 650 LYDCLSDPECLDEKRELSKVHAKRLSDERNLQDPNFKGINRQDLDRGWRGSTDITIQ 709

QY 704 GDDVFKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSQDLEILYLYNA 763

DB 710 GDDVFKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSQDLEILYLYNA 769

QY 764 KHTVNVLTGSLWPLSVQSPKRCGEPNRCAPHLWNPDLDCSCRDGKCAHSHHPSL 823

DB 770 KHTVNVLTGSLWPLSAQSPKRCGEPNRCAPHLWNPDLDCSCRDGKCAHSHHPSL 829

QY 824 DIDVGTDLNEDLDYVWIFKIKTQDGHARLGNLEPEEKPLVGEALARYKRAKKWRDKR 883

DB 830 DIDVGTDLNEDLDYVWIFKIKTQDGHARLGNLEPEEKPLVGEALARYKRAKKWRDKR 889

QY 884 EKLELETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHRIEAYLPESLVI 943

DB 890 EKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHRIEAYLPESLVI 949

QY 944 PGVNDIFPEELKGRIFTAPFLYDARNVKNGLSCWNVKGHVDEEQQNHRSLVIV 1003

DB 950 PGVNAIIFEELKGRIFTAPFLYDARNVKNGLSCWNVKGHVDEEQQNHRSLVIV 1009

QY 1004 PEWEAEVSOEVRVCGRGYILRVYAVKEGYGEGCVTHIENNTDELKFSNCVEEVPYN 1063

DB 1010 PEWEAEVSOEVRVCGRGYILRVYAVKEGYGEGCVTHIENNTDELKFSNCVEEVPYN 1069

QY 1064 NTVTCNDYATANOEEYGGAYTSRRNGYDEYTGSSNSVPADYASVYEKSYTDGRRDNPCES 1123

DB 1070 NTVTCNDYATANOEEYGGAYTSRRNGYDEYTGSSNSVPADYASVYEKSYTDGRRDNPCES 1125

QY 1124 NRGYGYDTPLPAGYVTKLEYFPETDKVWIEGTETGTFIVDSVELLMEE 1174

DB 1126 NRGYRDYTPLPYGVYTKLEYFPETDKVWIEGTETGTFIVDSVELLMEE 1176

# RESULT 5

CIAD\_BACTA

ID CIAD\_BACTA STANDARD; PRT; 1179 AA.

AC Q03744;

DT 30-MAY-2000 (Rel. 39, Created)

DT 10-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pesticidal crystal protein cryIAD (insecticidal delta-endotoxin

DE CryIA(d)) (crystalline entomocidal protoxin) (133 kDa crystal protein).

GN CRYIAD OR CRYIA(D).

OS Bacillus thuringiensis (subsp. aizawai).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1433;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NRRL B-18484 / PS811;

RA Payne J.M., Sick A.J.;

RT genes encoding novel lepidopteran-active toxins.";

RL Patent number US5246852, 21-SEP-1993.

CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.

CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING

CC SPOGULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.

CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE

CC N-TERMINUS.

CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC modified and this statement is not removed. Usage by and for commercial

QV 890 TNIVYKEAKESVDALFVNSOYDQIQADTNIAMTHAADKRVHRIEAYLPELSVIPGVNVD 949

DQ 950 IFBELKGRIFTAPFLYDARNVKNKGDNNGSLSCNNVKGHVDVEONNHRSVLVVPWEAE 1009  
 DQ 956 IFEELGRIFFATXSLYDARNVKNKGDNNGSLSCNNVKGHVDVESQNHRSVLVVPWEAE 1015  
 QY 1010 VSQVRVCPCRGYTLRTAYKEGYEGECVTIHELENNTDELKFSNCVEEEYPNNTVTGN 1069  
 DB 1016 VSQVRVCPCRGYTLRTAYKEGYEGECVTIHEEDNTDELKFSNCVEEEYPNNTVTGN 1075  
 QY 1070 DYTAQOEYGAGYTNRNKGDDETYSNSNPADYASVIYEKSYYTDGRDPCESNRQYGD 1129  
 DB 1076 DYTAQOEYGAGYTNRNKGESYESNSSIPAEYPIEB-AFYIDGRKENPCESNRQYGD 1134  
 QY 1130 YTPLPAGVVTKELYFPETDKWIEIGETEGETFIVDSVELLMBE 1174  
 DB 1135 YTPLPAGVVTKELYFPETDKWIEIGETEGETFIVDSVELLMBE 1179

```

RESULT 6
CIGA_BACTU
ID CIGA_BACTU STANDARD; PRT: 1166 AA.
AC O45746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cryIIA (insecticidal delta-endotoxin
GN CRYLGA OR CRYIG(A).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1428;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTS003494;
RA Lambert B.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF INSECTS.
CC -! DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPOROULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
CC -! MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
N-TERMINUS.
CC -! SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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DR EMBL; Z22510; CAA80233.1; -.  
 DR HSSP; P02965; ICYI.  
 DR InterPro; IPR001178; Endotoxin.  
 DR Pfam; PF00555; endotoxin; 1.  
 KW Toxin; Sporulation.  
 SQ SEQUENCE 1166 AA; 132003 MW; 3A98B2D2CA086DCC CRC64;

---

Query Match 68.9%; Score 4303; DB 1; Length 1166;  
 Best Local Similarity 71.1%; Pred. No. 4.3e-270;  
 Matches 851; Conservative 76; Mismatches 214; Indels 54; Gaps 12;

Qy	1	MENNIONCPYNCLNPNPEVLNEERSTGELPLDLISLTRELLSEFVGCVAFGLFD	60
		:     :                             :	
Db	1	MEISDOQQYIPYCNLPNPFESIFARNSGFNVSQVSGLTFRLLAEAVPAFGALGFD	60
		:	:
Qy	61	LWGFTFPSDWSLFOQLIOEQIRITLFERNRAITLRGLADSYYEITDALREWEANPN	120

Db	61	IIWAGLQWDSLFLRQIEQLRQIEITELRNRTAILGLSSYNYLVEAREWENDEN	120
Qy	121	NAOZLRVIRFANTD DALITAINNF <sup>1</sup> LTISFEIPLSVYQAA <sup>1</sup> NHL <sup>1</sup> SLLRDAVSFGQGW	180
Db	121	NPASQERVTRERLTDDAIVTGLPTLAIN <sup>1</sup> LEVNL <sup>1</sup> SVITQAA <sup>1</sup> NHL <sup>1</sup> SLLRDAVYFGERW	180
Qy	191	GLDIATVNNHYNRLINLHRYTHKCLD <sup>1</sup> TYNOGLE <sup>1</sup> NRGTNTOWARFNOFRDLTLVLVD	240
Db	181	GLTQANIEDL <sup>1</sup> TRTSLNIOEYSHCARWYNOGLE <sup>1</sup> NIJG <sup>1</sup> IS <sup>1</sup> ---RRYLD <sup>1</sup> Q <sup>1</sup> RD <sup>1</sup> L <sup>1</sup> TS <sup>1</sup> VLVD	236
Qy	241	IVALFPNVDRV <sup>1</sup> TYPIOTSSOL <sup>1</sup> TR <sup>1</sup> EIY <sup>1</sup> TSV <sup>1</sup> IED <sup>1</sup> SP <sup>1</sup> YSAN <sup>1</sup> IPNG <sup>1</sup> FN <sup>1</sup> RGV <sup>1</sup> RP <sup>1</sup> HLMD <sup>1</sup> PM	300
Db	237	IVALFPNI <sup>1</sup> DI <sup>1</sup> RYPIQ <sup>1</sup> OS <sup>1</sup> LT <sup>1</sup> REI <sup>1</sup> Y <sup>1</sup> SP <sup>1</sup> ----VAG <sup>1</sup> IN <sup>1</sup> FGL <sup>1</sup> SI <sup>1</sup> AN <sup>1</sup> -LRAPHLM <sup>1</sup> OFI	290
Qy	301	NSL <sup>1</sup> VFAT <sup>1</sup> RSQ <sup>1</sup> VTW <sup>1</sup> GG <sup>1</sup> HLV <sup>1</sup> SSR <sup>1</sup> NTA <sup>1</sup> --GN <sup>1</sup> RIN <sup>1</sup> FP <sup>1</sup> SV <sup>1</sup> GV <sup>1</sup> FN <sup>1</sup> PG <sup>1</sup> CA <sup>1</sup> IA <sup>1</sup> ED <sup>1</sup> DR <sup>1</sup> PF <sup>1</sup> YR	357
Db	291	DRIVIY <sup>1</sup> NSVR <sup>1</sup> STPY <sup>1</sup> WAG <sup>1</sup> HEV <sup>1</sup> SR <sup>1</sup> TCOG <sup>1</sup> OG <sup>1</sup> NEIR <sup>1</sup> PL <sup>1</sup> GV-----AANAEP-----	337
Qy	358	TLSDPV <sup>1</sup> FVR--GGFNPH---YVLGLRGVAPQO <sup>1</sup> TG <sup>1</sup> NHT-----RTFRN--S	397
Db	338	---PVTIR <sup>1</sup> TG <sup>1</sup> FTDEORQWYRARS <sup>1</sup> RV <sup>1</sup> SP <sup>1</sup> SGQ <sup>1</sup> DFSL <sup>1</sup> VD <sup>1</sup> AVG <sup>1</sup> FLT <sup>1</sup> IFS <sup>1</sup> AV <sup>1</sup> SIY <sup>1</sup> RNG <sup>1</sup> FG	393
Qy	398	GTIDSLDEIPQD <sup>1</sup> NSGAPW <sup>1</sup> NDY <sup>1</sup> SHVLNHY <sup>1</sup> TFV <sup>1</sup> KW <sup>1</sup> PC <sup>1</sup> EISGS <sup>1</sup> DSWRAP <sup>1</sup> MTSW <sup>1</sup> THRSAT <sup>1</sup> PTN	457
Db	394	FNTD <sup>1</sup> IDEI <sup>1</sup> PIEG <sup>1</sup> D--PFTGY <sup>1</sup> SHR <sup>1</sup> CH <sup>1</sup> VGF <sup>1</sup> CLASS <sup>1</sup> PF <sup>1</sup> --SGYARAP <sup>1</sup> FSW <sup>1</sup> THRSAT <sup>1</sup> LTN	449
Qy	458	TIDPER <sup>1</sup> TQI <sup>1</sup> PLVKAHT <sup>1</sup> LSQGT <sup>1</sup> W <sup>1</sup> RG <sup>1</sup> PT <sup>1</sup> G <sup>1</sup> GDIL <sup>1</sup> RR <sup>1</sup> TSG <sup>1</sup> GFAY <sup>1</sup> TVIN <sup>1</sup> IGQ <sup>1</sup> LPOR <sup>1</sup> YR	517
Db	450	TIAPDV <sup>1</sup> TQI <sup>1</sup> PLVKA <sup>1</sup> FN <sup>1</sup> HS <sup>1</sup> AI <sup>1</sup> VK <sup>1</sup> GP <sup>1</sup> TG <sup>1</sup> GDIL <sup>1</sup> RR <sup>1</sup> TVN <sup>1</sup> VSFG <sup>1</sup> DMRVN <sup>1</sup> ITAP <sup>1</sup> LSQR <sup>1</sup> YR	509
Qy	518	ARIRYAST <sup>1</sup> N <sup>1</sup> RIY <sup>1</sup> VTVAG <sup>1</sup> ERIFAG <sup>1</sup> OFN <sup>1</sup> K <sup>1</sup> MTD <sup>1</sup> GPL <sup>1</sup> TFQ <sup>1</sup> FSYAT <sup>1</sup> INTAF <sup>1</sup> TFP <sup>1</sup> MSQS <sup>1</sup> SF	577
Db	510	VRIRYAST <sup>1</sup> DLQ <sup>1</sup> FY <sup>1</sup> TNING <sup>1</sup> T <sup>1</sup> IN <sup>1</sup> GFSS <sup>1</sup> TM <sup>1</sup> SD <sup>1</sup> GD <sup>1</sup> LY <sup>1</sup> GR <sup>1</sup> ERVAG <sup>1</sup> TF <sup>1</sup> PT <sup>1</sup> FS <sup>1</sup> DAN <sup>1</sup> STF	569
Qy	578	TVGAD <sup>1</sup> TSSS <sup>1</sup> NEW <sup>1</sup> YID <sup>1</sup> R <sup>1</sup> FELI <sup>1</sup> PTAF <sup>1</sup> EAY <sup>1</sup> DL <sup>1</sup> ERAK <sup>1</sup> AVN <sup>1</sup> ALFT <sup>1</sup> SI <sup>1</sup> NOIG <sup>1</sup> IK <sup>1</sup> T <sup>1</sup> DT <sup>1</sup> YD <sup>1</sup> H	637
Db	570	TIGAFG <sup>1</sup> SPN <sup>1</sup> NEI <sup>1</sup> DI <sup>1</sup> RIE <sup>1</sup> VP <sup>1</sup> AEV <sup>1</sup> TFEAY <sup>1</sup> DL <sup>1</sup> EKAQ <sup>1</sup> AVN <sup>1</sup> ALFT <sup>1</sup> SS <sup>1</sup> NOIG <sup>1</sup> LK <sup>1</sup> T <sup>1</sup> DT <sup>1</sup> YD <sup>1</sup> H	629
Qy	638	IDQY <sup>1</sup> SN <sup>1</sup> VD <sup>1</sup> CLS <sup>1</sup> DEF <sup>1</sup> CL <sup>1</sup> DEK <sup>1</sup> REL <sup>1</sup> SEK <sup>1</sup> VK <sup>1</sup> AK <sup>1</sup> RLS <sup>1</sup> DERN <sup>1</sup> LQ <sup>1</sup> DP <sup>1</sup> N <sup>1</sup> FK <sup>1</sup> IN <sup>1</sup> Q <sup>1</sup> LD <sup>1</sup> RGW <sup>1</sup> RST	697
Db	630	IDK <sup>1</sup> VSN <sup>1</sup> LECL <sup>1</sup> SD <sup>1</sup> BF <sup>1</sup> CL <sup>1</sup> DEK <sup>1</sup> REL <sup>1</sup> SEK <sup>1</sup> VK <sup>1</sup> AK <sup>1</sup> RLS <sup>1</sup> DERN <sup>1</sup> LQ <sup>1</sup> DP <sup>1</sup> N <sup>1</sup> FK <sup>1</sup> IN <sup>1</sup> Q <sup>1</sup> LD <sup>1</sup> RGW <sup>1</sup> RST	689
Qy	698	DI <sup>1</sup> TIQ <sup>1</sup> GD <sup>1</sup> VD <sup>1</sup> V <sup>1</sup> KN <sup>1</sup> Y <sup>1</sup> LP <sup>1</sup> GT <sup>1</sup> DEC <sup>1</sup> Y <sup>1</sup> TY <sup>1</sup> LQ <sup>1</sup> ID <sup>1</sup> ES <sup>1</sup> LK <sup>1</sup> PY <sup>1</sup> TRY <sup>1</sup> LQ <sup>1</sup> RGY <sup>1</sup> IED <sup>1</sup> SOD <sup>1</sup> LEI <sup>1</sup> Y	757
Db	690	DI <sup>1</sup> ITQ <sup>1</sup> GD <sup>1</sup> VD <sup>1</sup> V <sup>1</sup> KN <sup>1</sup> Y <sup>1</sup> LP <sup>1</sup> GT <sup>1</sup> DEC <sup>1</sup> Y <sup>1</sup> TY <sup>1</sup> LQ <sup>1</sup> ID <sup>1</sup> ES <sup>1</sup> LK <sup>1</sup> VY <sup>1</sup> TRY <sup>1</sup> LQ <sup>1</sup> RGY <sup>1</sup> IED <sup>1</sup> SOD <sup>1</sup> LEI <sup>1</sup> Y	749
Qy	758	LIRYN <sup>1</sup> AKHET <sup>1</sup> VN <sup>1</sup> VLGT <sup>1</sup> SLW <sup>1</sup> PLSVQ <sup>1</sup> SP <sup>1</sup> IRK <sup>1</sup> CGEP <sup>1</sup> N <sup>1</sup> PCAP <sup>1</sup> HL <sup>1</sup> EW <sup>1</sup> NFD <sup>1</sup> LC <sup>1</sup> SD <sup>1</sup> RG <sup>1</sup> EKCA <sup>1</sup> HH	817
Db	750	LIRYN <sup>1</sup> AKHET <sup>1</sup> VN <sup>1</sup> VG <sup>1</sup> GSU <sup>1</sup> W <sup>1</sup> PLSAQ <sup>1</sup> SP <sup>1</sup> IGK <sup>1</sup> CGEP <sup>1</sup> N <sup>1</sup> PCAP <sup>1</sup> HL <sup>1</sup> EW <sup>1</sup> NFD <sup>1</sup> LC <sup>1</sup> SD <sup>1</sup> RG <sup>1</sup> EKCA <sup>1</sup> HH	809
Qy	818	SHH <sup>1</sup> FLSD <sup>1</sup> IDV <sup>1</sup> CG <sup>1</sup> TD <sup>1</sup> LN <sup>1</sup> ED <sup>1</sup> DV <sup>1</sup> W <sup>1</sup> IFK <sup>1</sup> IQ <sup>1</sup> DGH <sup>1</sup> ARL <sup>1</sup> GN <sup>1</sup> LEF <sup>1</sup> E <sup>1</sup> KE <sup>1</sup> PLV <sup>1</sup> GEAL <sup>1</sup> ARV <sup>1</sup> KRA <sup>1</sup> EK	877
Db	810	SHH <sup>1</sup> FLSD<	

[illegible]



Db 241 DIVAFPPNIDINTYPIQTATQTLREVLDLFFINENLSPAASYPT-FSAESAIRSPHL 299  
 QY 297 MDENSLFVTAETVRSQTVGSHLVSS--RNTAGRNFPDSYG-VFNEPGGAIMIADDEPR 353  
 Db 300 VDFLNSFTIYDLSARAYWGSHLVNFRFTGTTNLIRSPDLYGREGTERPVTITASPSV 359  
 QY 354 PFYRTLSDEVFVRGFGNPHYVLGRVAFQOQTGNTHTIRFNRSNGTIDSLDEIPQDMSG 413  
 Db 360 PIFRFLS--YIT-GLDLSNFPVAGIEGVFQNTISR--SIYRKSGPIDSFSELPPQDASV 413  
 QY 414 APWNDYSHVLNHFVVRPWPGLISGSDSHRAPMFSWTHRSAPTNTIPERITQIPLVKAH 473  
 Db 414 SPAIGYSHRLCHATELE---RISG-PRTAGTVFSWTHRSAPTNEVSPSRITQIPWKAH 469  
 QY 474 TIQSGTIVVRGPGFTGGDILRRTSGGPAYTIVNINGLPQRYRARIYASGTNLRIVYT 533  
 Db 470 TLASGASVKGFGFTGGDILRNSNGELGLRVFTGRLPOSYYIRFYASVANRSGETR 529  
 QY 534 VAGERIFAGQFNKMTDGTPLTFQSFYATINTAFTPFMSOSSFTVGADTFSSNEVIID 593  
 Db 530 YSQPPSYGISFPKTDAGEPLTISRFAHTLTPTTFRAQEEFDL---YIQSG--YIID 584  
 QY 594 RELPLVATPAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDDFC 653  
 Db 585 RLFPVTATPAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVACLSDDFC 644  
 QY 654 LDEKRELSEKVKHAKRLSDERNLLODPNPKGINROLDRGWSGTDITIQRGDDVFKENYV 713  
 Db 645 LDEKRELSEKVKHAKRLSDERNLLODPNPKGINROLDRGWSGTDITIQRGDDVFKENYV 704  
 QY 714 TLPGFFDECYPYLYOKIDESKLYPYRYQLRGYEDSDQLEIYLIRYNAKHETVNVLTG 773  
 Db 705 TLPGFFDECYPYLYOKIDESKLYPYRYQLRGYEDSDQLEIYLIRYNAKHETVNVLTG 764  
 QY 774 GSWLPLSVQSPYIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHPSLDDVGCETDLN 833  
 Db 765 GSWLPLSVENQIGCGEPNRCAPHLEWNPDLHCSRDGKCAHSHHPSLDDVGCETDLN 824  
 QY 834 EDLDVWVIFKIKTODGHARGLNLEFLEKPLVGEALARKVRAEKKWRDKREKLENTIV 893  
 Db 825 EDLGVWVIFKIKTODGHARGLNLEFLEKPLVGEALARKVRAEKKWRDKREKLENTIV 884  
 QY 894 YKEAKESVDALFVNQYDQLOQADTNIAHAAKRVHRIREAYLPESLVIPGVNVDIPEE 953  
 Db 885 YKEAKESVDALFVNQYDQLOQADTNIAHAAKRVHRIREAYLPESLVIPGVNVAIFEE 944  
 QY 954 LKGRIFTAFELDARVINKGDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWEAEVSQEE 1013  
 Db 945 LEERIFTAFSLDARNIKGDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWEAEVSQEE 1004  
 QY 1014 VRVCPGRGVLIRVATYKEGYGGCVTIHEIENNTDELAFNSCVEEVEYVNNVTCDNYTA 1073  
 Db 1005 VRVCPGRGVLIRVATYKEGYGGCVTIHEIENNTDELAFNSCVEEVEYVNNVTCDNYTA 1064  
 QY 1074 NOEYGGATSNRNGYDETYGNSVYPADYASVYEKSYTDGRRONPCESNRGYGDTPL 1133  
 Db 1065 TOEYEGTYSNRNGYDEAYGNPSYPADYASVYEKSYTDGRRONPCESNRGYGDTPL 1124  
 QY 1134 PAGYVTKLEYPEPTDKVWIEIGETEGTIVDSVLELLMEE 1174  
 Db 1125 PAGYVTKLEYPEPTDKVWIEIGETEGTIVDSVLELLMEE 1165

RESULT 8  
 ID CLHA\_BACTU  
 AC Q45748; STANDARD; PRT: 1172 AA.  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Pesticidal crystal protein cryIIHa (insecticidal delta-endotoxin  
 DE CRYIIH(a)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).  
 GN CRYIIA OR CRYIIA(A).

OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 RN NCBI\_TaxID=1428;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BTS02069AA;  
 RA Lambert B.;  
 RL Submitted B.;  
 CC Sub-!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPITHELIAL CELLS OF INSECTS.  
 CC DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
 CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
 CC OF THE SPORE COAT.  
 CC MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE  
 CC N-TERMINUS.  
 CC SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; Z22513; CAA80236.1; ..  
 DR HSSP; P02965; LCIIY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR Pfam; PF00555; endotoxin; 1.  
 KW Toxin; Sporulation.  
 SQ SEQUENCE 1172 AA; 132980 MW; 9BEC1B1071C71270 CRC64;

Query Match 67.8%; Score 4230.5; DB 1; Length 1172;  
 Best Local Similarity 69.9%; Pred. No. 2.1e-265;  
 Matches 834; Conservative 92; Mismatches 220; Indels 47; Gaps 11;

QY 4 NIQNCQVYNCLNPNVEIILNEERSTGR---LPLDLSLSITRELLSEFVPGVGAFLGF 60  
 Db 5 NNQNVVYNCLSNPENEIILDESRSREQVAEISGLITRELLSLLPGASFGFALED 64  
 QY 61 LINGFTPPDSNLSFLQIEQRIETLERNAITITRLGLADSYEIIYEALEWEANPN 120  
 Db 65 IIMGVIGDPQDNFLAQIEQRIETLERNAITITRLGLADSYEIIYEALEWEANPN 124  
 QY 121 NAOLREDVRIRFANTDALLITANNFTLTSFELPLSVYVQAAANLHLSLLRDVSEGGW 180  
 Db 125 NEALQDVRNRFSNTDALLITAPILLREQGFELPLSVYVQAAANLHLSLLRDVSEGGW 184  
 QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNOGLENGRNTROWARNFRRDLITVLID 240  
 Db 185 GLDPTVTVNNHYNRLINLIHRYTKHCLDLYNOGLENGRNTROWARNFRRDLITVLID 240  
 QY 241 IVALFPNDVTRPIQTSOLTRIEYTSVIE--DSPVSANIPNGFNRAEFGVRPPHMDP 299  
 Db 241 IVALFPNDVTRPIQTSOLTRIEYTSVIE--DSPVSANIPNGFNRAEFGVRPPHMDP 293  
 QY 300 MNSLFTVTAETVRSTQVGGHLSVSRNTA--GNRINFPSTGVFNPGGAIWIADEDPRFF-- 355  
 Db 294 LTRLVITGVQSGIYHWAGHEISSRTTGNLSSNIQPLPYCT-----AASADAFNM 344  
 QY 356 -----YRTLSDPVVRGFGFNPHVVLGRVACQQTGNTNTRT-----FRNSGIDSL 403  
 Db 345 NIHSETIYRTLAPYISVSGISPNRTRVVEGRVRLIARDNNLDLPFLYRKRGDLDF 404  
 QY 404 DEIPQDMSGAPWNDYSHVLNHNVTFFVRWPGCEISGDSWRAPMFSWTHRSAPTNTIDP 463  
 Db 405 TELPDESTPPYIGYSHRCHARFARSPVILPSPNFARLPVFSWTHRSAPTNEVSPSR 464  
 QY 464 ITQIPLVKAHTLQSGTIVRGPGFTGGDILERT--SCGPFAYTIVNINGLPQRYRARIR 521  
 Db 465 ITQIPLVKAHTLQSGTIVRGPGFTGGDILERT--SCGPFAYTIVNINGLPQRYRARIR 524  
 QY 522 YASTTNRIYVTVAGERIFAGQFNKMTDGTPLTFQSFYATINTAFTPFMSOSSFTVGA 581

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Db 525 YASVANSNGVFRHLPOPSYGISPTMGTDPLTSRSFALTITLTPITLRAQEFNL-- 582
QY 582 DTSSGNEVVIDPELIPVATAEAEYDLERAQKAVNALTSINQIGIKTDYDHYDQV 641
Db 583 -TIPRG--VVIDRIEFYVPDVAEAGYDLERAQKAVNALTSINQIGIKTDYDHYDQV 639
QY 642 SNLVDCLSEDFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGINRDLDRGWSGTDITI 701
Db 640 SNLVECLSEDFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGINRDLDRGWSGTDITI 699
QY 702 QRGDDVFKENYVTLPGTFDECYTYLYQKIDESKLPYTRYQLRGYLEDSDQLEIYLIRY 761
Db 700 QGSDDVFKENYVTLPGTFDECYTYLYQKIDESKLPYTRYQLRGYLEDSDQLEIYLIRY 759
QY 762 NAKHETVNLVGTSLWPLSVQSPIRKCGENRCAPHLEWNPDLDCSCRDGKCAHSHHF 821
Db 760 NAKHEIVNVPGTSLWPLSVQSPIRKCGENRCAPHLEWNPDLDCSCRDGKCAHSHHF 819
QY 822 SLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEBEKPLVGEALARKRAKKWRD 881
Db 820 SLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEBEKPLVGEALARKRAKKWRD 879
QY 882 KREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAKRVHRIEAYLPELS 941
Db 880 KREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAKRVHRIEAYLPELS 939
QY 942 VIPGVNVDIFEEELKGRIFTAFYLDARNVKNKGNDFNGLSCWNVKGVHDVVEQNNHRSVL 1001
Db 940 VIPGVNVDIFEEELKGRIFTAFYLDARNVKNKGNDFNGLSCWNVKGVHDVVEQNNHRSVL 999
QY 1002 VPEWEAEVSQEVRCVPGRGYILRVATYKEGYGEGCVTIEIENNTDELKFSNCVEEYV 1061
Db 1000 VPEWEAEVSQEVRCVPGRGYILRVATYKEGYGEGCVTIEIENNTDELKFSNCVEEYV 1059
QY 1062 PNNVTVCNDYTAQOEYGGAYTGRNRYDETYGNSVSPADYASVYEEKSYTDGRRDNC 1121
Db 1060 PSNTVTCNDYTAQOEYGGAYTGRNRYDETYGNSVSPADYASVYEEKSYTDGRRDNC 1119
QY 1122 ESNRGYGDYTPAGYVTRKLEYPFETDKWVIEGTEGTFIVDSVELLMEE 1174
Db 1120 EFNRGYRDYTPAGYVTRKLEYPFETDKWVIEGTEGTFIVDSVELLMEE 1172

RESULT 9
C1GB_BACTZ
ID C1GB_BACTZ STANDARD; PRT: 1169 AA.
AC Q9ZAZ6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIgb (Insecticidal delta-endotoxin
DE CryIgb(b)) (Crystalline entomotoxin) (133 kDa crystal protein).
GN CRYIGB OR CRYIGB(B) OR CRYH2.
OS Bacillus thuringiensis (subsp. wuhanensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=52024;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-525;
RX MEDLINE=20153386; PubMed=10688690;
RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
RT "Cloning of two new cry genes from Bacillus thuringiensis subsp.
RT wuhanensis strain ";
RL Curr. Microbiol. 40:227-232(2000).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PIERIS RAPAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC -----
DR EMBL; U70725; AAD10291.1; -.
DR HSSP; P02965; ICIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1169 AA; 132904 MW; D1EFCL508A8B10BD CRC64;

Query Match 67.7%; Score 4224.5; DB 1; Length 1169;
Best Local Similarity 70.1%; Pred. No. 5.1e-265;
Matches 834; Conservative 78; Mismatches 241; Indels 37; Gaps 10;

QY 1 MENNQNOCVPYNCNLPNPEVEILNEERSTGRPLDLSLSTRLLSEFVGVGAFGLFD 60
Db 1 MEINNQOCVPYNCNLPNPEVEILNEERSTGRPLDLSLSTRLLSEFVGVGAFGLFD 60
QY 61 LIWGFITPDSWLSFLQIEOLIEQRIETLERNRAITTLGLADSYETIYIEALREWEANPN 120
Db 61 LIWGFITPDSWLSFLQIEOLIEQRIETLERNRAITTLGLADSYETIYIEALREWEANPN 120
QY 121 NAOLREDVRIRFANTDDALITAINNFTLTSFEIPLSVVQAAANLHSLRLDADVSFQGW 180
Db 121 NPASKERVTRFRTDDALLTGYPLMAIPGFEATLSVYAQSANLHALLRDADVFFGERW 180
QY 181 GLDIATVNNHYNKLNLHRYTKHCLDLYNOGLENLGNTNROMARNQFRDLTLVLD 240
Db 181 GLQTNIDLYSLKNSIRDYTNHCVFYNIGLNLNVR---PEYRQRELTISVLD 236
QY 241 IVALFNVDYRTYPIOTSSOLTRFETIYSSVIEDSPYSANIPNGFNRAEFVGRPHLMDFM 300
Db 237 LVALFFNYDIRTYPIPTKLSOLTREIYTDPII---SPGAQAGYTLQDV-LREPHLMDFL 290
QY 301 NSLFTVAETVRSQTVWGGHLV-SSRTAGNKRINFPSPYGVNPGGAIWADBDP----- 352
Db 291 NLLIYTGVEGRHGWAGHEVESRGTGMNIRFLYGT-----AATAETRTFTPS 342
QY 353 -----RPFYTLSDPVFVRGGFN--PHYVLGL-RGYAFOQTGTNHTRTFRNSGTIDSLD 404
Db 343 TFPGLNLFYTLTSAPIFRDEPGANIIIRYRTSLVEGVGTQP--NNGQLYRVRGTLDSLD 401
QY 405 EIPPDNSGAPNDYSHVLNHYTVFVRWPGELSGSDSWRAPMFWTHESATPTWIDPERI 464
Db 402 QLPLEGESSL--TEYSHRUCHVRFPAQSLRNAEPLDYARVPMFWTHESATPTWIDPDVI 459
QY 465 TQIPLVKAHTLOSQTTVVRGPGFTGGDILARTSGGPFAYTVININGQLPQRYRARIYAS 524
Db 460 TQIPLVKAFLHSSATVVRGPGFTGGDILARTNAGNEDMRVNTITAPLSQRYRVRIYAS 519
QY 525 TTNRILYIVVAGRIIFAGQPKMTMDGDLTFQSFYSATINTAFTPMSSOSTVVGADTF 584
Db 520 TANLQFHTSINGRAINQANFPATMNSGENLQSGSERVAGFTTPTFTSDALSTETIGAFSF 579
QY 585 SSGNEVYIDRFELIPVATAEAEYDLERAQKAVNALTSINQIGIKTDYDHYDQVSNL 644
Db 580 SSGNEVYIDGIEFVPAEVTATESDQDRAQKAVNALTSINQIGIKTDVNTYHIDQVSNL 639
QY 645 VDLCLSEDFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGINRDLDRGWSGTDITIQRG 704
Db 640 VECLSEDFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGINRDLDRGWSGTDITIQRG 699
QY 705 DVDFKENYVTLPGTFDECYTYLYQKIDESKLPYTRYQLRGYIEDSDQLEIYLIRYNAK 764
Db 700 DVDFKENYVTLPGTFDECYTYLYQKIDESKLPYTRYQLRGYIEDSDQLEIYLIRYNAK 759
QY 765 HETVNVLTGSLWPLSVQSPIRKCGENRCAPHLEWNPDLDCSCRDGKCAHSHHFSLD 824

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Db 760 HETVNPVGTSLWPLSAQSPIGKCGEPNRCATHLEWPNFLDSCRDGKCAHSHHFSLD 819
QY 825 IDVGCTDLNEDLVWVFIKIKQDGHARGNLGFLKPLVGEALARKVRAEKWKROKRE 884
Db 820 IDVGCTDLNEDLVWVFIKIKQDGHARGNLGFLKPLVGEALARKVRAEKWKROKRE 879
QY 885 KLELETIVVYKEAKESVDALFVNSQYDQLOADTNIAHRAADKRVHRIREAYLPESVIP 944
Db 880 KLELETIVVYKEAKESVDALFVNSQYDQLOADTNIAHRAADKRVHRIREAYLPESVIP 939
QY 945 GVNVDIFEELKGRFTFAFFLYDARNVJKNQDFNGLSCWNVKGVHVDVEQNNHRSVLVVP 1004
Db 940 GVNAAIFEELKGRFTFAFFLYDARNVJKNQDFNGLSCWNVKGVHVDVEQNNHRSVLVVP 999
QY 1005 EWEAEVSOEVRVCPGRGYILRVYAKGYGEGCVTIHEIENNTDELKFSNCEVEEYPNN 1064
Db 1000 EWEAEVSOEVRVCPGRGYILRVYAKGYGEGCVTIHEIENNTDELKFSNCEVEEYPNN 1059
QY 1065 TVTCNDYNTAQEEYGGAYTSRNGYDTEYGSNSVSPADYASVYEKSYTDGRRDNPCESN 1124
Db 1060 TVTCNDYNTAQEEYGGAYTSRNGYDTEYGSNSVSPADYASVYEKSYTDGRRDNPCESN 1119
QY 1125 RGYGDTPIPAAGVYKLEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174
Db 1120 RGYGDTPIPAAGVYKLEYPETDKVWIEIGETEGTFIVDSVELLMEE 1169

RESULT 10
C1CA_BACTE STANDARD; PRT; 1189 AA.
AC F05518; P10327; Q03742; Q45725;
DT 01-NOV-1988 (Rel. 09, Created)
DT 30-NOV-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin
GN CryIc(a)) (Crystalline entomocidal protoxin) (134 kDa crystal protein).
OS Bacillus thuringiensis (subsp. entomocidus), and
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436, 1433;
RN [1]_TaxID=1436, 1433;
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=60.5;
RX MEDLINE=88289380; PubMed=3399402;
RA Honee G., van der Salm T.P.M., Visser B.;
RT "Nucleotide sequence of crystal protein gene isolated from B.
RT thuringiensis subspecies entomocidus 60.5 coding for a toxin highly
RT active against Spodoptera species.";
RL Nucleic Acids Res. 16:6240-6240(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=NRRL B-18484 / PS811;
RA Payne J.M., Sick A.J.;
RT "Bacillus thuringiensis isolate active against lepidopteran pests, and
RT genes encoding novel lepidopteran-active toxins.";
RL Patent number US5246852, 21-SEP-1993.
RN [3]
RP SEQUENCE OF 1-823 FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=7-29;
RX MEDLINE=89343627; PubMed=2548060;
RA Sanchis V., Lerechus D., Menco M., Chauaux J., Guo S., Lecadet M.-M.;
RT "Nucleotide sequence and analysis of the N-terminal coding region of
RT the Spodoptera-active delta-endotoxin gene of Bacillus thuringiensis
RT aizawai 7-29";
RL Mol. Microbiol. 3:229-238(1989).
RN [4]
RP SEQUENCE OF 1-756 FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=7-29 / K26-21;
RA Strizhov N.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

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CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE INCLUDING SPODOPTERA
CC SPECIES.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC EMBL; X07518; CAA30396.1; -
CC EMBL; M73251; AAA22343.1; -
CC EMBL; X13620; CAA31951.1; -
CC EMBL; X96682; CAA65457.1; -
CC PIR; S00944; S00944.
CC PIR; S04181; S04181.
CC HSSP; P02965; ICIV.
CC InterPro; IPR001178; Endotoxin.
CC Pfam; PF00555; endotoxin; 1.
CC Toxin; Sporulation.
CC CONFLICT 124 124 A -> E (IN REF. 1).
CC CONFLICT 294 294 A -> R (IN REF. 1).
CC CONFLICT 366 366 A -> I (IN REF. 3).
CC CONFLICT 376 380 WPAPP -> CORHH (IN REF. 3).
CC CONFLICT 386 386 V -> G (IN REF. 3).
CC CONFLICT 405 405 T -> Q (IN REF. 2).
CC CONFLICT 453 453 H -> D (IN REF. 1).
CC CONFLICT 775 775 R -> A (IN REF. 3).
CC CONFLICT 853 853 V -> L (IN REF. 2).
CC CONFLICT 864 864 G -> N (IN REF. 2).
CC CONFLICT 931 931 D -> N (IN REF. 2).
CC SEQUENCE 1189 AA; 134715 MW; 362768685916A0DF CRC64;

Query Match 67.6%; Score 4223.5; DB 1; Length 1189;
Best Local Similarity 68.9%; Pred. No. 6e-265;
Matches 834; Conservative 95; Mismatches 224; Indels 57; Gaps 17;

QY 1 MENNIOQCVPYNCNLANPEVEILNEER-STGRULPDLISLITRFLSEFPYGVGVARGLF 59
Db 1 MENNIOQCVPYNCNLANPEVEILNEER-STGRULPDLISLITRFLSEFPYGVGVARGLF 59
QY 60 DLWGFITPESDWSLFLIQIBQLIEQRIETLERNRAITTLRGLADSYEITAEALREWEANP 119
Db 61 DFVWGVGPSOWDAFLVQIBQLINERAEFARNAATANLEGLNNTNFIYVEAFKEWEEDP 120
QY 120 NNAQLREDVRIREFANTDDALITAINNFTLTSFIPILSVYVQAANLHSLLRDAVSFGQG 179
Db 121 NNPATRVIDRFRILDLGLERDIPSRFISGFEVPLSVYAQAANLHSLLRDAVSFGQG 180
QY 180 WGLDIATVNNHYNRLNLHRYTKHCLDTYNOGLENLGNTTQWARFNQFRDLTLTVL 239
Db 181 WGLTTVNNVNNYRLNRHIDEYADHCANLNLKSTYQDWTYNNRLRDLTLTVL 240
QY 240 DIVALFPNYDVRTYPTQTSQTREIYTSVIEDSP---VSANIPNGFNRAE-FGVRPPH 295
Db 241 DIAAAPPYNDNRRYPLOPVQQLTRVYVTPDLNPNFQLOLSVAQLPT-FNVMESSAIRNPH 299
QY 296 LMDFMNSLFTVAB--TVRSQTVWGHVLSRNTAGNRINFPSPYGVENPGGAIWAIEDP- 352
Db 300 LFDILNLNLTFTDWFVSGRNFYWGGRHVITSSLLGGNITSPIVG-----REANQEP 351
QY 353 -----RPFYRLSDPV--FVGGGFNPHYVL-GLRGVAFQQTGTNHTTFRNSGIDSL 403
Db 352 RSFTENGPFVRLSNPTLRLLOQPWPAPPNLRGVGEVF-STPTN-SFTYRGRGVDSL 409
QY 404 DEIPPDNSGAPWNDYSHVNLNHTVFRVWFGEISGDSWRAP-----MFSWTHRSATPIN 457

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Db 410 TELPPEDNSVPPREGYSHRLCHATFVQSG-----TPFLTGGVTSWTHRSATLTN 460
QY 458 TIDPERITDIPVKAHTLOSITVVGPGFTGGDILIRRTSGGPPATYVNINGQLPQRYR 517
Db 461 TIDPERINIPVKGPRVGGSVITGPGFTGGDILIRRTSGGPPATYVNINGQLPQRYR 520
QY 518 ARIRYASTNLIYV-TVAGERIFAGQ-----FNKMTDGTDPDLTQFSFYATINTAFWF 570
Db 521 LRFYASSRDARVILVTGAAGTGVGGQVSNMPLQKTMGEIGNLTSTRTYTDSPFPF 580
QY 571 PMSQSFV-----GADTFSSNEWIDRFELIPVTAFTFAEYDLERAKAVNALFTSI 624
Db 581 RANPDIGISEQPLFGAGTSSG-ELYIDKIELILADATFAESDLERAKAVNALFTSS 639
QY 625 NOIGIKITDVTYHIDOVSNLVDCLSEDFCLDEKRELSKVKKAKRLSDENLLQDNFKG 684
Db 640 NQIGLKITDVTYHIDOVSNLVDCLSEDFCLDEKRELSKVKKAKRLSDENLLQDNFKG 699
QY 685 INRQDRGRGSTDIITIQRGDDVFKENYVTLPGTFDECYPTLYIQKIDSKLPYTRYQL 744
Db 700 INRQDRGRGSTDIITIQGDVDFKENYVTLPGTVDECYPTLYIQKIDSKLKAYTRYEL 759
QY 745 RGYEDSQLEIYLIRYNKAKHETVNLGTSLWPLSVQSPPIKCGEPNRCAPHLEWNPDL 804
Db 760 RGYEDSQLEIYLIRYNKAKHETVNLGTSLWPLSVQSPPIKCGEPNRCAPHLEWNPDL 819
QY 805 DCSRGCEKCAHSHSFSLDIDVGCITDLNEDLDVWVIEFKITQDGHARLGNLEFLEKPL 864
Db 820 DCSRGCEKCAHSHSHFTLIDVGCITDLNEDLDVWVIEFKITQDGHARLGNLEFLEKPL 879
QY 865 VGEALARVRAEKWKDRKLELENTIYVKEAKESVDALFVNSQYDQLQADTNIAIHA 924
Db 880 LGEALARVRAEKWKDRKLELENTIYVKEAKESVDALFVNSQYDQLQADTNIAIHA 939
QY 925 AKRVHRIEALPELSPVPGVNDVIFELKGRIFTAFELYDARNVKGDFPNNGLSOWN 984
Db 940 AKRVHRIEALPELSPVPGVNAALFEELEGRIFTAFELYDARNVKGDFPNNGLLCWN 999
QY 985 VKGHVDVEQNHRSLVVPWEAEYSQEVRCVPCGRGYILRTVAYKEGYGEGCVTTHEIE 1044
Db 1000 VKGHVDVEQNHRSLVVPWEAEYSQEVRCVPCGRGYILRTVAYKEGYGEGCVTTHEIE 1059
QY 1045 NNTDELKFSNCVEEYYPNNTVTCNDYTANQEEYGAITSRNGYDITYGSNSVSPADYA 1104
Db 1060 DNTDELKFSNCVEEYYPNNTVTCNNYTGQEEYEGYTSRNGYDEAYGNVSPADYA 1119
QY 1105 SYVEEKSYTDGRDPCSNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETGTFIV 1164
Db 1120 SYVEEKSYTDGRDPCSNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETGTFIV 1179
QY 1165 DSVLELLMEE 1174
Db 1180 DSVLELLMEE 1189

RESULT 11
CLAB_BACTK
ID CLAB_BACTK STANDARD: PRT: 1155 AA.
AC P06578; P06577; P21257; P09666; P09667;
DT 01-JAN-1988 (Rel. 06, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cryIAB (Insecticidal delta-endotoxin
GN CRYIA(b) (Crystalline entomocidal protoxin) (130 kDa crystal protein).
OS Bacillus thuringiensis (subsp. kurstaki),
OS Bacillus thuringiensis (subsp. berliner), and
OS Bacillus thuringiensis (subsp. aizawai).
OC Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1434, 1433;
RN [1]
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RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RX MEDLINE=87163505; PubMed=3557124;
RA Geiser M., Schweitzer S., Grimm C.;
RT "The hypervariable region in the genes coding for entomopathogenic
RT crystal proteins of Bacillus thuringiensis: nucleotide sequence of
RT the kurhd1 gene of subsp. kurstaki HD1.";
RL Gene 48:109-118(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RA Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
RT "Cloning and nucleotide sequencing of two insecticidal delta-
RT endotoxin genes from Bacillus thuringiensis var. kurstaki HD-1 DNA.";
RL Agric. Biol. Chem. 51:455-463(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=NRD-12;
RA Hefford M.A., Brousseau R., Prefontaine G., Hanna Z., Condie J.A.,
RA Lau P.C.K.;
RT "Sequence of a lepidopteran toxin gene of Bacillus thuringiensis
RT subsp kurstaki NRD-12.";
RL J. Biotechnol. 6:307-322(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RX MEDLINE=86223796; PubMed=3011746;
RA Thorne L., Garduno F., Thompson T., Decker D., Zounes M., Wild M.,
RA Walfield A.M., Pollock T.J.;
RT "Structural similarity between the lepidoptera- and diptera-specific
RT insecticidal endotoxin genes of Bacillus thuringiensis subsp.
RT 'kurstaki' and 'israelensis'.";
RL J. Bacteriol. 166:801-811(1986).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=S93;
RA Silva-Werneck J.O., De-Souza M.T., Dias J.M.C.S., Ribeiro B.M.;
RT "Characterization of Bacillus thuringiensis subsp. kurstaki strain S93
RT effective against the Fall armyworm, Spodoptera frugiperda and cloning
RT of a cryIAB gene.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.berliner; STRAIN=1715;
RX MEDLINE=86300092; PubMed=3743328;
RA Wabiko H., Raymond K.C., Bulla L.A. Jr.;
RT "Bacillus thuringiensis entomocidal protoxin gene sequence and gene
RT product analysis.";
RL DNA 5:305-314(1986).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.berliner; STRAIN=1715;
RX MEDLINE=87054026; PubMed=3023091;
RA Hoeft H., de Greve H., Seurinck J., Jansens S., Mahillon J.,
RA Ampe C., Vandeckerckhove J., Vanderbruggen H., van Montagu M.,
RA Zabeau M., Vaeck M.;
RT "Structural and functional analysis of a cloned delta endotoxin of
RT Bacillus thuringiensis berliner 1715.";
RL Eur. J. Biochem. 161:273-280(1986).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=HD-133;
RA Chak K.-F., Jen J.C.;
RT "Complete nucleotide sequence and identification of a putative
RT promoter region for the expression in Escherichia coli of the cryIA(b)
RT gene from Bacillus thuringiensis var. aizawai HD133.";
RL Proc. Natl. Sci. Coun. Repub. China 17B:7-14(1993).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=IPL7;
RX MEDLINE=87248103; PubMed=3297927;
RA Oeda K., Oshie K., Shimizu M., Nakamura K., Yamamoto H., Nakayama I.,
RA Ohkawa H.;
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"Nucleotide sequence of the insecticidal protein gene of *Bacillus thuringiensis* strain aizawai IPL7 and its high-level expression in *Escherichia coli*.";  
Gene 53:113-119(1987).  
[10]  
SEQUENCE FROM N.A.  
SPECIES=B.t.aizawai; STRAIN=IC1;  
MEDLINE=89083518; PubMed=3205732;  
RA Halder M.Z., Ellar D.J.;  
RT "Nucleotide sequence of a *Bacillus thuringiensis* aizawai IC1 entomocidal crystal protein gene.";  
RL Nucleic Acids Res. 16:10927-10927(1988).  
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.  
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.  
CC -!- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in insect-resistant maize by Monsanto, Northrup King and Ciba Geigy.  
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.  
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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DR EMBL; M15271; AAA22561.1; -  
DR EMBL; M13898; AAA22330.1; -  
DR EMBL; M37263; AAA22420.1; -  
DR EMBL; M12661; AAA22613.1; -  
DR EMBL; AF059670; AAC64003.1; -  
DR EMBL; D00117; BAA00071.1; -  
DR EMBL; X04698; CAA28405.1; -  
DR EMBL; X54939; CAA38701.1; -  
DR EMBL; A09398; CAA00840.1; -  
DR EMBL; A03793; CAA00303.1; -  
DR EMBL; M16463; AAA22551.1; -  
DR EMBL; M13233; CAA31620.1; -  
DR PIR; JD0002; JD0002.  
DR PIR; S11446; S11446.  
DR PIR; S14555; S14555.  
DR PIR; A26461; A26461.  
DR PIR; A29838; A29838.  
DR PIR; A26513; A26513.  
DR PIR; S02134; S02134.  
DR HSSP; P02965; IC1V.  
DR InterPro; IPR001178; Endotoxin.  
DR Pfam; PF00555; endotoxin; 1.  
KW Toxin; Sporulation; Plasmid; Genetically modified food.  
FT CONFLICT 207 207 GS -> AL (IN REF. 4).  
FT CONFLICT 282 283 R -> P (IN REF. 4).  
FT CONFLICT 382 406 LKGGPPYKEAEP (IN REF. 4).  
FT FT 410 410 VLDGTEFYGTSSNLPFAVYKSGT -> GPDGGRICLWNL  
FT CONFLICT 430 432 L -> P (IN REF. 4).  
FT CONFLICT 437 437 LSH -> CLAY (IN REF. 4).  
FT CONFLICT 447 447 R -> Y (IN REF. 4).  
FT CONFLICT 450 450 I -> V (IN REF. 4).  
FT CONFLICT 450 450 A -> P (IN REF. 10).  
FT CONFLICT 452 458 MFSWHR -> NDSSWTYC (IN REF. 4).  
FT CONFLICT 461 461 E -> N (IN REF. 3).  
FT CONFLICT 463 465 NNI -> GDV (IN REF. 4).  
FT CONFLICT 479 486 STNLGSGT -> LQSLWN (IN REF. 4).  
FT CONFLICT 492 492 P -> L (IN REF. 4).  
FT CONFLICT 501 505 RTSP -> EELT (IN REF. 4).  
FT CONFLICT 537 537 F -> L (IN REF. 10).  
FT CONFLICT 542 542 D -> H (IN REF. 3).  
FT CONFLICT 545 545 T -> I (IN REF. 10).  
FT CONFLICT 568 568 P -> I (IN REF. 10).  
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FT CONFLICT 568 569 TV -> HL (IN REF. 3).  
FT CONFLICT 665 665 K -> E (IN REF. 3).  
FT CONFLICT 675 676 KR -> NG (IN REF. 3).  
FT CONFLICT 703 703 S -> N (IN REF. 4).  
FT CONFLICT 712 712 D -> H (IN REF. 4).  
FT CONFLICT 731 731 P -> L (IN REF. 7 AND 10).  
FT CONFLICT 785 785 P -> R (IN REF. 7 AND 10).  
FT CONFLICT 836 836 N -> I (IN REF. 3).  
FT CONFLICT 978 978 H -> Q (IN REF. 9).  
FT CONFLICT 1016 1016 E -> T (IN REF. 3).  
FT CONFLICT 1036 1036 C -> F (IN REF. 9).  
FT CONFLICT 1060 1060 E -> G (IN REF. 3).  
SQ SSEQUENCE 1155 AA; 130623 MW; 43461A64C7AC7CAF CRC64;  
Query Match 67.4%; Score 4211.5; DB 1; Length 1155;  
Best Local Similarity 70.0%; Pred. No. 3.4e-264;  
Matches 831; Conservative 83; Mismatches 228; Indels 45; Gaps 9;  
QY 1 MENNIO-NOCVPYNCLNPNVEILNEER-STGRPLDLSLRLFLSEFVPGVGAVGL 58  
DB 1 MDNPNINECIPNCLSNPEVVLGGERITGTTPDISLSLQFLSEFVPGAGFVGL 60  
QY 59 FDIWGFITPSDMSLFLQLEQLIEQRIETLERNRAITLRLGLADSYEYIEALREWEAN 118  
DB 61 VDIWGFIFGSPWDALFVQLEQLINQRIEFARNAQLISLGLSNLYQIYAESFREWEAD 120  
QY 119 PNAQILREDYRIRFANTDDALITAINFTLTSTFEIPLLSYVQAAANHLSLRDVAFSGQ 178  
DB 121 PTPALREEMRIQFNDKNSALTAIPLFAVONTQVPLLSYVQAAANHLSLRDVSVFGQ 180  
QY 179 GWGLDIAIVNHNINLINLTHRYTKHCLDTYNOGLNLTNTRTROMARENOFRDLTLTV 238  
DB 181 RWGFDATINSRYNDLTRIGNTDHVRWYNGLERWGPDSRWIRYNOFRDLTLTV 240  
QY 239 LDIVALFPNDYRTYPIQTSSQLTREIYTSVIEDSPVSAINPFGNRA---EFGVRRP 294  
DB 241 LDIVSLFPNDYRTYPIQTSSQLTREIYTVSLE---NFDGSPGSAQIEGSIKSP 294  
QY 295 HLMDFMNSLFTVTAETVRSQIVWGGH-LVSSRNTAGNRINFPISGVF-NFGGAIWADED 351  
DB 295 HLMDFMNSLFTVTAETVRSQIVWGGH-LVSSRNTAGNRINFPISGVF-NFGGAIWADED 351  
QY 352 PRPFYRTLSDPFVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNRSQITDLSDEIP 407  
DB 355 GQGVYRTLSSTLYRPPNIGINNOQLSVLDGTEFAVGTSSNLSAVYRKSGTVDLSDEIP 414  
QY 408 PQDSCAPNDYSHVLNHNFTVFWPGEISGDSWRAPMFSWTHRSATPTTIDPERITQI 467  
DB 415 PNNNVPPRQGFSHRLSHVSMFRSGFSNVSIIRAPMFSWTHRSATPTTIDPERITQI 474  
QY 468 PLVKAHTLOSSTVVRGPGFTGGDILRRSTSGGPFAYTIVNINQLPQRYEARIRYASTTN 527  
DB 475 PLTKSTNLGSGTSVVRGPGFTGGDILRRSTSGGPFAYTIVNINQLPQRYEARIRYASTTN 534  
QY 528 LRIYTVAGERIFAGFNKMTGDDPLTFOSFSYATINTAFTPPMSQSSFTGADTFSSG 587  
DB 535 LQPTSIDGRPINQGNFSAATMSSGSLNCGSFRTVGTFTTFFNFGSSSVFTLSAHFVNSG 594  
QY 588 NEYVIDRFELIPVATFEAYDLERAKAVNALFTINQIGIKTDYTDYHDIVSNLVC 647  
DB 595 NEYVIDRFELIPVATFEAYDLERAKAVNALFTINQIGIKTDYTDYHDIVSNLVC 654  
QY 648 LSDEFCLDEKRELSKVKHAKRLSDERNLLODPNFGINRQLDRGWRGSTDITIQGGDDV 707  
DB 655 LSDEFCLDEKRELSKVKHAKRLSDERNLLODPNFGINRQLDRGWRGSTDITIQGGDDV 714  
QY 708 FKENVYTLPGTDECYPTLYQKIDESKLPYTRYQLRGVIEDSQLELYLYRYNAKHET 767  
DB 715 FKENVYTLPGTDECYPTLYQKIDESKLPYTRYQLRGVIEDSQLELYLYRYNAKHET 774  
QY 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPOLDSCRDGKCAHSHHFLSDIDV 827  
DB 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPOLDSCRDGKCAHSHHFLSDIDV 808

QY 828 GCTDLNEDLDVWVIEFKIKTODGHARLGNLEFLLEKPLVUGALARKVRAEKKWRDKREKLE 887  
 DB 809 GCTDLNEDLCVWVIFKIKTODGHARLGNLEFLLEKPLVUGALARKVRAEKKWRDKREKLE 868  
 QY 888 LETNIVYKEAKESVDALFVNSQYDQADQNIAMIHAADRVRHRIREAYLPELSIVPGVN 947  
 DB 869 WETNIVYKEAKESVDALFVNSQYDQADQNIAMIHAADRVRHRIREAYLPELSIVPGVN 928  
 QY 948 VDFPEELKGRIFAPFLYDARNVKGDFNGLSCWNKGVHDVVEQNNHRSVLVVPWE 1007  
 DB 929 AALFELEGRIFTAFSLYDARNVKGDFNGLSCWNKGVHDVVEQNNHRSVLVVPWE 988  
 QY 1008 AYSQVQVRCVPGRGYILRVATYKGVGEGCVTHIEFNNTDELKFSNCVBEVYPPNVT 1067  
 DB 989 AYSQVQVRCVPGRGYILRVATYKGVGEGCVTHIEFNNTDELKFSNCVBEVYPPNVT 1048  
 QY 1068 CNDYTANQEEYGGAYTSRNRGYDETYGSNSVPADYASVYEKSYTDGRRDNPCESNRGY 1127  
 DB 1049 CNDYTATQEEYEGCTYTSRNRGYDGAYESNSVPADYASVYEKAYTDGRRDNPCESNRGY 1108  
 QY 1128 GDTPLPAGVYKLEYFPETDKVWIEIGETGTFIVDSVELLMEE 1174  
 DB 1109 GDTPLPAGVYKLEYFPETDKVWIEIGETGTFIVDSVELLMEE 1155

RESULT 12  
 C12A\_BACTX STANDARD; PRT; 1171 AA.  
 ID C12A\_BACTX  
 AC Q57458; Q03741;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin  
 CryIIa(a)) (crystalline entomocidal protoxin) (133 kDa crystal protein).  
 GN CRYIIA OR CRYIE(A) OR CRYIC(B) OR BTXI OR BTII.  
 OS Bacillus thuringiensis (subsp. kenyaee).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=33930;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91081338; PubMed=2259636;  
 RA Bosse M., Masson L., Brousseau R.;  
 RT "Nucleotide sequence of a novel crystal protein gene isolated from  
 RT Bacillus thuringiensis subspecies kenyaee";  
 RL Nucleic Acids Res. 18:7443-7443(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=4F1;  
 RX MEDLINE=91072224; PubMed=2254254;  
 RA Visser B., Munsterman E., Stoker A., Dirkse W.G.;  
 RT "A novel Bacillus thuringiensis gene encoding a Spodoptera exigua-  
 RT specific crystal protein";  
 RL J. Bacteriol. 172:6783-6788(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PS81F;  
 RA Payne J.M., Sick A.J.;  
 RT "Novel Bacillus thuringiensis isolate denoted B.t. PS81F, active  
 RT against lepidopteran pests, and a gene encoding a lepidopteran-active  
 RT toxin";  
 RL Patent number US039523, 13-AUG-1991.  
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE INCLUDING SPODOPTERA  
 CC SPECIES.  
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
 CC SPOROGATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
 CC OF THE SPORE COAT.  
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE  
 CC N-TERMINUS.  
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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 CC -----  
 DR EMBL; X56144; CAA39609.1; -;  
 DR EMBL; X53985; CAA37933.1; -;  
 DR EMBL; M73252; AAA22345.1; -;  
 DR HSSP; P02965; IC1Y.  
 DR InterPro; IPR001178; Endotoxin.  
 DR Pfam; PF00555; endotoxin; 1.  
 KW Toxin; Sporulation.  
 FT CONFLICT 862 N -> K (IN REF. 3).  
 SQ SEQUENCE 1171 AA; 133252 MW; 5758FBE5ABDB5ABE CRC64;  
 Query Match 66.8%; Score 4173; DB 1; Length 1171;  
 Best Local Similarity 69.1%; Pred. No. 1.le-261;  
 Matches 822; Conservative 103; Mismatches 223; Indels 42; Gaps 13;  
 QY 4 NIONQCVYPNCLNNPEVEILNEERSTGRPLDIDLSLTRFLLSEFFVGVGAFGLFLDIW 63  
 DB 5 NNONQCVYPNCLNNPENEILDIERSNSTVATNALEISR-LLASATPIGGILLGLFDAIW 63  
 QY 64 GEITPDSWSLFLQIEOLIEORLETLRNRAITLRLGLADSYETIIEALREWEANPNAQ 123  
 DB 64 GSIGPSOWDLFLQIEILLIDOKIEEFARNQAIKLEGISLYIYTAFAWEADPTNPA 123  
 QY 124 LREDVRIRFANTDDALITANNFTLSFEIPLLSVYVQAANLHLSILRDVAFQCGWGLD 183  
 DB 124 LKEEMRTQFNQDMSILVTAIPFSVQNVQVPLSVYVQAANLHLSVLRDVSFQAGWGD 183  
 QY 184 IAVNNHKLINLIHRYTKHCLDITYNQLENL-RGNTROWARFNFRDLTLTVLDIV 242  
 DB 184 IATINSRYNDLRLPIYTDYAVRWYNTGLDRLPRTGGLRNWARFNQFRRELATVSLDII 243  
 QY 243 ALFPNDVRYPIQTSSQLTREIYTSVIE--DSPVSANIPNGFNRAEFGVRPHLDFM 300  
 DB 244 SFRNVDRLYPIPTSQLPREYITDPIVNTIYRVGSPFENIENSA---IRSHLMDFL 300  
 QY 301 NSLFVTAETVRSQTVMGHVLVSSRNATAGN-IPNPSYGVFNPGGAIWADDPDP----- 354  
 DB 301 NNLITDILLRGVYHAGHRYVTSHTGSSQVITPQYGI-----TAAEPRTIAPS 352  
 QY 355 -----FYRTLSDPVEVRGFGFNPHVVLGL---RGVAFQOTGTNNHRTFNGSTIDSLD 404  
 DB 353 TFPGLNLFYRTLSPNPFRRSENITP--TLGINVQGVGFIQ-PNNAEVLVRSRGTVDSL 409  
 QY 405 EIPPDNSGAPWNDYSHVLNHTVVRKPGEISGDSWRAPMFSKWTBRSATNTIDPERI 464  
 DB 410 ELPIDGENSLV--GYSHRLSHVTLTR---SLYNTNITSLTFVWTHHSATNTINPDI 464  
 QY 465 TQPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPAYIVNINGQLPQRYARIYAS 524  
 DB 465 TQPLVKGFRLLGGTSVVKPGFTGGDILRNTIGEVSQVNSPITQRYLRFRYAS 524  
 QY 525 TTNLRIVTVAGERIFAGQPNKMTDGPDLTFQSFVSATINTAFTPFMSOSSFTVGADTF 584  
 DB 525 SRDARITVAIGQIRVDMTLEKMEIGESLTSRTSYTNSNPFSPRANPDIIRIAELP 584  
 QY 585 SSGNEVYIDREFLIPYTATAEVDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL 644  
 DB 585 IRGELYIDKIEILADATFEEDYDLERAQKAVNALFTSNQLGLKTDVTDYHIDQVSNL 644  
 QY 645 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINFQLDGRGWSGTDITQRG 704  
 DB 645 VECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINFQLDGRGWSGTDITQGG 704  
 QY 705 DDVFKENYVLPGTDECYPTIYLYQKIDESKLPYTRYQLRGYIEDSQDLEILYIRYNAK 764  
 DB 705 DDVFKENYVLPGTDECYPTIYLYQKIDESKLPYTRYQLRGYIEDSQDLEILYIRYNAK 764

```

leafroller (Lepidoptera, Tortricidae).";
New Zealand J. Crop Hortic. Sci. 20:27-36(1992).
[5]
SEQUENCE FROM N.A.
STRAIN=YET-1520;
Sun M., Yu Z.;
Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in
CC insect-resistant cotton and tomato by Calgene (Monsanto) and in
CC maize by Dekalb Genetics.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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[illegible]



Db 415 PQNNVPQROGFSRLSHVMSFRSGFNSVSIIRAPMFSWIHRSAEFNIIASDSTIQI 474  
 QY 468 PLVKAHTLQSGTTVVRPGTGGDILRRITSGGPFAYIVING-----QLP-----QRY 516  
 Db 475 PAVKGNFLNG-SWISGPGTGGDLVRLNNGN-----NIQNGEYIEVPIHFSTSTRY 527  
 QY 517 RARIRYASTNLRIYVTVAGERIFAGQFNKTMGTGDLTTFQSFYATINTAFTFPMQSS 576  
 Db 528 RVRVYASVTPHILNVNMGSSIFSNVTPATATSLDNLQSSDPCYFESANAFT---SSLG 584  
 QY 577 FTVGADTFSSGNEVYIDRFELIPVTAIFEAEDYLERAKAVNALFTSINQIGIKIDVTDY 636  
 Db 585 NIVGVNFSGTAGVILDRFEIPVTALEAEYNLERAKAVNALFTSTNQLGKINTYDY 644  
 QY 637 HIDQVSNLVCLSDFECLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGRGS 696  
 Db 645 HIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGRGS 704  
 QY 697 TDITIQRGDDVFKENYVTLPGTDECTPTLYQKIDSKLKPTRYQLRGYIEDSQBLEI 756  
 Db 705 TGITIQGGDDVFKENYVTLPGTDECTPTLYQKIDSKLKAFTRYQLRGYIEDSQBLEI 764  
 QY 757 YLIRYNAKHETVNVLGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSRDGEKCAH 816  
 Db 765 YLIRYNAKHETVNVGSLWPLSAQSPICGKEPNRCAPHLEWNPDLDCSRDGEKCAH 824  
 QY 817 HSHFSLDIDVGCTDLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAE 876  
 Db 825 HSHFSLDIDVGCTDLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAE 884  
 QY 877 KVRDRKREKLEETNIVYKAKESVDALFVNSQYDQLOADTNIAHAAKRVHRIREAY 936  
 Db 885 KVRDRKREKLEETNIVYKAKESVDALFVNSQYDQLOADTNIAHAAKRVHSIREAY 944  
 QY 937 LPESLVPVGNVDIFELKGRITAFPLXDARNVKNKDNGLSCWNVKGVHDVVEQNN 996  
 Db 945 LPESLVPVGNVAIFELKGRITAFPLXDARNVKNKDNGLSCWNVKGVHDVVEQNN 1004  
 QY 997 HRSVLVPEWEAEVQSVRVCPOGRIYLTAYKEGYGEGCVTIHETENNTDELKFSNCV 1056  
 Db 1005 QRSVLVPEWEAEVQSVRVCPOGRIYLTAYKEGYGEGCVTIHETENNTDELKFSNCV 1064  
 QY 1057 EEEVYNNVTQNDYFANQBEYGAITSNRNGYDETYGSSNPADYASVYEKSYTDGR 1116  
 Db 1065 EEEIYNNVTQNDYFANQBEYGAITSNRNGYDETYGSSNPADYASVYEKSYTDGR 1120  
 QY 1117 RNPCEENRGYDYPPLPAGYVTKLEYFPETDKVMEIGETGTFIVDSVLELLMEE 1174  
 Db 1121 RNPCEENRGYDYPPLPAGYVTKLEYFPETDKVMEIGETGTFIVDSVLELLMEE 1178  
 RESULT 14  
 C1DB.BACTU STANDARD; PRT; 1160 AA.  
 ID C1DB.BACTU  
 AC 045747;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Pesticidal crystal protein cryIb (Insecticidal delta-endotoxin  
 DE CryIb(b) (Crystalline entomocidal protoxin) (131 kDa crystal protein).  
 GN CRYIb OR CRYIb(B).  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxId=1428;  
 RN [1]  
 RC STRAIN=BTS0349A;  
 RP SEQUENCE FROM N.A.  
 RA Lambert B.;  
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPIHELIAL CELLS OF INSECTS.  
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
 CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.  
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE DELTA ENDOTOXIN IS LOCATED IN THE  
 CC N-TERMINUS.  
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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 CC -----  
 DR EMBL; 222511; CAA80234.1; -  
 DR HSSP; P02965; 1CIV.  
 DR InterPro; IPR001178; Endotoxin.  
 DR Pfam; PF00555; endotoxin; 1.  
 KW Toxin; Sporulation.  
 SQ SEQUENCE 1160 AA; 130968 MW; B18B18748B40695E CRC64;  
 Query Match 66.4%; Score 4146; DB 1; Length 1160;  
 Best Local Similarity 69.2%; Pred. No. 5.9e-260;  
 Matches 817; Conservative 98; Mismatches 238; Indels 28; Gaps 15;  
 QY 1 MENNIOQCVPYCNLNNPEVEILNEER-STGRPLPLDISLSTREFLLSEFPVGVGVAFLF 59  
 Db 1 MDINHQCIPYCNLSPDAILLDAERLETGNTVADISGLINFLYFNFGGFIYVGLL 60  
 QY 60 DLWGFPTPSWSLFLQIEQLIEQRIETLERNRAITTLRLGLADSYEYIEALREWNP 119  
 Db 61 ELIWGFVPSQWEIFLAQIEQLISORTTEFARQCAISRLGSLNNYIYETTFRAWEKDP 120  
 QY 120 NNAQLREDDVIRANTDDALITAINNETLTSFEPLISVYVQAAHLHLSDRAVSQGG 179  
 Db 121 SNPALREEMTQPNWMSALIAIPLLRVRYEALLSVYVQAAHLHLVLRDVSVYVQ 180  
 QY 180 WGLDIAFVNNHYNRLINLHRYTKHCLDTYNOGLELRTNTROWAFNFRRLDTLTVL 239  
 Db 181 WGDPAVTVNSRYSDTLRLIHVYTDHCVTDYNDGLKNLEGSRLSDWVYVNRRLTLISVL 240  
 QY 240 DIVALFPNVDVRYPIOTSSQLTREIYTSVIEDSPVS--ANIPNGFNRAEFG-VRPFHL 296  
 Db 241 DIIAFAFPNDIEAYPIQTASOLTREVYLDLPFVNETLSPASYPY-PSAAESAIRSPL 299  
 QY 297 MDMNSLFTVAEVRVSTVWGHLVSS--RNTAGNRINFFSYG-VFNPGGAIWIADEDR 353  
 Db 300 VDELSFTIITDLSAYYWGHLVNSFRGTGTTNLRISPLYREGTERPFTVISA 359  
 QY 354 PFYRTLSDPVFVRGGFNGPHYVLGRVAFQQTGTHNTRFRNSGTIDSLDETPPODNG 413  
 Db 360 PIFRTLS--YFT--GLNPNPVAGIEGVFQNTISR--SIYKSGPIDSELPQDVSV 413  
 QY 414 APWNDYSHVNLNHTVFWPCEIGSDSWRAPMFSWTHRSATPTNTIDPRTIOLPKAH 473  
 Db 414 SPAIGYSHRLCHATFLE---RISG-PRIAGTVFSWTHRSASPINEVSPSRITQIPVYKAH 469  
 QY 474 TLOGGTVVRGPGTGDILRRTSGGPFAYIVYINGQLPQRYRARIKRYASTNLRIYVT 533  
 Db 470 TLASGASVINGPGTGDILTRNSMGDLGALRVTFGRUPQSYIIRFRYASVANRSGTFR 529  
 QY 534 VAGERIFAGQFNKMTDGTPLTFQSFYSYATINTAFTFPMQSSFTVGDATFFSGNEVYID 593  
 Db 530 YSOPPSYGISFPKTMAGEALTSERFAHTLTFPIFSAQAEEDL---YIQSG--VYID 584  
 QY 594 RFELIPVTATFEAYEDLERAKAVNALFTSINQIGIKTDVTHYDQVSNLVCLDSEFC 653  
 Db 585 RIEFIPVDATFESEINLERAKAVNALFTSTNQLGLKTDVTHYDQVSNLVCLDSEFC 644  
 QY 654 LDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGRGSTDTIQRGDDVFKENY 713  
 Db 645 LDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGRGSTDTIQRGDDVFKENY 704  
 QY 714 TLPGTDECYPTLYQKIDSKLKPTRYQLRGYIEDSQBLEIYLRYNKAKHETVNLGT 773



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Db 705 TLTFDECYPTLYQKIDESKLKAYTYQLRGYIEDSQDLEIYLIRYNAKHEIVNPGT 764
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Db 765 GSLWPLSVQSPILRKGEFNRCPHLEWNPDLDCSCRDCEKCAHSHHFSLSLDIDVGCDDL 824
QY 834 EDLDVWVTFKIKTDQGHARLGNLEFLEKPLVGEALARKRAEKWRDKREKLELETNIV 893
Db 825 EDLGVWVTFKIKTDQGHARLGNLEFLEKPLVGEALARKRAEKWRDKREKLELETNIV 884
QY 894 YKEAKESVDALFVNSOYDQADTNIAHHAADKRVHRIEAYLPELSVIGVNDVIFEE 953
Db 895 YKEAKESVDALFVNSOYDQADTNIAHHAADKRVHRIEAYLPELSVIGVNDVIFEE 944
QY 954 LKGRIFTAFLLYDARNVKNGDFNGLSCWNVKGVHDVVEEQNNHRSVLVWPWEAEYSQE 1013
Db 945 LKGRIFTAFLLYDARNVKNGDFNGLSCWNVKGVHDVVEEQNNHRSVLVWPWEAEYSQE 1004
QY 1014 VRVCGRGYILRVATYKSGYGGCVTHIEIENNTDELKFSNCEBVEEYVNNVTTCNDYTA 1073
Db 1005 VRVCGRGYILRVATYKSGYGGCVTHIEIENNTDELKFSNCEBVEEYVNNVTTCNDYTA 1062
QY 1074 NOEGEGGYATSRNRYDETYGSSVVPADYASVYEEKSYTGDGRNDPNCESNRGYGDYTPL 1133
Db 1063 NKNHGANCSSNRGYDESYESSNSIPADYAPVYEEAYTDGQRNCPCEFFNRG---HTPL 1119
QY 1134 PAGYVTKLEYPPETDKVWIEGTEGTFIVDSVLELLMEE 1174
Db 1120 PAGYVTKLEYPPETDKVWIEGTEGTFIVDSVLELLMEE 1160

RESULT 15
ID C1CB_BACTG STANDARD: PRT: 1176 AA.
AC P56953;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cryIcb (insecticidal delta-endotoxin
DE CryIc(b)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).
GN CryIc(b) OR CryIc(b).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-29;
RX MEDLINE=93236401; PubMed=8476286;
RA Kalman S.S.;
RT "Cloning a novel cryIc-type gene from a strain of Bacillus
RT thuringiensis galleriae.";
RL Appl. Environ. Microbiol. 59:1131-1137(1993).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS. TOXIC TO SPODOPTERA EXIGUA AND
CC TRICHLIUSIA NI.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC DR EMBL: M97880; ; NOT_ANNOTATED_CDS.
CC DR HSP: P02965; 1C1Y.

```

```

DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1176 AA; 132867 MW; 108233494C2AC018 CRC64;

Query Match 66.2%; Score 4134; DB 1; Length 1176;
Best Local Similarity 68.3%; Pred. No. 3.6e-259;
Matches 819; Conservative 98; Mismatches 234; Indels 48; Gaps 15;

QY 1 MENNIOQCVPYCLNNEPVEILNEER-STGRPLPLDISLSLRFLESEFVPGVGVAFGLF 59
Db 1 MENNIOQCVPYCLNNEPVEILNEER-STGRPLPLDISLSLRFLESEFVPGVGVAFGLF 60
QY 60 DLWGTFTPSDWSLFLQLEQIELELRNRAITTLRGLADSEIYIEALREWEANP 119
Db 61 DFVWGVGPSDFDAFLVQIEQLINERIAAYARSAALNLEGLNENIYIEAFKEWADP 120
QY 120 NNAQLREDVRIRFANTDDALITAINNFTLTSPRIPLSVVVOAANLHLSLRDVAVSFGOG 179
Db 121 DNPVTRVVDREPRILDGLLERDIPSPERTAGFEVPLSVYACAAANLHLAILRDSIFGAR 180
QY 180 WGLDIATVNNHYNRLINLHRYTKHCLDYYNOGLEMLRGNTTQWARFNOFRDLTLVL 239
Db 181 WGLTTINNVNENYRLIRHIDYAHNCADTYNRLNLPKSTYQDWITYNLRDLTLVL 240
QY 240 DIVALPENVDVRYPIOTSSOLTRREIYTSVIEDSP---VSANIPNGFNRAEP-GVRPPH 295
Db 241 DIAAFPSYDNRRYPIQSVGLTREIYTDPLTFNFQOLASVAOLPT-FVWESNAIRTEH 299
QY 296 LMDFMNLSLFTAE--TVRSQTVMGHLSNRNTAGNRINFPSPSYGVNFGGAIWAIEDP- 352
Db 300 LEDVLNLTFTDWSVGRNRYGWHGRVINSRIGGNGNITSPIYG-----REANQEP 351
QY 353 -----RPFYRTLSDPVF--VRGFGNPHVYL-GLRGVAFQQTGCTNHTFRNSGIDSL 403
Db 352 RSFTNGFVFTLSNPTFLPQOPFAPPENLRGVGEVEF-STPLN-SFTYRGRTVDSL 409
QY 404 DEIPPODSGAPWNDXSHVLNHTVFRWPCGE---ISGDSWRAPMFSWTHRSATPTNTID 460
Db 410 TELPPEDNSVPPREGYSRHLCHATFVQRSCTPELTIG-----PVFSWTHRSATDNIY 463
QY 461 PERITQIPLKANTHLOGSTVVRGPGFTGGDIILRRSGGPPATVIVNINGQLPQRTARI 520
Db 464 PDVINQIPLKAFNLATSGTSVVRGPGFTGGDIIRTVNNGSVLSMSLNFSTTLQRYRVY 523
QY 521 RYASTTNLRIVTVVAGERIFAGOFNKMTDGTPLTFQSPSYATINTAFTPPMSQSFTVG 580
Db 524 RYASQTMVMSVTVGGSTTGCGFPSTMSANGALTQSFEFA-----EPVVISASGSQ 577
QY 581 ADTFSSGNEV-----YIDREFLIPVATFAEYDLERAQKAVNALFTSINQIGKIDVTD 635
Db 578 GASISNNVGRQMFHLDRIEFLPVTSTFEEDYDLERAQAVNALFTSTNQLGLKIDVTD 637
QY 636 YHIDQVSNLVDCLSDPECLDEKRELSKVKHAKRLSDERNLLQDPNFKGNOLDGRWRG 695
Db 638 YHIDQVSNLVECLSDPECLDEKRELSKVKHAKRLSDERNLLQDPNFRSTINGOLDGRWRG 697
QY 696 STDTIIRGDDVFKENYVTLFGTFDECYPYLYQKIDESKLKPYTRYQLRGYIEDSQDLE 755
Db 698 STDTIIRGDDVFKENYVTLFGTFDECYPYLYQKIDESKLKPYTRYQLRGYIEDSQDLE 757
QY 756 IYLIRYNAKHEIVNPGTGLSWPLSVQSPILRKGEFNRCPHLEWNPDLDCSCRDCEKA 815
Db 758 IYLIRYNAKHEIVNPGTGLSWPLSVQSPILRKGEFNRCPHLEWNPDLDCSCRDCEKA 817
QY 816 HSHHFSLDIDVGCDDLNEEDLVWVTFKIKTDQGHARLGNLEFLEKPLVGEALARKRA 875
Db 818 HSHHFSLDIDVGCDDLNEEDLVWVTFKIKTDQGHARLGNLEFLEKPLVGEALARKRA 877
QY 876 EKKWRDKREKLELETNIVTYKEAKESVDALFVNSOYDQADTNIAHHAADKRVHRIEA 935
Db 878 EKKWRDKREKLELETNIVTYKEAKESVDALFVNSOYDQADTNIAHHAADKRVHRIEA 937

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QY 936 YLPESVIPGVNVDIPEELKGRIFTAFFLYDARNVIKNGDFNNGLSQWNVKGVHDVVEQN 995
||||| 938 YLPESVIPGVNAGIFEELKGRIFTAYSLYDARNVIKNGDFNNGLLCWNLKGHDVVEQN 997
Db 938 YLPESVIPGVNAGIFEELKGRIFTAYSLYDARNVIKNGDFNNGLLCWNLKGHDVVEQN 997
QY 996 NHRSLVVPWEAEVSVQEVRCVPCRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNC 1055
Db 998 NHRSLVVPWEAEVSVQEVRCVPCRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNC 1057
QY 1056 VEEVYPNNITVTNDYTANQOEYGGAYTSRNGYDETYGSNSSVPADYASVYEEKSYTDG 1115
Db 1058 VEEVYPNNITVTNDYTATQEEYGGAYTSRNGYDETYGSNSSVQADYASVYEEKADTDG 1117
QY 1116 RRDNPESNRGYGDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174
Db 1118 RRDNPESNRGYGDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1176
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Search completed: November 27, 2002, 20:22:34  
Job time : 41 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 27, 2002, 18:33:24 ; Search time 54 seconds  
(without alignments)  
2090.034 Million cell updates/sec

Title: US-09-837-961-8  
Perfect score: 6244  
Sequence: 1 MENNIOQCVPYNCLNNPEV.....IGETEGTIVDSVELLMEE 1174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6244	100.0	1174	2 A42459	parasporal crystal
2	5406	86.6	1174	2 S32649	parasporal crystal
3	4424.5	70.9	1181	2 A41052	parasporal crystal
4	4342	69.5	1176	2 J0241	parasporal crystal
5	4329	69.3	1176	2 S02215	parasporal crystal
6	4328	69.3	1176	2 JC2219	parasporal crystal
7	4326	69.3	1176	2 A22617	parasporal crystal
8	4303	68.9	1166	2 S32645	parasporal crystal
9	4282.5	68.6	1165	2 S11446	parasporal crystal
10	4230.5	67.8	1172	2 S32689	parasporal crystal
11	4217.5	67.5	1189	2 S00944	parasporal crystal
12	4211.5	67.4	1155	2 JD0002	parasporal crystal
13	4194.5	67.2	1155	2 I39838	parasporal crystal
14	4191.5	67.1	1155	2 A26513	parasporal crystal
15	4189.5	67.1	1155	2 S02134	parasporal crystal
16	4186	67.0	1156	2 A29125	parasporal crystal
17	4173	66.8	1171	2 I40572	parasporal crystal
18	4151.5	66.5	1177	2 A49785	parasporal crystal
19	4148	66.4	1171	2 A37829	parasporal crystal
20	4148	66.4	1178	1 USBSXH	parasporal crystal
21	4146	66.4	1160	2 S32647	parasporal crystal
22	4134	66.2	1176	2 A48970	parasporal crystal
23	4037	64.7	1156	2 A29838	parasporal crystal
24	3465	55.5	1228	2 S00873	parasporal crystal
25	3120	50.0	934	2 A22798	parasporal crystal
26	2367.5	37.9	823	2 S04181	parasporal crystal
27	2129.5	34.1	1138	2 A48944	parasporal crystal
28	1947.5	31.2	1157	1 S49247	parasporal crystal
29	1850	29.6	1154	2 S39536	parasporal crystal

30 1685.5 27.0 1160 2 I40589 parasporal crystal  
31 1630.5 26.1 1156 2 S19306 parasporal crystal  
32 1519 24.3 1136 1 USBS81 parasporal crystal  
33 1515.5 24.3 655 2 JC7140 protoxin - Bacillu  
34 1495.5 24.0 1180 2 I39870 parasporal crystal  
35 1486.5 23.8 1180 2 A26858 parasporal crystal  
36 1368.5 21.9 618 2 S11445 parasporal crystal  
37 1367 21.9 719 2 I40590 cryV465 protein -  
38 1360 21.8 719 2 I39815 insecticidal prote  
39 1359 21.8 719 2 S25383 parasporal crystal  
40 1353 21.7 719 2 I39814 insecticidal prote  
41 898.5 14.4 652 2 I39811 parasporal crystal  
42 892.5 14.3 659 2 S10228 parasporal crystal  
43 883.5 14.1 652 2 A27323 parasporal crystal  
44 874.5 14.0 934 2 B29838 parasporal crystal  
45 802 12.8 649 1 JH0261 parasporal crystal

ALIGNMENTS

RESULT 1  
A42459  
parasporal crystal protein cryIFal - Bacillus thuringiensis (strain aizawai)  
N:Alternate names: parasporal crystal protein cryIF  
C:Species: Bacillus thuringiensis  
C:Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 01-Dec-2000  
C:Accession: A42459  
R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, J. Bacteriol. 173, 3966-3976, 1991  
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene  
A:Reference number: A42459; MUID:91286178; PMID:2061280  
A:Accession: A42459  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <CHA>  
A:Cross-references: GB:M63897; NID:gi42757; PIDN:AAA22348.1; PID:gi42758  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 100.0%; Score 6244; DB 2; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIOQCVPYNCLNNPEVEILNEERSTGRPLDLSLTRFLLSFVPGVGFGLFD 60  
Db 1 MENNIOQCVPYNCLNNPEVEILNEERSTGRPLDLSLTRFLLSFVPGVGFGLFD 60  
QY 61 LINGFITPDSWLSFLQIEQIETLERNRAITTLRGLADSYEYIIEALREWEANPN 120  
Db 61 LINGFITPDSWLSFLQIEQIETLERNRAITTLRGLADSYEYIIEALREWEANPN 120  
QY 121 NAQLREDVRIRFANTDDALITANNFTLTSTFEIPLLSVYVQAAANHLHLRLDAVSFGQGW 180  
Db 121 NAQLREDVRIRFANTDDALITANNFTLTSTFEIPLLSVYVQAAANHLHLRLDAVSFGQGW 180  
QY 181 GLDIATVNNHYNLNLHRYTHKCLDYNQGLENLGRTNQTWARPNQFRDLTLTFLD 240  
Db 181 GLDIATVNNHYNLNLHRYTHKCLDYNQGLENLGRTNQTWARPNQFRDLTLTFLD 240  
QY 241 IVALFPNDYVRTPIOTSSOLTREITTSVIEDSPYSANIPNGFNRAEFCVRPPLHMDFM 300  
Db 241 IVALFPNDYVRTPIOTSSOLTREITTSVIEDSPYSANIPNGFNRAEFCVRPPLHMDFM 300  
QY 301 NSLFVTAETVRSQTVGGHLYSSRNTAGNRINFPSTGYVFNPGGAIWIADEDDPPFYRTL 360  
Db 301 NSLFVTAETVRSQTVGGHLYSSRNTAGNRINFPSTGYVFNPGGAIWIADEDDPPFYRTL 360  
QY 361 DPVFVGGGNGNHYVGLRGVAFQQTGTNTRFRNSGTIDSLDEIPPDNSGAPNDYS 420  
Db 361 DPVFVGGGNGNHYVGLRGVAFQQTGTNTRFRNSGTIDSLDEIPPDNSGAPNDYS 420  
QY 421 HVLNHTVFEWPGCEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKATLQSGTT 480

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Db 421 HVLNHWTFVRWPGETISGDSWRAPMFSTHRSATPTNIDPERITQIPLVKAHTLQSGTT 480
Qy 481 VVRGPGETGDDTLRTSGGPFAYTIVNNGQLPQRYRIRYASTNLRIVTVAGERIF 540
Db 481 VVRGPGETGDDTLRTSGGPFAYTIVNNGQLPQRYRIRYASTNLRIVTVAGERIF 540
Qy 541 AGQFNKTMIDTGDPLTFQSFYSATINTAFTFPMSSQSFYTGADTFSSGNEVYIDREFELIPV 600
Db 541 AGQFNKTMIDTGDPLTFQSFYSATINTAFTFPMSSQSFYTGADTFSSGNEVYIDREFELIPV 600
Qy 601 TATFAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFECLDEKREL 660
Db 601 TATFAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFECLDEKREL 660
Qy 661 SEKVHAKRLSDERNLLQDPNPKGINRQLDRGWRGSDITITQGGDDVFKENYVTLPGTFD 720
Db 661 SEKVHAKRLSDERNLLQDPNPKGINRQLDRGWRGSDITITQGGDDVFKENYVTLPGTFD 720
Qy 721 EGYPTLYQKIDESKLPYTRQYLRGYIEDSDQLEIYLIRYNAKHETVNVLTGSLWPLS 780
Db 721 EGYPTLYQKIDESKLPYTRQYLRGYIEDSDQLEIYLIRYNAKHETVNVLTGSLWPLS 780
Qy 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
Db 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
Qy 841 IFKIKTQDGHARGLNLEFLEEKPLVGEALARVKRAKKWRDKREKLELETNIVYKEAKES 900
Db 841 IFKIKTQDGHARGLNLEFLEEKPLVGEALARVKRAKKWRDKREKLELETNIVYKEAKES 900
Qy 901 VDALFVNSQYDQLOADNTAMIAHADKRVHRIREAYLPELSVIPGVNVDIPEELGRIFT 960
Db 901 VDALFVNSQYDQLOADNTAMIAHADKRVHRIREAYLPELSVIPGVNVDIPEELGRIFT 960
Qy 961 AFFLYDARNVIRKNGDFNGLSCWNKGVHDVEEQNNHRSVLVVPWEAEVSEVRCVPCR 1020
Db 961 AFFLYDARNVIRKNGDFNGLSCWNKGVHDVEEQNNHRSVLVVPWEAEVSEVRCVPCR 1020
Qy 1021 GYLIRVTAYKEGEGCVTTHIEINNTDELKFSNCVBEVEYVNNVTCTNDYTANQEEYGG 1080
Db 1021 GYLIRVTAYKEGEGCVTTHIEINNTDELKFSNCVBEVEYVNNVTCTNDYTANQEEYGG 1080
Qy 1081 AYTSNRNGYDEYGSNSVPADYASVYEKSYTDGRRNCPNCSNRGYGDTPLPAGYVTK 1140
Db 1081 AYTSNRNGYDEYGSNSVPADYASVYEKSYTDGRRNCPNCSNRGYGDTPLPAGYVTK 1140
Qy 1141 ELEYPTOKVWIEIGETEGTIFVDSVELLMEE 1174
Db 1141 ELEYPTOKVWIEIGETEGTIFVDSVELLMEE 1174

```

## RESULT 2

S32649

paraspore crystal protein cryIpa3 - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C&gt;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S32649

R:Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645

A:Accession: S32649

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1174 &lt;LAW&gt;

A:Cross-references: EMBL:222512; NID:g295865; PIDN:CAA80235.1; PID:g295866

C:Superfamily: paraspore crystal protein

C:Keywords: delta-endotoxin

Query Match

Best Local Similarity 86.6%; Score 5406; DB 2; Length 1174;

Matches 1017; Conservative 60; Mismatches 95; Indels 4; Gaps 3;

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Qy 1 MENNIOQCVPYNCLNPEVEILNEERSTGRPLDLSLSLRELLSEFVPGVGVAGFLD 60
Db 1 MKNNIQOCVPYNCLNPEVEILNEERSTGRPLDLSLSLRELLSEFVPGVGVAGFLD 60
Qy 61 LINGFITPSDWSFLQIQEQLIEQRIETLERNRAITLRLGLADSYEIIYALREWZANPN 120
Db 61 LINGFITPSDWSFLQIQEQLIEQRIETLERNRAITLRLGLADSYEIIYALREWZANPN 120
Qy 121 NAOLREDVRIRFANTDALLITANNPTLTSFEIPLLSVYVQAANLHLSLLRDVAFSGQW 180
Db 121 NAOLREDVRIRFANTDALLITANNPTLTSFEIPLLSVYVQAANLHLSLLRDVAFSGQW 180
Qy 181 GLDIATVNNHYNLNLHRYTHKCHLDYVNGLENLGNINTRQWARPNFRRLDTITVLID 240
Db 181 GLDIATVNNHYNLNLHRYTHKCHLDYVNGLENLGNINTRQWARPNFRRLDTITVLID 240
Qy 241 IVALFPNVDYRTYPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRAEGVRPPLMDFM 300
Db 241 IVALFPNVDYRTYPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRAEGVRPPLMDFM 300
Qy 301 NSLFTAETVRSQTVMGCHLVSSRNTAGNRINFPYSYGVFNPGGAIWIADEDPRPFYRTLS 360
Db 301 NSLFTAETVRSQTVMGCHLVSSRNTAGNRINFPYSYGVFNPGGAIWIADEDPRPFYRTLS 360
Qy 361 DPVVRGFGNPNHVLGRLGVAFOQTGNTFRNRTFRSGTIDSLDEIPQDNSCAPNDYS 420
Db 361 DPVVRGFGNPNHVLGRLGVAFOQTGNTFRNRTFRSGTIDSLDEIPQDNSCAPNDYS 420
Qy 421 HVLNHWTFVRWPGETISGDSWRAPMFSTHRSATPTNIDPERITQIPLVKAHTLQSGTT 480
Db 421 HVLNHWTFVRWPGETISGDSWRAPMFSTHRSATPTNIDPERITQIPLVKAHTLQSGTT 480
Qy 481 VVRGPGETGDDTLRTSGGPFAYTIVNNGQLPQRYRIRYASTNLRIVTVAGERIF 540
Db 481 VVRGPGETGDDTLRTSGGPFAYTIVNNGQLPQRYRIRYASTNLRIVTVAGERIF 540
Qy 541 AGQFNKTMIDTGDPLTFQSFYSATINTAFTFPMSSQSFYTGADTFSSGNEVYIDREFELIPV 600
Db 541 AGQFNKTMIDTGDPLTFQSFYSATINTAFTFPMSSQSFYTGADTFSSGNEVYIDREFELIPV 600
Qy 601 TATFAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFECLDEKREL 660
Db 601 TATFAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFECLDEKREL 660
Qy 661 SEKVHAKRLSDERNLLQDPNPKGINRQLDRGWRGSDITITQGGDDVFKENYVTLPGTFD 720
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Qy 721 EGYPTLYQKIDESKLPYTRQYLRGYIEDSDQLEIYLIRYNAKHETVNVLTGSLWPLS 780
Db 721 EGYPTLYQKIDESKLPYTRQYLRGYIEDSDQLEIYLIRYNAKHETVNVLTGSLWPLS 780
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Db 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
Qy 841 IFKIKTQDGHARGLNLEFLEEKPLVGEALARVKRAKKWRDKREKLELETNIVYKEAKES 900
Db 841 IFKIKTQDGHARGLNLEFLEEKPLVGEALARVKRAKKWRDKREKLELETNIVYKEAKES 900
Qy 901 VDALFVNSQYDQLOADNTAMIAHADKRVHRIREAYLPELSVIPGVNVDIPEELGRIFT 960
Db 901 VDALFVNSQYDQLOADNTAMIAHADKRVHRIREAYLPELSVIPGVNVDIPEELGRIFT 960
Qy 961 AFFLYDARNVIRKNGDFNGLSCWNKGVHDVEEQNNHRSVLVVPWEAEVSEVRCVPCR 1020
Db 961 AFFLYDARNVIRKNGDFNGLSCWNKGVHDVEEQNNHRSVLVVPWEAEVSEVRCVPCR 1020
Qy 1021 GYLIRVTAYKEGEGCVTTHIEINNTDELKFSNCVBEVEYVNNVTCTNDYTANQEEY 1078
Db 1021 GYLIRVTAYKEGEGCVTTHIEINNTDELKFSNCVBEVEYVNNVTCTNDYTANQEEY 1078
Qy 1079 GGAYTSNRNGYDEYGSNSVPADYASVYEKSYTDGRRNCPNCSNRGYGDTPLPAGYV 1138

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Db 1079 TDCNVANRGEDAYGHNPTVHYTTPYEETVYDERRNPCEANKGYNYTLPVGYV 1138  
QY 1139 TKELEYFPETDKVWIEGTEGTFIVDSVLLMEE 1174  
Db 1139 TKELEYFPETDVWIEGTEGTFIVDSVLLMEE 1174  
RESULT 3  
A41052  
parasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)  
C:Species: Bacillus thuringiensis  
C:Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 01-Dec-2000  
C:Accession: A41052  
R;Lee, C.S.; Aronson, A.I.  
J. Bacteriol. 173, 6635-6638, 1991  
A:Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp  
A:Reference number: A41052; MUID:92011442; PMID:1655719  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1161 <LE>  
A:Cross-references: GB:M65252; NID:g142874; PIDN:AAA22410.1; PID:g142875  
C:Superfamily: Parasporal crystal protein  
C:Keywords: delta-endotoxin  
Query Match 70.9%; Score 4424.5; DB 2; Length 1181;  
Best Local Similarity 72.1%; Pred. No. 7.4e-280;  
Matches 857; Conservative 93; Mismatches 216; Indels 23; Gaps 9;  
QY 1 MENNIO-NOCVPYNCLNPNPEVILNEER-STGRPLDLSLTRLFLSEFVPGVAFGL 58  
Db 1 MDNPNKINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSLQFLLSEFVPGAGFVLG 60  
QY 59 FDLIWFITPDSNLSFLQLEQIEQRIETLERNRAITIRGLADSEYIIEALREWEAN 118  
Db 61 IDLIWFGVPSQWDAFLVQLEQISRIEFAFARQAISRLGLESLNYQIYAEAFREWEAD 120  
QY 119 PNAQLREDVRIRFANTDDALITAINFTLTSFEIPLSVYVQAAHLHLILLRDVAFSG 178  
Db 121 PTPALREEMRIQFNDMNSALTATPFTVQNVQVPLSVYVQAVNLHLVLRLDVSVFG 180  
QY 179 GWGLDIATVNNHRLNLHRYTKHCLDTYNOGLELRTNQWARFNQFRDLALT 238  
Db 181 RWGLDVATINSRYNDLRLCTGYDAVRMYNGLERWVGPDSDRYNQFRDLALT 240  
QY 239 LDIVALFPNDVRYTPLOTSSQLTREIYTSVIEDSPVSNIPNFGNRAEFGVRPHLMD 298  
Db 241 LDIVLFPNDVRYTPLOTSSQLTREIYTNVLEN--FDGSRGSAQRIEQSIRSPHMD 298  
QY 299 FMNSLFTAEVRSQVTWGGH--LVSSRNATAGNRINPSPYGVF-NPGGAIWIADEDPRPF 355  
Db 299 ILNSIITYTDAHGYYWWSHQIMASPVGSGEFPFLYGTWGNAPQORIVQAOLCGV 358  
QY 356 YRLSDPVPVVRGEGFNHYVLGRG-----VAFOQTGNHTFRFNSGTIDSLDE 405  
Db 359 YRTLSS-TFYR---NP-FIIGINNQLSLVDGTEFAFGSSNLPASVAYKRGVGVDSLDE 412  
QY 406 IPQDASGAPWNDYSHVLNHTVFRNPEGEISGDSWRAPMFSWTHRSATNTIDPRIT 465  
Db 413 IPQDNNVPQROGFSHRLSVMSFRSGFSNVSYSITRAPMFSWIHRSAEFNIPSSQIT 472  
QY 466 QIPLVRAHTLQSGTIVYRGFGGDTLRTSGPPAYTTVNNINGQLPQRYRARIRYAST 525  
Db 473 QIPLTSTNLGSGTSVVGKFGGDTLRTSPQISTLRVNTAPLSQRYRIRYAST 532  
QY 526 TNLRIYVTVAGERIFAGQFNKMTDGLPFTQSPFSYATINTAFTFPMSSQSFTVGADTF 585  
Db 533 TNLQFHTSIDGRPINQGNFSAATSSGGNLSQSGSFRVGTFTPFNFSSNGSVFTLSAHVN 592  
QY 586 SGNEVIDRELIPVTATFAEDYDLERAQAVNALFTSINQIGIKTDVTDYHIDQVSNLV 645  
Db 593 SGNEVIDRIEFVPAEYFDLERAQAVNALEFTSPNQIGIKTDVTDYHIDQVSNLV 652

QY 646 DCLSDFECLDEKRELSKVHAKRLSDERNLLQDPNFKGINRDLRGWRGSTDITIIQRGD 705  
Db 653 ECLSDFECLDEKRELSKVHAKRLSDERNLLQDPNFKGINRDLRGWRGSTDITIIQGGD 712  
QY 706 DVPKENVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSOOLEIYLIRYNAKH 765  
Db 713 DVPKENVTLPGTFDECYPTLYQKIDESKLKAYTRYELRGYIEDSQDLEIYLIRYNAKH 772  
QY 766 ETYNVLGTSGIWPISVQSPIKCGEPNRCAPHLNPNPDLCSDRGDKCAHSHHFLSDI 825  
Db 773 ETYNVPGTSLWPLSFESSIGKCGEPNRCAPHLNPNPDLCSDRGDKCAHSHHFLSDI 832  
QY 826 DVGCTDLNEDLDVWVIFIKITQDGHARLGNLEFLPEEPLVGEALARYKRAKRWDRKREK 885  
Db 833 DVGCTDLNEDLDVWVIFIKITQDGHARLGNLEFLPEEPLVGEALARYKRAKRWDRKREK 892  
QY 886 LELETNIVYKEAKESVDALFVNSOYDQLOADNTIAMIAADKRVHRIEAYLPESLVP 945  
Db 893 LQLETNIVYKEAKESVDALFVNSOYDQLOADNTIAMIAADKRVHRIEAYLPESLVP 952  
QY 946 VNYDIEELKGRIFTAPFLYDARNVIKNGDFNGLSCWNVKGVHDVBEQNNHRSVLVPE 1005  
Db 953 VNAGIFEELEGRIFTAVSLYDARNVIKNGDFNGLSCWNVKGVHDVBEQNNHRSVLVPE 1012  
QY 1006 WEAEVSOEVRVCPGRGYILRVATYKEGYGCGCVTHIENNTDELKFSNCVVEEYVNPNT 1065  
Db 1013 WEAEVSOEVRVCPGRGYILRVATYKEGYGCGCVTHIENNTDELKFSNCVVEEYVNPNT 1072  
QY 1066 VTCNDYTANQEEGGAYTSNRNGYDETYGSSVSPADYASVYEKSYTDGRRDPCESNR 1125  
Db 1073 VTCNXYTANQEEGGAYTSNRNGYDETYGSSVSPADYASVYEKSYTDGRRDPCESNR 1132  
QY 1126 GYGDYTPPLPAGYVTKLEYFPETDKVWIEGTEGTFIVDSVLLMEE 1174  
Db 1133 GYGDYTPPLPAGYVTKLEYFPETDKVWIEGTEGTFIVDSVLLMEE 1181  
RESULT 4  
JT0241  
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
N:Alternate names: 135K insecticidal protein  
C:Species: Bacillus thuringiensis  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 01-Dec-2000  
C:Accession: JT0241  
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
Agric. Biol. Chem. 52, 1565-1573, 1988  
A:Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal prote  
A:Reference number: JT0241  
A:Accession: JT0241  
A:Molecule type: DNA  
A:Residues: 1-1176 <SHI>  
C:Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal pro  
C:Comment: The 135K protein has insecticidal activity against Plutella xylostella lar  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin  
Query Match 69.5%; Score 4342; DB 2; Length 1176;  
Best Local Similarity 71.5%; Pred. No. 1.7e-274;  
Matches 852; Conservative 86; Mismatches 221; Indels 32; Gaps 12;  
QY 1 MENNIO-NOCVPYNCLNPNPEVILNEER-STGRPLDLSLTRLFLSEFVPGVAFGL 58  
Db 1 MDNPNKINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSLQFLLSEFVPGAGFVLG 60  
QY 59 FDLIWFITPDSNLSFLQLEQIEQRIETLERNRAITIRGLADSEYIIEALREWEAN 118  
Db 61 IDLIWFGVPSQWDAFLVQLEQISRIEFAFARQAISRLGLESLNYQIYAEAFREWEAD 120  
QY 119 PNAQLREDVRIRFANTDDALITAINFTLTSFEIPLSVYVQAAHLHLILLRDVAFSG 178  
Db 121 PTPALREEMRIQFNDMNSALTATPFTVQNVQVPLSVYVQAVNLHLVLRLDVSVFG 180

QY 179 GGLDIATVNNHYNRLINLIHRYTKHCLDYYNOGLENLRGNTNQWAFENQFRRLDITLV 238  
 Db 181 RWGFAAATINSYNDLRLTGLNNTDYAVRWYNTGLERVWGPDSRWYRINQFRRLDITLV 240  
 QY 239 LDIVALFPMNDVRYTPYIOTSSOLTREITSSVIEDSPVSANIPNGF---NRAEFGVRPP 294  
 Db 241 LDIVALFPMNDVRYTPYIOTSSOLTREITSSVIEDSPVSANIPNGF---NRAEFGVRPP 294  
 QY 295 HLMDFMNSLFTVTAETVRSQTVWGGHLSVR--NTAGNRINPFSYGVENPGGAI--WIADE 350  
 Db 295 HLMDFMNSLFTVTAETVRSQTVWGGHLSVR--NTAGNRINPFSYGVENPGGAI--WIADE 350  
 QY 351 DRPPYRILSDPVFVR-----GGFNGPHYVLGRVAFQQTGNTNRT--FRNSGTIDSLD 404  
 Db 353 TGLGIFRTLSPLRYRIILGSGPNNOELFVLDGTEFASLTNLPSTIYRQGVVDSLD 412  
 QY 405 EIPPDNSGAPWNDYSHVLNHTVFRWPGETSGS--DSMRAPMFSWTHRSATPTNIDPER 463  
 Db 413 VIPPDNSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFSWQHSRAEFNNIPSSQ 469  
 QY 464 ITQIPLVKAHTIQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYA 523  
 Db 470 ITQIPLVKAHTIQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYA 523  
 QY 524 STTNLRIVTVAGERIFAGQNKMTMDGDLTFFQSFYATINTAFTFMSQSSFTVGADT 583  
 Db 530 STTNLRIVTVAGERIFAGQNKMTMDGDLTFFQSFYATINTAFTFMSQSSFTVGADT 583  
 QY 584 FSSGNEVYIDRFELIPVTATFEAYDLERAKAYNALTSINQIGIKTDVTDYHIDQVSN 643  
 Db 590 FNSGNEVYIDRFELIPVTATFEAYDLERAKAYNALTSINQIGIKTDVTDYHIDQVSN 649  
 QY 644 LVDCLSDEFCLDERKELSEKVKHAKRLSDERNLLQDPNFKGINRQDLGRWGSTDITQ 703  
 Db 650 LVDCLSDEFCLDERKELSEKVKHAKRLSDERNLLQDPNFKGINRQDLGRWGSTDITQ 709  
 QY 704 GDDVFKENYVTLPGTDFECYPTLYQKIDESKLPYTRYOLRGYVIEDSQLEIYLIRYNA 763  
 Db 710 GDDVFKENYVTLPGTDFECYPTLYQKIDESKLPYTRYOLRGYVIEDSQLEIYLIRYNA 769  
 QY 764 KHTVNVLTGSLWPLSAQSPICKGEPNRCAPHLENNPDLDCSCRGECAHSHHFSL 823  
 Db 770 KHTVNVLTGSLWPLSAQSPICKGEPNRCAPHLENNPDLDCSCRGECAHSHHFSL 829

RESULT 5  
 S02215

parasporal crystal protein cryA - *Bacillus thuringiensis* (strain entomocidus)  
 C:Species: *Bacillus thuringiensis*

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 01-Dec-2000  
 C:Accession: S02215  
 R:Masson, L.; Marcotte, P.; Prefontaine, G.; Brousseau, R.  
 Nucleic Acids Res. 17, 446, 1989  
 A:Title: Nucleotide sequence of a gene cloned from *Bacillus thuringiensis* subspecies  
 A:Reference number: S02215; MUID:89098405; PMID:2911478  
 A:Accession: S02215  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1176 <MAS>  
 A:Cross-references: EMBL:X13535; NID:g40266; PIDN:CAA31886.1; PID:g40267  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 69.3%; Score 4329; DB 2; Length 1176;

Best Local Similarity 71.4%; Pred. No. 1.2e-273;

Matches 850; Conservative 86; Mismatches 223; Indels 32; Gaps 12;

QY 1 MENNIQ-NOCVPYNCLNNPEVEILNEER-STGRLLDLIDLSLTRLLSEFPVGVGATGL 58  
 Db 1 MDNPNINECIPNCLSNPEVEVLGGERIEGTYPIDISLSTQFLLEFPVAGFVLGL 60  
 QY 59 FDLWGFITPDSWLSFLQIQIEQRIETLERNRAITTLRGLADSYEITYEALREWEAN 118  
 Db 61 VDIWIGFPGSQWDAPFVQIEQLINQRIEETARQAISLECLSNLYQIYAESFREWAD 120  
 QY 119 PNNQRLREDVRIRANTDDALITANNFTLSFEIPLSVYVQAANHLSLRLDVSFGQ 178  
 Db 121 PTNPALEEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANHLSLRLDVSFGQ 180  
 QY 179 GWWGLDIAVNNHYNRLINLIHRYTKHCLDYYNOGLENLRGNTNQWAFENQFRRLDITLV 238  
 Db 181 RWGFAAATINSYNDLRLTGLNNTDYAVRWYNTGLERVWGPDSRWYRINQFRRLDITLV 240  
 QY 239 LDIVALFPMNDVRYTPYIOTSSOLTREITSSVIEDSPVSANIPNGF---NRAEFGVRPP 294  
 Db 241 LDIVALFPMNDVRYTPYIOTSSOLTREITSSVIEDSPVSANIPNGF---NRAEFGVRPP 294  
 QY 295 HLMDFMNSLFTVTAETVRSQTVWGGHLSVR--NTAGNRINPFSYGVENPGGAI--WIADE 350  
 Db 295 HLMDFMNSLFTVTAETVRSQTVWGGHLSVR--NTAGNRINPFSYGVENPGGAI--WIADE 350  
 QY 351 DRPPYRILSDPVFVR-----GGFNGPHYVLGRVAFQQTGNTNRT--FRNSGTIDSLD 404  
 Db 353 TGLGIFRTLSPLRYRIILGSGPNNOELFVLDGTEFASLTNLPSTIYRQGVVDSLD 412  
 QY 405 EIPPDNSGAPWNDYSHVLNHTVFRWPGETSGS--DSMRAPMFSWTHRSATPTNIDPER 463  
 Db 413 VIPPDNSVPPRAGFSHRLSHVTML---SQAAGAVYTLRAPTFSWQHSRAEFNNIPSSQ 469  
 QY 464 ITQIPLVKAHTIQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYA 523  
 Db 470 ITQIPLVKAHTIQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYA 529  
 QY 524 STTNLRIVTVAGERIFAGQNKMTMDGDLTFFQSFYATINTAFTFMSQSSFTVGADT 583  
 Db 530 STTNLRIVTVAGERIFAGQNKMTMDGDLTFFQSFYATINTAFTFMSQSSFTVGADT 589  
 QY 584 FSSGNEVYIDRFELIPVTATFEAYDLERAKAYNALTSINQIGIKTDVTDYHIDQVSN 643  
 Db 590 FNSGNEVYIDRFELIPVTATFEAYDLERAKAYNALTSINQIGIKTDVTDYHIDQVSN 649  
 QY 644 LVDCLSDEFCLDERKELSEKVKHAKRLSDERNLLQDPNFKGINRQDLGRWGSTDITQ 703  
 Db 650 LVDCLSDEFCLDERKELSEKVKHAKRLSDERNLLQDPNFKGINRQDLGRWGSTDITQ 709  
 QY 704 GDDVFKENYVTLPGTDFECYPTLYQKIDESKLPYTRYOLRGYVIEDSQLEIYLIRYNA 763  
 Db 710 GDDVFKENYVTLPGTDFECYPTLYQKIDESKLPYTRYOLRGYVIEDSQLEIYLIRYNA 769  
 QY 764 KHTVNVLTGSLWPLSAQSPICKGEPNRCAPHLENNPDLDCSCRGECAHSHHFSL 823  
 Db 770 KHTVNVLTGSLWPLSAQSPICKGEPNRCAPHLENNPDLDCSCRGECAHSHHFSL 829

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QY 824 DIDVGCDDLNEEDLVWVIFIKITODGHARLGNLEFLEKPLVGEALARKVKAEEKWRDKR 883
D 830 DIDVGCDDLNEEDLVWVIFIKITODGHARLGNLEFLEKPLVGEALARKVKAEEKWRDKR 889
QY 884 EKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHAAKRVHRIREAYLPELSVI 943
D 890 EKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHAAKRVHRIREAYLPELSVI 949
QY 944 PGVNVDIFEELKGRIFTAFILYDARNVKNKGNGLSCWNVKGVHDVEEQNNHRSVLV 1003
D 950 PGVNAALFEELKGRIFTAFILYDARNVKNKGNGLSCWNVKGVHDVEEQNNHRSVLV 1009
QY 1004 PEWEAEYSQEVRCVPCRGYILRVTAKEGYGEGCVTTHIEINNTDELKFSNCVEEYVFN 1063
D 1010 PEWEAEYSQEVRCVPCRGYILRVTAKEGYGEGCVTTHIEINNTDELKFSNCVEEYVFN 1069
QY 1064 NTVTCNDYTANOEYGGAYTSRNGYDETYGNSVADYASVYEKSYTDGRDNPCES 1123
D 1070 NTVTCNDYTANOEYGGAYTSRNGYDETYGNSVADYASVYEKSYTDGRDNPCES 1125
QY 1124 NRGYDTPPLPAGVYVTKLEYFPETDKVWIEIGTEGTFIVDSVELLMEE 1174
D 1126 NRGYDTPPLPAGVYVTKLEYFPETDKVWIEIGTEGTFIVDSVELLMEE 1176

RESULT 6
JC2219
parasporal crystal protein cryIAa - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C:Accession: JC2219
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
Biosci. Biotechnol. Biochem. 58, 830-835, 1994
A:Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an
A:Reference number: JC2219; MUID:94289859; PMID:7764972
A:Accession: JC2219
A:Molecule type: DNA
A:Residues: 1-1176 <UDA>
A:Cross-references: DDBJ:D17518; NID:g506190; PIDN:BA04468.1; PID:g535781
C:Genetics:
A:Gene: cryIA(a)
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 69.3%; Score 4328; DB 2: Length 1176;
Best Local Similarity 71.4%; Pred. No. 1.4e-273;
Matches 850; Conservative 86; Mismatches 223; Indels 32; Gaps 12;

QY 1 MENNIQ-NQCVPYNCLNPEVEILNEER-STGRPLDLSLTLRFLSEFVPGVGVAFGL 58
D 1 MDNPNINECIPYNCLSNPEVGLGERIETGYTPIDISLSLTQFLSEFVPGGVGL 60
QY 59 FDLTWGFTPSDWSLFLQLEQRIETLERNAITTLRGLADSYEYIEALREHNEAN 118
D 61 VDIWIGFGPSQMDAFVLQLEQINRIEFAFNQAISRLGLESLNLYQIYAESFREWAD 120
QY 119 PNAQREDVRIRFANTDDALITAINFTTSPEIPLLSVYVQAANLHSLRLDVAESFG 178
D 121 PTPALREEMRIQFNDMNSALITPAIPALVQNYQVPLSVYVQAANLHSLRLDVSVFG 180
QY 179 GWGLDIATVNNHRLNLHRYTKHCLDTYNOGLRGTNTQWAFRQFRDLTLTV 238
D 181 RWGFDAAATINSYNDLRLIGNTYDAVWYNTGLRWGPDSDRWYRQFRDLTLTV 240
QY 239 LDIVALEPNDVRYPTQTSOLTRREYTSVIEDSPVSANIPNGF----NRAEFGVRPP 294
D 241 LDIVALEFNSDRIYRTYTSOLTRREYTSVIEDSPVSANIPNGF----NRAEFGVRPP 294
QY 295 HLMDFMNSLVTAETVRSQVFWGSHLYSSR--NTAGNRINFPSPGVFNPGGAI--WIADE 350
D 295 HLMDFMNSLVTDVHRGFNWSHQITASPVGFSGPEFAPPLFG--NAGNAAPPLVL 352
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QY 351 DPRPFYRTLSDPVFR-----GGFGNPHYVLGRVAFQQTGNHTRT-FRNSGTDISLD 404
D 353 TGLGIFRTLSPLRYRILILGSPNNQELFVLDGTEFSASLTNTLPSTIYIQRGVDSLD 412
QY 405 EIPQDNSGAFWNDYSVHLNHTFVRNPFGEISGS--DSWRAPMFMSWTHRSATPTTIDPER 463
D 413 VIPQDNSVPRAGFSHRLSHVTML--SQAAGAVYTLRAFTSQWHSRAEFNNIIPSSQ 469
QY 464 ITQIPLVKAHTLQSGTTVVVRGPGTGGDILRRTSGGPPAYTIVNINGQLPORYRARIYA 523
D 470 ITQIPLTKSNLGSSTSVKPGTGGDILRRTSGGISTLRVNTITAPLSORYRARIYA 529
QY 524 STTNLRIVTVAGRIIRFAGQFNKMTDGTPLTFOSFVSATINTAFTFPMSSOSTVAGDT 583
D 530 STTNLRQPHTSIDGRPIINQGNFSATMSSGNSLQSGSFRVTGTTTFFNFGSNGSVFTLSAHV 589
QY 584 PSSNEVYIDFELIPVATFAEYDLERAKAVNALFTSINOIGIKTDVDYHIDQVSN 643
D 590 FNSGNEVYIDRIEFVPAEVTFAEYDLERAKAVNELFTSSNQIGLKTDDVTDYHIDQVSN 649
QY 644 LVDCLSDFECLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDGRGWGSDTITQR 703
D 650 LVECLSDFECLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDGRGWGSDTITQ 709
QY 704 GDDVFKENYVTLPGTFDECYTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRNA 763
D 710 GDDVFKENYVTLPGTFDECYTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRNA 769
QY 764 KHEVNVVLGTGSLWPLSVQSPDKGPNRCAPHLENNPDLDCSROGCEKCAHSHHFS 823
D 770 KHEVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLENNPDLDCSROGCEKCAHSHHFS 829
QY 824 DIDVGCDDLNEEDLVWVIFIKITODGHARLGNLEFLEKPLVGEALARKVKAEEKWRDKR 883
D 830 DIDVGCDDLNEEDLVWVIFIKITODGHARLGNLEFLEKPLVGEALARKVKAEEKWRDKR 889
QY 884 EKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHAAKRVHRIREAYLPELSVI 943
D 890 EKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHAAKRVHRIREAYLPELSVI 949
QY 944 PGVNVDIFEELKGRIFTAFILYDARNVKNKGNGLSCWNVKGVHDVEEQNNHRSVLV 1003
D 950 PGVNAALFEELKGRIFTAFILYDARNVKNKGNGLSCWNVKGVHDVEEQNNHRSVLV 1009
QY 1004 PEWEAEYSQEVRCVPCRGYILRVTAKEGYGEGCVTTHIEINNTDELKFSNCVEEYVFN 1063
D 1010 PEWEAEYSQEVRCVPCRGYILRVTAKEGYGEGCVTTHIEINNTDELKFSNCVEEYVFN 1069
QY 1064 NTVTCNDYTANOEYGGAYTSRNGYDETYGNSVADYASVYEKSYTDGRDNPCES 1123
D 1070 NTVTCNDYTANOEYGGAYTSRNGYDETYGNSVADYASVYEKSYTDGRDNPCES 1125
QY 1124 NRGYDTPPLPAGVYVTKLEYFPETDKVWIEIGTEGTFIVDSVELLMEE 1174
D 1126 NRGYDTPPLPAGVYVTKLEYFPETDKVWIEIGTEGTFIVDSVELLMEE 1176

RESULT 7
A22617
parasporal crystal protein cryIAa - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 01-Dec-2000
C:Accession: A22617
R:Schnepf, H.E.; Wong, H.C.; Whiteley, H.R.
J. Biol. Chem. 260, 6264-6272, 1985
A:Title: The amino acid sequence of a crystal protein from Bacillus thuringiensis ded
A:Reference number: A22617; MUID:85207613; PMID:2581950
A:Accession: A22617
A:Molecule type: DNA
A:Residues: 1-1176 <SCH>
A:Cross-references: GB:M11250; NID:g142764; PIDN:AAA22353.1; PID:g142765
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
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```
Query Match      69.3%; Score 4326; DB 2; Length 1176;
Best Local Similarity 71.3%; Pred. No. 1.9e-273;
Matches 849; Conservative 87; Mismatches 223; Indels 32; Gaps 12;

QY 1 MENNIO-NQCVNYNCLNPEVEILNEER-STGRLLDLDLSLTRFLLSEFVGVGAFGL 58
Db 1 MNNPNINCEIPYCNLSNPEVLAGERTETGTITDIDSLTQFLLSEFVGVGAFGL 60

QY 59 FDLWGFITPDSWLSFLQIEOLIBORIETLERNRAITLRLGADSYEYIEALREWEAN 118
Db 61 VDIINGIGPSOWDAPVOIEOLINQRIEERFARNOAISLEGLSNLYQIYAESFREWEAD 120

QY 119 PNAQLREDVRIRFANTDDALITAINNETLTSFEPLLSVYVQAAANLHLSLLRDVAFSG 178
Db 121 PTPALREEMRIQFNDMSALTATPALLAVQNYQVPLLSVYVQAAANLHLSVLRDVSFG 180

QY 179 GGLDIAIVNNHYNLNLHRYTHKCLDITNOGLENLGNTROWARFNQFRDLTIV 238
Db 181 RWGDDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWGPDSRDWRVYNQFRRLTIV 240

QY 239 LDIVALFNYDRTYPIOTISSOLTREIYTSVIEDSPYSANIPNGF----NPAEFGVRPP 294
Db 241 LDIVALFNSYDSRRPIKTVSOLTREIYTNPVLE-----NPDGFRGMAQRIEQNIQP 294

QY 295 HLMDFMNSLFTVTAETVRSQTVWGGHLVSSR--NTAGNRINPSPYGVNFPNGAI--WIADE 350
Db 295 HLMDILNSITIVDHRGENYWSGHQITASPVGSGPEFAFLFG--NAGNAAPVLVSL 352

QY 351 DPREFYRLSDPVFR-----GGFONPHYVLGRVAFQQTGNHRT--FRNSGTIDSID 404
Db 353 TGLGIFRLSPLVRYRIILIGSGPNQNELFLVDGTBFSASLTTLNLPSTIYRQRGVDSID 412

QY 405 BIPPDNSGAPWNDYSHVLNHWTFVRWPGETSGS--DSWRAPMFWTHESAPTNTIDPER 463
Db 413 VIPQDNSVPRAGFSHLSVHTL---SQAAGAVYTRAFTFSMOHSRSEFNLIIPSSQ 469

QY 464 ITQIPLVKAHTLQSGTTVVRGPGTGGDILRRISGPPFAYTIVNINGOLPORARIRYA 523
Db 470 ITQIPLKSTNLGSGTSVKGPGTGGDILRRISGPPQISTLRVNTAPLSQRYRIRYA 529

QY 524 STTNLRIVTVAGBRIFAGQNKMTDGDPLTFQSFVATINTAFTFPMSSQSFVTGADT 583
Db 530 STTNLQHTSIDGRPINQGNESATMSGNSLQSGSFRTVGTTFPNSGSSVETLSAHV 589

QY 584 FSSGNEVYIDREFLIPYATFAEYDLERAKAVNALFTSINOIGKTDVTDYHIDQVSN 643
Db 590 FNSGNEVYIDRIEVPFAEYDLERAKAVNELFTSSNQIGLKTVDYHIDQVSN 649

QY 644 LVCLSDFECLDKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITQR 703
Db 650 LVECLSDFECLDKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITQ 709

QY 704 GDDVFKENYVTLPGTFDECPTYLYQIDESKLKPYTRYQLRGYIESQDLEIYLIRYNA 763
Db 710 GDDVFKENYVTLPGTFDECPTYLYQIDESKLKAYTRYQLRGYIESQDLEIYLIRYNA 769

QY 764 KHETVNLVGLGSLWPLSQSPIRKCGPNRCAPHLENNPDLDCSCROGKCAHSHHFS 823
Db 770 KHETVNPVGLSLWPLSAQSPFKCGPNRCAPHLENNPDLDCSCROGKCAHSHHFS 829

QY 824 DIDVGCFLDNEDLVWVIFKIQDQGHARLGNLEFLEKPLVGEALARKVRAEKWKDKR 883
Db 830 DIDVGCFLDNEDLVWVIFKIQDQGHARLGNLEFLEKPLVGEALARKVRAEKWKDKR 889

QY 884 EKLENTNIVYKEAKESVDALFVNSQDQLQADNTIAMIHAADKRVHIREAYLPESLVI 943
Db 890 EKLENTNIVYKEAKESVDALFVNSQDQLQADNTIAMIHAADKRVHIREAYLPESLVI 949

QY 944 PGVNVDFEELKGRIFTAFELIADARNVKNKGDFNNGLSCHNVKGVHDVQONNERSVLV 1003
Db 950 PGVNAAFEELEGRIFTAFSLYDARNVKNKGDFNNGLSCHNVKGVHDVQONNERSVLV 1009

Query Match      68.9%; Score 4303; DB 2; Length 1166;
Best Local Similarity 71.1%; Pred. No. 6e-272;
Matches 851; Conservative 78; Mismatches 214; Indels 54; Gaps 12;

QY 1 MENNIOQCVPYCNCLNPEVEILNEERSTGRLLDLDLSLTRFLLSEFVGVGAFGLFD 60
Db 1 MEISDQNYIYPYCNCLNPESEIFNARNNSFGLVQSVSSGLTRFLLAAVPAAGFALGFD 60

QY 61 LIWGFITPDSNLSFLQIEOLIBORIETLERNRAITLRLGADSYEYIEALREWEANPN 120
Db 61 IINGALGVQDWSFLRQIEOLIBORIETLERNRAITLRLGSSSNLYVEALREWEANPN 120

QY 121 NAQLREDVRIRFANTDDALITAINNETLTSFEPLLSVYVQAAANLHLSLLRDVAFSG 180
Db 121 NPASQERVTRFRUTDDAIVTGLPTLAIRNLEVNLSVYTOAANLHLSLLRDVAFSGRW 180

QY 181 GLDIATVNNHYNLNLHRYTHKCLDITNOGLENLGNTROWARFNQFRDLTLTVID 240
Db 181 GLTQANTEDLYRLTSNIQEYSDHCARWYNOGLEIGIS---RRYLDFFORDLITVID 236

QY 241 IVALFPNYDRTYPIQTSQTLREIYTSVIEDSPYSANIPNGNRAEFGVVRPHLMDFM 300
Db 237 IVALFPNYDRTYPIQTSQTLREIYTSV---VAGNINFGLSIANV-LRAPHLMDFI 290

QY 301 NSLFWTAETVRSQTVWGGHLVSSRNTA---GNRINPSPYGVNFPNGALWIADEPRFYR 357
Db 291 DRIYIYNSVRSTPYWAGHEVISRTQGGQNEIRFPLYGV-----AANAEP----- 337

QY 358 TLDSPVFEVR--GGFONPH---YVLGLRGVAFQQTGNHT-----RFRN--S 397
Db 338 ---PVTRIRPTFDEQQRWVRARSRVVSRSSQDLSLVDVAGFLIFPSAVSYRNGFG 393

QY 398 GTDLSDEIPEQNSGAPWNDYSHVLNHWTFVRWPGEISGSDSWRAPMFWTHESAPTNT 457
Db 394 FNTDTIDEIPIEGTD---PFTGYSHRLCHVGFLASSPFI--SOYARAPIFSWTHESAPLTN 449

QY 458 TIDPERTQIPLVKAHTLQSGTTVVRGPGTGGDILRRISGPPFAYTIVNINGOLPOR 517
Db 450 TIAPDVITQIPLVKAHTLQSGTTVVRGPGTGGDILRRISGPPFAYTIVNINGOLPOR 509

QY 518 ARIRYASTTNLRIVTVAGBRIFAGQNKMTDGDPLTFQSFVATINTAFTFPMSSQSF 577
Db 510 VRIRYASTTDLQTYTNGTITNGINFSSTMDSDGLDLYGFRVAGFTTPTFFTSANSTF 569
```





## RESULT 10

parasporal crystal protein cry1Hal - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S32689

submitted to the EMBL Data Library, April 1993

R:Lambert, B.

A:Reference number: S32645

A:Accession: S32689

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: EMBL:22513; NID:g296086; PIDN:CAA80236.1; PID:g296087

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 67.8%; Score 4230.5; DB 2; Length 1172;  
Best Local Similarity 69.9%; Pred. No. 3.2e-267;  
Matches 834; Conservative 92; Mismatches 220; Indels 47; Gaps 11;

Qy 4 NTQNCVYVNCNNPEVILNEERSTGR---LPDLSLSLRFLLSEFVPGVGVAFLPD 60  
Db 5 NNQNYVYVNCNPNPEVILNEERSTGR---LPDLSLSLRFLLSEFVPGVGVAFLPD 64  
Qy 61 LIWGFIPTSDNSLFLQIEQLTEQRIETLRNRAITTLRGLADSYEIXIEALREWEANPN 120  
Db 65 IIWVGIGPDQWNLFLAQIEQLDQRIEIAHVRNQALSRLEGDSYEYIESUREWEASN 124  
Qy 121 NQALREDVRIIRFANTDDALITAINFTLTFSFEIPLLSVYVQAANLHLSLRDAVSFGQW 180  
Db 125 NEALQDVRNRFNTDNALITAIPILEQGFPEIPLLSVYVQAANLHLSLRDAVSFGQW 184  
Qy 181 GLDIATVNNHYNRLNLIHRYTKHCLDYNOGLENLRTNQWAFNQFRDLTLVLD 240  
Db 185 GLDTVTVNNHYNRLNLIHRYTKHCLDYNOGLENLRTNQWAFNQFRDLTLVLD 240  
Qy 241 IVALPFPNDVRYPIQTSQTLREIYTSVIE-DSPVSANIPNGFNRAEFVGRPHLMD 299  
Db 241 IVALPFPNDVRYPIQTSQTLREIYTSVIE-DSPVSANIPNGFNRAEFVGRPHLMD 293  
Qy 300 MNSLVTAEIVRSQVWGSHLVSSRNTA--GNRINFPYSGVFNPGGAIWADEDRPPT-- 355  
Db 294 LTRLYIVTGVSGIYHWAGHESITRTGTLNLSNIQFPLYGT-----AASADRAFNM 344  
Qy 356 -----YRLSDPVEVGGFGNHYVLGLGVAPOQTGTHNHT-----FRNSTIDSL 403  
Db 345 NIHSETYRLTSAPYISVSGISPNRTVRVGVFLIARDNNLDSLPFLYRKEGTLD 404  
Qy 404 DEIPQDNGAPWNDYSHVLNHTVVRVPGELSGSDSWRAPMFWTHRSATPTNIDPER 463  
Db 405 TELPPEDESTPPYIGYSHRLCHAREARSPVILEPNSFARLPVFSWTHRSASTNEVSPSR 464  
Qy 464 ITQIPLVKAHLQSTTVVRGPGTGGDILRT--SGGPFAYTVINNGOLPQRYARIR 521  
Db 465 ITQIPWKAHLTASGAYIKGPGFTGGDITMRNNNLGLDGLTLRTVTCRPLQSYIIRL 524  
Qy 522 YASTNLRIYTVACERIFAGQFNKMTDGPDLTQFSQSYATINFTAFPKSQSFTVGA 581  
Db 525 YASVANSSGVFRLHPQPSYISFTPTMGTDLPTRSGRSALTFTPIITLTRAQEFNL-- 582  
Qy 582 DTFSSGNEVYIDRFELIPVTAFEAEDYLERAKAVNALFTSINQIGKTDVTDYHIDQV 641  
Db 583 -TIPRG--VYIDRIEFVPVDAFTEAGYDLERAKAVNALFTSTNORGLKTDITDHIQV 639  
Qy 642 SNLVDCLSDFCCLKRELSKVKHAKLSDERNLQDPNFKGINRQLDRGWRGSTDITI 701  
Db 640 SNLVECLSDFCCLKRELSKVKHAKLSDERNLQDPNFKGINRQLDRGWRGSTDITI 699  
Qy 702 ORGDDVKNVNTVLPGTDECYPTLYQKIDESKLKPTTRVOLRGYIEDSQDLEYILRY 761  
Db 700 QGSDVDFKNVNTVLPGTDECYPTLYQKIDESKLKAYTRYQLRGYIEDSQDLEYILRY 759

Qy 762 NAKHETVNVLTGSLWPLSVQSPFIRKCGFNRCAHPLEWNPDLDCSCRDGKCAHSHHF 821  
Db 760 NAKHEIVNVPGTGLWPLSVENSIGPCGSNRCAPHEWNPDLDCSCRDGKCAHSHHF 819  
Qy 822 SLIDIVGCTDLNEDLDVWIFIKITQDGHARLGNLEFLEKPLVGFALARVRAEKKWD 881  
Db 820 SLIDIVGCTDLNEDLDVWIFIKITQDGHARLGNLEFLEKPLVGFALARVRAEKKWD 879  
Qy 882 KREKLEETNIYVKEAKESVDALFVNSQDQLQADNTIAMIHAAADKRVHRIEAYLP 941  
Db 880 KKKLEFETNIYVKEAKESVDALFVNSQDKLKADNTIAMIHAAADKRVHRIEAYLP 939  
Qy 942 VIPGVNVDIFEBELKGRIFTAFPLYDARNVYKNGDFNGLSCWNVKGHVDFEONNHR 1001  
Db 940 VIPGVNADIFELEGRIFTAYSLSYDARNVYKNGDFNGLSCWNVKGHVDFEONNHR 999  
Qy 1002 VYPEWEAEVSQEVRCVPCGRGYILRYTAYKEGEGCVTITETNNNTDELKFCNCEVEEY 1061  
Db 1000 VYPEWEAEVSQEVRCVPCGRGYILRYTAYKEGEGCVTITETNNNTDELKFCNCEVEEY 1059  
Qy 1062 PNNTVTCNDYTANQOEYGGATSRNRYDETYGSSNVPADYASVYEKSYTDGRDNP 1121  
Db 1060 PNNTVTCNDYTANQOEYEGTYTSRNOGYDEAYESNVPANYSVYEKAYTDGRRENS 1119  
Qy 1122 ESNRGYGYDTPLPAGYVTKLEYFPETDKWIEIGETEGTFIVDSVELLMEE 1174  
Db 1120 EFNRGYRDTPLPAGYVTKLEYFPETDKWIEIGETEGTFIVDSVELLMEE 1172

RESULT 11  
S00944

parasporal crystal protein cry1cal - Bacillus thuringiensis (strain entomocidus 60.1)

C:Species: Bacillus thuringiensis

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 01-Dec-2000

C:Accession: S00944

R:Honee, G.; van der Salm, T.; Visser, B.

A:Title: Nucleotide sequence of crystal protein gene isolated from B. thuringiensis

A:Reference number: S00944; MUID:8829380; PMID:3399402

A:Accession: S00944

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-1189 &lt;HON&gt;

A:Cross-references: EMBL:X07518; NID:g40293; PIDN:CAA30396.1; PID:g40294

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 67.5%; Score 4217.5; DB 2; Length 1189;  
Best Local Similarity 68.8%; Pred. No. 2.3e-266;  
Matches 833; Conservative 96; Mismatches 224; Indels 57; Gaps 17;

Qy 1 MENNQNCVYVNCNNPEVILNEER-STGRPLDLSLSTRLFLSFBFVGVAFLGF 59  
Db 1 MEENNQNCIYVNCNPNPEVILNEERSTGRPLDLSLSTRLFLSFBFVGVAFLGF 60  
Qy 60 DLINGFITPDSNLSLFLQIEQLTEQRIETLRNRAITTLRGLADSYEIXIEALREWEANP 119  
Db 61 DFWGVIGPQWDAFLVQIEQLINERIAEFARNAALNLEGNNFNFIYVEAFKEWEDP 120  
Qy 120 NNAQLREDVRIIRFANTDDALITAINFTLTFSFEIPLLSVYVQAANLHLSLRDAVSFGQ 179  
Db 121 NNPTRTVRIDRFRLDGLLERDIPFSGFVEYPLLSVYQAANLHLSLRDAVSFGIF 180  
Qy 180 WGLDIATVNNHYNRLNLIHRYTKHCLDYNOGLENLRTNQWAFNQFRDLTLVLD 239  
Db 181 WGLTITVNNHYNRLNLIHRYTKHCLDYNOGLENLRTNQWAFNQFRDLTLVLD 240  
Qy 240 DIVALFPNDVRYPIQTSQTLREIYTSVIEDSP---VSANIPNGFNRAEFVGRPH 295  
Db 241 DIAAFFPNDRRYPIQPVGQLTREVTDPLINFPNQLQSVQALPT-FNNMESSIRNPH 299  
Qy 296 LMDFMNSLFTVAE--TVRSQTVWGHSLVSSRNTAGNRINFPYSGVFNPGGAIWADEDP- 352  
Db 294 LTRLYIVTGVSGIYHWAGHESITRTGTLNLSNIQFPLYGT-----AASADRAFNM 344

Db 300 LFDILNLTITFDWFSVGRNFYWGHRVYSSILGGNITSPIYG-----REANQEP 351

QY 353 -----RPFYRTLSDPV--FVRGGFGNPHYVL-GLRGVAFQOCTNHTFRNSGTDLSL 403

Db 352 RSTFNGPVRTUSNPLRLQLQWPAPPFNLRGVGEVFEF-STPTN-SFTYGRGTVDLSL 409

QY 404 DEIPPDQNSGAPWMDYSHVLNHNVTFFVRWPGEISGDSWRAP-----MFSWTHRSAYPTN 457

Db 410 TELPPEDNSVPPRGYSHRLLCHAFVQVRSQ-----TPFLTGVVFSWTSALITN 460

QY 458 TIDPERITQPLVKAHLQSGTTVVVRGGFTGGDILRRTSGGPFAYTIVNINGLQRPYR 517

Db 461 TIDPERINQPLVGRFVWGVTGVTGTTGGDILRNTFGDFVSQVQVNSITQYR 520

QY 518 ARIRYASTTNRIYV-TVAGERIFAGQ-----FNKMDTGDPDTTFOSESYATINTATFF 570

Db 521 LRFRYASRDARVILVIGASTGVGGQVSNMPLQKMEIGENUTSRIFRTDFSNPFSF 580

QY 571 PMSQSSFTV-----GADTFSSGNEVYIDRPELIPVTATFEAYDLERAQAVNALETSI 624

Db 581 RANPDIIIGISEQPLFGAGSISG-ELYIDKIEIILADATFEASDLERAQAVNALETS 639

QY 625 NQIGIKTDVTDYHIDQVSNLVDCLDFEKLSEKVKHAKRLSDERNLLQDPNFKG 684

Db 640 NQIGLKTVDVTDYHIDQVSNLVDCLDFEKLSEKVKHAKRLSDERNLLQDPNFKG 699

QY 685 INPOLDRGWRGSTDITQRGDDVFKENAVTLPGTDFECYPTLYKQIDESKLKPYTRYQL 744

Db 700 INQPDGRGWRGSTDITQGGDDVFKENAVTLPGTDFECYPTLYKQIDESKLKAYTRYEL 759

QY 745 RGYTEDSQDLEIYLIRYNAKHETVNLGTSGLWPLSVQSPYRKCGEPNRCAPHLEWNPDL 804

Db 760 RGYTEDSQDLEIYLIRYNAKHETVNLGTSGLWPLSVQSPYRKCGEPNRCAPHLEWNPDL 819

QY 805 DCSRCDEKCAHSHHSLSLDVCGTDLNEDLVVWIFKIKTQGHARLGNLEFLEKPL 864

Db 820 DCSRCDEKCAHSHHSLSLDVCGTDLNEDLVVWIFKIKTQGHARLGNLEFLEKPL 879

QY 865 VGEALARKVRAEKWRKREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNIAHI 924

Db 880 LGEALARKVRAEKWRKREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNIAHI 939

QY 925 ADKRVHRIEAYLPSELSVPGVNVVDIPEELKGRIFTAFFLYDARNVKNKGFNNGLSOWN 984

Db 940 ADKRVHRIEAYLPSELSVPGVNVVDIPEELKGRIFTAYSLYDARNVKNKGFNNGLSOWN 999

QY 985 VKGHVDVEQNHRSLVVPBWEAEVQEVRCGRGYLKVATYKEGEGCVTIHEIE 1044

Db 1000 VKGHVDVEQNHRSLVVPBWEAEVQEVRCGRGYLKVATYKEGEGCVTIHEIE 1059

QY 1045 NNTDELAFSCVVEEVPNNVTTCNDXTANQOEYGGAYTSRNGYDETYGSSNSVPADYA 1104

Db 1060 NNTDELAFSCVVEEVPNNVTTCNDXTANQOEYGGAYTSRNGYDETYGSSNSVPADYA 1119

QY 1105 SVYEKSYTDGRNPNCESNRGQYDTPLPAGYVTKLEYPPETDKWVIEIGETEGFIV 1164

Db 1120 SVYEKSYTDGRNPNCESNRGQYDTPLPAGYVTKLEYPPETDKWVIEIGETEGFIV 1179

QY 1165 DSVELLMLLEE 1174

Db 1180 DSVELLMLLEE 1189

RESULT 12

JD00002

N;Alternate names: Delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal protein

C;Species: Bacillus thuringiensis

C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 01-Dec-2000

C;Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002

R;Kondo, S.; Tamura, N.; Kunitake, A.; Hattori, M.; Akashi, A.; Ohmori, I.

Agric. Biol. Chem. 51, 455-463, 1987

A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from

A;Reference number: A90025

A;Accession: A90025

A;Molecule type: mRNA

A;Residues: 1-1155 <KON>

R;Experimental source: subsp. kurstaki

R;Geiser, M.; Schweitzer, S.; Grimm, C.

Gene 48, 109-118, 1986

A;Title: The hypervariable region in the genes coding for entomopathogenic crystal protein

A;Reference number: A91560; MUID:87163505; PMID:3557124

A;Accession: A91560

A;Molecule type: DNA

A;Residues: 1-1155 <GEI>

A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124

R;Experimental source: subsp. kurstaki

R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.

DNA 5, 305-314, 1986

A;Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product a

A;Reference number: A90955; MUID:86300092; PMID:3743328

A;Accession: A90955

A;Molecule type: DNA

A;Residues: 1-1155 <WAB>

A;Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720

R;Experimental source: subsp. berliner

R;Chak, K.F.; Jen, J.C.

submitted to the EMBL Data Library, October 1990

A;Description: Complete nucleotide sequence and expression in Escherichia coli of a c

A;Reference number: S14555

A;Accession: S14555

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1155 <CHA>

A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273

R;Hofte, H.; de Greve, H.; Seuring, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandeker

Eur. J. Biochem. 161, 273-280, 1986

A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus t

A;Reference number: A26461; MUID:87054026; PMID:3023091

A;Accession: A26461

A;Molecule type: DNA

A;Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>

A;Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255

R;Experimental source: strain berliner 1715

C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.

C;Genetics:

A;Gene: cry-1-2; bt2

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

F;82-586/Product: toxic peptide #status predicted <TXP>

F;82-300/Region: toxic #status predicted

F;300-586/Region: insecticidal #status predicted

Query Match 67.4%; Score 4211.5; DB 2; Length 1155;

Best Local Similarity 70.0%; Pred. No. 5.4e-266;

Matches 831; Conservative 83; Mismatches 228; Indels 45; Gaps 9;

QY 1 MENNIO-NOCVPYCLNPNVEIILNEER-STGRPLDLSLTLRFLSEFVPGVGVAFGL 58

Db 1 MDNPNNECIPYCNLSNPVEVLGGERIETGYTFIDLSLTQFLSEFVPGAGVGL 60

QY 59 FDLIWGITPDSWLSFLQIBQLIETRIETLERNAITTLRGLADSYEITYEALREWEAN 118

Db 61 VDIWGITPDSWDAFLVQIQLNRIEERFARQALSLRLEGLSNLYQIYAESFREWAD 120

QY 119 PNAQLREDVRIRFANTDDALITAINNFTLSFEIPLSVYVQANLHLLLRDAVSFG 178

Db 121 PTPNPALEEMRIQFNDMNSALTTPAIFVQNYQVPLSVYVQANLHLLSRVSVFG 180

QY 179 GWDLDIATVNNHNLNLHRYTHKCLDVTYNOGLENLGRNTNTROWAFENFRDLITV 238

Db 181 RWGDAATINRYNDLRLIGNYTHDVAWYNTGLERVWGPDSRDWRIRNGFRRLITV 240

QY 239 LDIVALEPNDVRYTPIQTSSQLTREYTSSTVEDSPVSANIPNGFNRA----BFGVRPP 294

Db 241 LDIVSLFPNDVRYTPIFTVSLTREYTNVPLE-----NFDGSRGSAOGIEGSRP 294

Qy 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINEPSYGVF-NPGGAIWIADRD 351  
 Db 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINEPSYGVF-NPGGAIWIADRD 351  
 Qy 352 PRPFYRTLDSPVVRG--GFGNPHY-VLGLRGVAFQOTGTNHTRTFRNSGTDLSDEIP 407  
 Db 352 PRPFYRTLDSPVVRG--GFGNPHY-VLGLRGVAFQOTGTNHTRTFRNSGTDLSDEIP 407  
 Qy 408 PODNSGAPNDYSHVNLHVTFVWPGEGISGDSWRAPFMSWTHRSATPNTIDPRTIQI 467  
 Db 408 PODNSGAPNDYSHVNLHVTFVWPGEGISGDSWRAPFMSWTHRSATPNTIDPRTIQI 467  
 Qy 415 PNNVPPRQGFQSHRSHVMSFRSFSNSVSIIRAPFMSWTHRSATPNTIDPRTIQI 474  
 Db 415 PNNVPPRQGFQSHRSHVMSFRSFSNSVSIIRAPFMSWTHRSATPNTIDPRTIQI 474  
 Qy 468 PLVKAHTLQSGTIVVVRGPGFTGGDILRTSGGPFYATVINGNQLPQRYRARIYASTIN 527  
 Db 468 PLVKAHTLQSGTIVVVRGPGFTGGDILRTSGGPFYATVINGNQLPQRYRARIYASTIN 527  
 Qy 475 PLTKSTNLGSGTVVVGPGFTGGDILRTSGGPFYATVINGNQLPQRYRARIYASTIN 534  
 Db 475 PLTKSTNLGSGTVVVGPGFTGGDILRTSGGPFYATVINGNQLPQRYRARIYASTIN 534  
 Qy 528 LRIYVTVAGERIFAGQFNKMTDGLTQFQSFYATINTAFTFMSQSFTVGDTPSSG 587  
 Db 528 LRIYVTVAGERIFAGQFNKMTDGLTQFQSFYATINTAFTFMSQSFTVGDTPSSG 587  
 Qy 535 LQFHTSIHGRPINQGNFSAATSSGNSGSGSFRHLGFTTPFNFSNGSVFTLSAHVNSG 594  
 Db 535 LQFHTSIHGRPINQGNFSAATSSGNSGSGSFRHLGFTTPFNFSNGSVFTLSAHVNSG 594  
 Qy 588 NEVYIDRELPVATFAEYDLERAQKAVNALFTSINOIGTKTDVTDYHIDQVSNLVD 647  
 Db 588 NEVYIDRELPVATFAEYDLERAQKAVNALFTSINOIGTKTDVTDYHIDQVSNLVD 647  
 Qy 595 NEVYIDRELPVATFAEYDLERAQKAVNELFTSSNOIGTKTDVTDYHIDQVSNLVD 654  
 Db 595 NEVYIDRELPVATFAEYDLERAQKAVNELFTSSNOIGTKTDVTDYHIDQVSNLVD 654  
 Qy 648 LSDFCLDEKRELSKVKHAKRLSDERNLQDPNFKINRQLDRGWRGSTDTIORGDV 707  
 Db 648 LSDFCLDEKRELSKVKHAKRLSDERNLQDPNFKINRQLDRGWRGSTDTIORGDV 707  
 Qy 655 LSDFCLDEKRELSKVKHAKRLSDERNLQDPNFKINRQLDRGWRGSTDTIORGDV 714  
 Db 655 LSDFCLDEKRELSKVKHAKRLSDERNLQDPNFKINRQLDRGWRGSTDTIORGDV 714  
 Qy 708 FKENVTLPGTFDECYPTLYQKIDESKLPYTRYQYQYQYQYQYQYQYQYQYQY 767  
 Db 708 FKENVTLPGTFDECYPTLYQKIDESKLPYTRYQYQYQYQYQYQYQYQYQYQY 767  
 Qy 715 FKENVTLPGTFDECYPTLYQKIDESKLPYTRYQYQYQYQYQYQYQYQYQYQY 774  
 Db 715 FKENVTLPGTFDECYPTLYQKIDESKLPYTRYQYQYQYQYQYQYQYQYQYQY 774  
 Qy 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSDRDEKCAHSHHSLDIDV 827  
 Db 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSDRDEKCAHSHHSLDIDV 827  
 Qy 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSDRDEKCAHSHHSLDIDV 808  
 Db 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSDRDEKCAHSHHSLDIDV 808  
 Qy 828 GCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKKWRDREKLE 887  
 Db 828 GCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKKWRDREKLE 887  
 Qy 809 GCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKKWRDREKLE 868  
 Db 809 GCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKKWRDREKLE 868  
 Qy 888 LETNIVYKEAKESVDALFVNSQYDQADNTIAMTHADKRVHRIREAYLPESLIPGVN 947  
 Db 888 LETNIVYKEAKESVDALFVNSQYDQADNTIAMTHADKRVHRIREAYLPESLIPGVN 947  
 Qy 869 WETNIVYKEAKESVDALFVNSQYDQADNTIAMTHADKRVHRIREAYLPESLIPGVN 928  
 Db 869 WETNIVYKEAKESVDALFVNSQYDQADNTIAMTHADKRVHRIREAYLPESLIPGVN 928  
 Qy 948 VDIFELKGRIFTAFPLDARVKNKGNFNGLSQWNVKGVVDVEEQNHRSVLPVPEWE 1007  
 Db 948 VDIFELKGRIFTAFPLDARVKNKGNFNGLSQWNVKGVVDVEEQNHRSVLPVPEWE 1007  
 Qy 929 AAIFEELEGRIFTAFPLDARVKNKGNFNGLSQWNVKGVVDVEEQNHRSVLPVPEWE 988  
 Db 929 AAIFEELEGRIFTAFPLDARVKNKGNFNGLSQWNVKGVVDVEEQNHRSVLPVPEWE 988  
 Qy 1008 AEVSQEVRCVPGRGVILRVATYKEGYGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1067  
 Db 1008 AEVSQEVRCVPGRGVILRVATYKEGYGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1067  
 Qy 989 AEVSQEVRCVPGRGVILRVATYKEGYGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1048  
 Db 989 AEVSQEVRCVPGRGVILRVATYKEGYGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1048  
 Qy 1068 CNDYTANOEYGGATSNRNGYDETYGNSVSPADYASVEKSTYDGRNPNCSNRY 1127  
 Db 1068 CNDYTANOEYGGATSNRNGYDETYGNSVSPADYASVEKSTYDGRNPNCSNRY 1127  
 Qy 1049 CNDYTANOEYGGATSNRNGYDETYGNSVSPADYASVEKSTYDGRNPNCSNRY 1108  
 Db 1049 CNDYTANOEYGGATSNRNGYDETYGNSVSPADYASVEKSTYDGRNPNCSNRY 1108  
 Qy 1128 GDTPLPAGYVTKLEYPEDDKWIEIGETEGTFIVDSVLELLMEE 1174  
 Db 1128 GDTPLPAGYVTKLEYPEDDKWIEIGETEGTFIVDSVLELLMEE 1174  
 Qy 1109 GDTPLPAGYVTKLEYPEDDKWIEIGETEGTFIVDSVLELLMEE 1155  
 Db 1109 GDTPLPAGYVTKLEYPEDDKWIEIGETEGTFIVDSVLELLMEE 1155

RESULT 13  
 139838  
 paraspore crystal protein - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 01-Dec-2000  
 C:Accession: I39838  
 R:Heford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.  
 J. Biotechnol. 6, 307-322, 1987  
 A:Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki  
 A:Reference number: I39838  
 A:Accession: I39838

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <RES>  
 A:Cross-references: GB:M37263; NID:g142885; PIDN:AAA22420.1; PID:g142886  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 67.2%; Score 4194.5; DB 2; Length 1155;  
 Best Local Similarity 69.8%; Pred. NO. 7e-265;  
 Matches 828; Conservative 83; Mismatches 231; Indels 45; Gaps 9;

Qy 1 MENNIQ-NOCVPYCNLNPEVILNEER-STGRLPDLSLSTRFLLSPFVPGVAVFGL 58  
 Db 1 MDNNEINCEPYNCLSPNEVEVLGGERIETGYTIDISLQFLLSFVPGVAVFGL 60  
 Qy 59 FDLINGFTPPSDWSLFLQIEQLIQRITLERNRAITLRLGLADSYEYIEALREWEAN 118  
 Db 61 VDIWIGIFGSPQWDAFLVQIEQLINORTEEPARNQAISRLGLSNLYQIYAESFREWEAD 120  
 Qy 119 PNAACOLREDVRIRFANTDDALITAINNTLSFEPLISVYVQAAANLHSLRLDVAFGQ 178  
 Db 121 PTPNALREMRIOFNDMSALTATPLFAVQNYQVPLLSVYVQAAANLHSLRLDVAFGQ 180  
 Qy 179 GWGLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENLRGNTROWARFNQFRDLITLV 238  
 Db 181 RWGFDATINSKYNLDLTRLIGNYTDHAYWNTGLERVWGPDSRDWRINQFRRLTLTV 240  
 Qy 239 LDIVALFNYDVRTPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA----EFGVRPP 294  
 Db 241 LDIVSLFNYDSRTPIRTVSOLTREIYTNVLE-----NFDGSGFRGSAQOIGESIRSP 294  
 Qy 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINEPSYGVF-NPGGAIWIADRD 351  
 Db 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINEPSYGVF-NPGGAIWIADRD 351  
 Qy 352 PRPFYRTLDSPVVRG--GFGNPHY-VLGLRGVAFQOTGTNHTRTFRNSGTDLSDEIP 407  
 Db 352 PRPFYRTLDSPVVRG--GFGNPHY-VLGLRGVAFQOTGTNHTRTFRNSGTDLSDEIP 407  
 Qy 408 PODNSGAPNDYSHVNLHVTFVWPGEGISGDSWRAPFMSWTHRSATPNTIDPRTIQI 467  
 Db 415 PNNVPPRQGFQSHRSHVMSFRSFSNSVSIIRAPFMSWTHRSATPNTIDPRTIQI 474  
 Qy 468 PLVKAHTLQSGTIVVVRGPGFTGGDILRTSGGPFYATVINGNQLPQRYRARIYASTIN 527  
 Db 475 PLTKSTNLGSGTVVVGPGFTGGDILRTSGGPFYATVINGNQLPQRYRARIYASTIN 534  
 Qy 528 LRIYVTVAGERIFAGQFNKMTDGLTQFQSFYATINTAFTFMSQSFTVGDTPSSG 587  
 Db 535 LQFHTSIHGRPINQGNFSAATSSGNSGSGSFRHLGFTTPFNFSNGSVFTLSAHVNSG 594  
 Qy 588 NEVYIDRELPVATFAEYDLERAQKAVNALFTSINOIGTKTDVTDYHIDQVSNLVD 647  
 Db 595 NEVYIDRELPVATFAEYDLERAQKAVNELFTSSNOIGTKTDVTDYHIDQVSNLVD 654  
 Qy 648 LSDFCLDEKRELSKVKHAKRLSDERNLQDPNFKINRQLDRGWRGSTDTIORGDV 707  
 Db 655 LSDFCLDEKRELSKVKHAKRLSDERNLQDPNFKINRQLDRGWRGSTDTIORGDV 714  
 Qy 708 FKENVTLPGTFDECYPTLYQKIDESKLPYTRYQYQYQYQYQYQYQYQYQYQY 767  
 Db 715 FKENVTLPGTFDECYPTLYQKIDESKLPYTRYQYQYQYQYQYQYQYQYQYQY 774  
 Qy 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSDRDEKCAHSHHSLDIDV 827  
 Db 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSDRDEKCAHSHHSLDIDV 808  
 Qy 828 GCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKKWRDREKLE 887  
 Db 809 GCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKKWRDREKLE 868  
 Qy 888 LETNIVYKEAKESVDALFVNSQYDQADNTIAMTHADKRVHRIREAYLPESLIPGVN 947  
 Db 888 LETNIVYKEAKESVDALFVNSQYDQADNTIAMTHADKRVHRIREAYLPESLIPGVN 947

Db 869 WETNIVYKEAKESVDALFVNSQYDRLQADTNIAHIAADKRVHSIREAYLPSELSVIPGVN 928  
 QY 948 VDIFEEELKGRIFTAFYLDARNVIKNGDFNGLSCWNKGVHDVVEEQNNHRSVLVVPWE 1007  
 Db 929 AAIFEEELKGRIFTAFYLDARNVIKNGDFNGLSCWNKGVHDVVEEQNNHRSVLVVPWE 988  
 QY 1008 AEVSQEVRCVGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEVPNNVT 1067  
 Db 989 AEVSQEVRCVGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEVPNNVT 1048  
 QY 1068 CNDYTAQEEYGGAYTSRNGYDYESNSSVPADYASVYEKSYTDDRNDPCESNRY 1127  
 Db 1049 CNDYTAQEEYGGAYTSRNGYDYESNSSVPADYASVYEKSYTDDRNDPCESNRY 1108  
 QY 1128 GDYTPLPAGYVTKLEYFPETDKWIEGEGTGFIVDSVELLMEE 1174  
 Db 1109 GDYTPLPAGYVTKLEYFPETDKWIEGEGTGFIVDSVELLMEE 1155

RESULT 14  
 A26513  
 parasporal crystal protein - Bacillus thuringiensis (strain aizawai)  
 C:Species: Bacillus thuringiensis  
 C:Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 01-Dec-2000  
 C:Accession: A26513  
 R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, H.  
 Gene 53, 113-119, 1987  
 A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
 A:Reference number: A26513; MUID:87248103; PMID:3297927  
 A:Accession: A26513  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <OE>  
 A:Cross-references: GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 67.1%; Score 4191.5; DB 2; Length 1155;  
 Best Local Similarity 69.8%; Pred. No. 1.1e-264;  
 Matches 829; Conservative 82; Mismatches 231; Indels 45; Gaps 9;

QY 1 MENNIQ-NOCPVYNCLNPEVEILNEER-STGRULPDLISLTFELSEFVGVGVAFGL 58  
 Db 1 MDNNINIECIPYCNLSNPEVGLSGRIETGYTPIDISLTOFLLESEFVGVGVAFGL 60

QY 59 FDLIWGFIPTSDSLFLQLOLEQRIETLERNRAITLRLGLADSYEIIYELARENEAN 118  
 Db 61 VDLIWGFIPTSDSLFLQLOLEQRIETLERNRAITLRLGLADSYEIIYELARENEAN 120

QY 119 PNAQLREVRIRFANTDDALITAINNFTLTSFPIPLSVVQAAANLHLSLLRDVAFSGQ 178  
 Db 121 PTPALREEMRIQFDMNSALTAPLFAVQYQVPLSVVQAAANLHLSVLRDVAFSGQ 180

QY 179 GWGLDITAVNNHNNLNLHRTKKHCLDYNQGLENLRTNTQWAFRNFQFRDLTLTV 238  
 Db 181 RWGFDAITNSRYNLDRLNLTGNTHAVRYNTGLERWVGPDSDRWIRYQFRDLTLTV 240

QY 239 LDIVALFPNDVRYPIQTSQSLTRETIVTSVIEDSPVSANIPNGENR---AEFGVRRP 294  
 Db 241 LDIVSLFPNDVRYPIQTSQSLTRETIVTSVIEDSPVSANIPNGENR---AEFGVRRP 294

QY 295 HLMDFMNSLFTVETVRSQVWGGH--LVSSRNTAGNRINFPSPYGVF-NPGGAIWIADED 351  
 Db 295 HLMDFMNSLFTVETVRSQVWGGH--LVSSRNTAGNRINFPSPYGVF-NPGGAIWIADED 354

QY 352 PRFYRTLSDPVFRG---GFGNPHY-VLGLRGVAFQOQTNTNTRTFRNSGTDLSLDEIP 407  
 Db 355 GQGYRTLSLTLRPPNIGINNQLSVLDCTEFAYCTSSNLPSAVYRKSGTVDSLDEIP 414

QY 408 PDNSGAPMNDYSLVNLHVTIVFRWPGFISGDSWRAPMFSTWHSATPTNTIDPRTQI 467  
 Db 415 PQNNVPPROGFSRHRUSHVSMFRSGFSNFSVITRAPMFWHSATPTNTIDPRTQI 474

QY 468 PLVKAHTLQSGTIVRVGPGFTGGDILRETSGSPFAYTIIVNINGQLPQRYRARIYASTTN 527  
 Db 475 PLTSTNLGSGTIVRVGPGFTGGDILRETSGSPFAYTIIVNINGQLPQRYRARIYASTTN 534  
 QY 528 LRIYTVAGERIFAQGNKMTMDTGDPLTFQSFYSYATINTAFTFPMSSQSFVGVADTFSSG 587  
 Db 535 LQFHTSIDGRFINQGNFSATSSGSLGSGSFRTVGVFTTFNFSGSSVFTLSAHVFNSSG 594  
 QY 588 NEVYIDRELIPVATFAEYDLERAKAVNALFTSINQIGIKTDVTDYHIDQVSNLVD 647  
 Db 595 NEVYIDRELIPVATFAEYDLERAKAVNALFTSINQIGIKTDVTDYHIDQVSNLVD 654  
 QY 648 LSDFECLDEKRELSEKVKHAKRLSDERNLLODPNFKINRLQDLDRGWRGSTDITQGGDDV 707  
 Db 655 LSDFECLDEKRELSEKVKHAKRLSDERNLLODPNFKINRLQDLDRGWRGSTDITQGGDDV 714  
 QY 708 FKENYVTLPGTFFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 767  
 Db 715 FKENYVTLPGTFFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 774  
 QY 768 VNVLTGSLNPLSVQSPKRCGEPNRCAPHLWNPDDLDCSCRDGEKCAHHSHHSLDIDV 827  
 Db 775 VNVLTGSLNPLSVQSPKRCGEPNRCAPHLWNPDDLDCSCRDGEKCAHHSHHSLDIDV 808

QY 828 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEPLLEKPLVGEALARKVRAEKRWKREKLE 887  
 Db 809 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEPLLEKPLVGEALARKVRAEKRWKREKLE 868

QY 888 LETNIVYKEAKESVDALFVNSQYDRLQADTNIAHIAADKRVHSIREAYLPSELSVIPGVN 947  
 Db 869 WETNIVYKEAKESVDALFVNSQYDRLQADTNIAHIAADKRVHSIREAYLPSELSVIPGVN 928

QY 948 VDIFEEELKGRIFTAFYLDARNVIKNGDFNGLSCWNKGVHDVVEEQNNHRSVLVVPWE 1007  
 Db 929 AAIFEEELKGRIFTAFYLDARNVIKNGDFNGLSCWNKGVHDVVEEQNNHRSVLVVPWE 988

QY 1008 AEVSQEVRCVGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEVPNNVT 1067  
 Db 989 AEVSQEVRCVGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEVPNNVT 1048

QY 1068 CNDYTAQEEYGGAYTSRNGYDYESNSSVPADYASVYEKSYTDDRNDPCESNRY 1127  
 Db 1049 CNDYTAQEEYGGAYTSRNGYDYESNSSVPADYASVYEKSYTDDRNDPCESNRY 1108

QY 1128 GDYTPLPAGYVTKLEYFPETDKWIEGEGTGFIVDSVELLMEE 1174  
 Db 1109 GDYTPLPAGYVTKLEYFPETDKWIEGEGTGFIVDSVELLMEE 1155

## RESULT 15

S02134

Parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai ICI)  
 N:Alternate names: delta-endotoxin ICI; entomocidal crystal protein  
 C:Species: Bacillus thuringiensis  
 A:Variety: strain aizawai ICI  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 01-Dec-2000  
 C:Accession: S02134; S04994  
 R:Haider, M.Z.; Ellar, D.J.  
 Nucleic Acids Res. 16, 10927, 1988

A:Title: Nucleotide sequence of a Bacillus thuringiensis aizawai ICI entomocidal crystal protein  
 A:Reference number: S02134; MUID:89083518; PMID:3205732  
 A:Accession: S02134

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-1155 &lt;HA&gt;

A:Cross-references: EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278

A:Experimental source: strain aizawai ICI

R:Haider, M.Z.; Ellar, D.J.

J. Mol. Biol. 208, 183-194, 1989

A:Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid chan

A:Reference number: S04994; MUID:89362455; PMID:2769751

A:Accession: S04994

A:Molecule type: DNA

A:Residues: 429-449, 'A', 451-724 <HAW>

A:Cross-references: EMBL:X16315

A:Experimental source: strain aizawai IC1

C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 67.1%; Score 4189.5; DB 2; Length 1155;  
Best Local Similarity 69.8%; Pred. No. 1.5e-264;  
Matches 828; Conservative 84; Mismatches 230; Indels 45; Gaps 9;

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QY 1 MNNNTQ-NOCVYNCLNPEVEILNEER-STGRPLDLISLSLTPLELLSEFVPGVGVAFGL 58
DB 1 MNNPNINEICPNCLSNPEVEVLGERIETGYTIDISLQTFLLSEFVPGAGFVLGL 60
QY 59 FOLINGFITPDSWLSFLQIEQLIQRIETLERNRAITTLRGLADSYEIIYEAALREWEAN 118
DB 61 VDIINGIFGPSQWDAFLVQIEQLINORIEEPARNQAISRLGSLNLYQIYAESFREWEAD 120
QY 119 PNAQLREOVRIFRANTUDALITANNFTLSFEPLISVYQAAANHLSDRLDAVSEGG 178
DB 121 PTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYQAAANHLSDRLDAVSEGG 180
QY 179 GGLDITATVNNHYNLINLIHRYTKHCLDITYNQGLENLRGNTROWARENOFRDLTLTV 238
DB 181 RWGFDAAITNSRYNDLRLIGNYTHAVRWYNTGLERWGPDSRDWIRYNQFRRELITLV 240
QY 239 LDVALFPNYDYRTPIQTSQLTREITSSVIEDSPVSANIPNGFNRA----EFGVRPP 294
DB 241 LDVLSLFPNDSRTYPIRTVSQLTREITNPVLE-----NFDGSRGSAQOIEGSIKSP 294
QY 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGRNINPSYGVF-NPGCAIWIADSD 351
DB 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGRNINPSYGVF-NPGCAIWIADSD 351
QY 352 PRPFYRTSLDPPVFVRG---GFGNPHY-VLGLRGVAFQQTGTNHTFRNSQSTIDSLDEIP 407
DB 355 GCGVYRTSLSTLYRRFPNIGINNQLSVLDGTGEFAVGTSNLPSSAVYRKSGTVDSLDEIP 414
QY 408 PQDSCAPNDYSHVLNHYTVFVWPGCEISGDSWRAPMSEWTHRSATNTIDPERITQI 467
DB 415 PQNNVPPRQGFSSHRLSHVSMFSGFSNVSIIIRPPMFSWTHRSAEFNIIIPSSQITQI 474
QY 468 PLVKAHTLQSGTVVRGPGTGGDILRRTSGGPFAYTVIWNINGQLPQRYRARIYASTIN 527
DB 475 PLTKSNLQSGTSYVKGPGTGGDILRRISPGQISTLRVNTAPLSQRYRARIYASTIN 534
QY 528 LRIYTVAGERIPAGOFNKTMDTGPLTFTQSFYSATINTAFTFPMSSQSFVAGDTFSSG 587
DB 535 LQHTSIDGRIINQGNFSAITMSGSLQSGSFRIVGFTTFFNFSGSSVFTLSAHVFNSSG 594
QY 588 NEVYIDRFELIPVATFEAYEDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLYDC 647
DB 595 NEVYIDRIEFVPAEVTFEAYEDLERAKAVNALFTSSNGIGLKTVDYHIDQVSNLYEC 654
QY 648 LSDPCLDEKRELSKVKHAKLSDERNLQDPNFKGINRQLDRGWRGSTDITIQGGDV 707
DB 655 LSDPCLDEKRELSKVKHAKLSDERNLQDPNFKGINRQLDRGWRGSTDITIQGGDV 714
QY 708 FKENVYTLPGTFDECYTYLYQKIDESKLPKPYRQLRCYIEDSQOLEIYLIRYNAKHET 767
DB 715 FKENVYTLPGTFDECYTYLYQKIDESKLPKPYRQLRCYIEDSQOLEIYLIRYNAKHET 774
QY 768 VNYLGTGSLMPLSVQSPIRKCQEPNRCAPHELNPNLDQSCRDEKCAHSHHSHFSLDIDV 827
DB 775 VNPVGTGSLMPLSVQSPIRKCQEPNRCAPHELNPNLDQSCRDEKCAHSHHSHFSLDIDV 808
QY 828 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARYKRAEKWRDRKLE 887
DB 809 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARYKRAEKWRDRKLE 868
QY 888 LETNIVYKEAKESVDALFVNSQDQLQADNTIAMIHAAADKRVHSIREAYLPSELSVPGVN 947
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Search completed: November 27, 2002, 20:25:28

Job time : 58 secs

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DB 869 WETNIVYKEAKESVDALFVNSQYDRLQADNTIAMIHAAADKRVHSIREAYLPSELSVPGVN 928
QY 948 VDIIFEELKGRIFTARFLYDARNVKNKGFNNGLSCHWNKGVHDVEEQNNHRSVLVYVPEWE 1007
DB 929 AALFELEGRIFTARFLYDARNVKNKGFNNGLSCHWNKGVHDVEEQNNHRSVLVYVPEWE 988
QY 1008 AEYSQEVRYVCPGRGYILRVYATYKGYGEGCVTHIETENNTDELKFSNCEVEEYYPNNTVT 1067
DB 989 AEYSQEVRYVCPGRGYILRVYATYKGYGEGCVTHIETENNTDELKFSNCEVEEYYPNNTVT 1048
QY 1068 CNDYTANQBEYGGAYTSRARGYDETYGSSNSVPADYASVYEKSYTDGRDNPCESNRGY 1127
DB 1049 CNDYTANQBEYGGAYTSRARGYDETYGSSNSVPADYASVYEKSYTDGRDNPCESNRGY 1108
QY 1128 GDTPLPAGYVTKLELYFFETDKVWIEIGETEGTFFIVDSVELLME 1174
DB 1109 GDTPLPAGYVTKLELYFFETDKVWIEIGETEGTFFIVDSVELLME 1155
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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 27, 2002, 20:27:55 ; Search time 157 Seconds

(without alignments)  
2879.780 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MENNIOQCVPYCNLNPEV.....IGETGTFIVDSVELLMEE 1174

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO.spool/US09837961/runat\_25112002\_142417\_5983/app\_query.fasta\_1.1351  
-DS=PublishedApplications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blotsum62  
-TRANS=human40.cgi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSI2B=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09837961.ecgn\_1\_1\_63 @runat\_25112002\_142417\_5983  
-NCPU=6 -ICPU=3 -NO\_XLPY -NO\_MMAPP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -YGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications\_NA:

1: /cgn2\_6/ptodata/2/pubna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubna/PTC\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubna/US06\_PUBCOMB.seq:\*  
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6: /cgn2\_6/ptodata/2/pubna/PTC\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubna/US08\_NEW\_PUB.seq:\*  
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9: /cgn2\_6/ptodata/2/pubna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	6244	100.0	3522	10 US-09-826-660-5
2	5879	94.2	3444	10 US-09-826-660-1
3	4812.5	77.1	3534	10 US-09-873-873-25
4	4804.5	76.9	3531	10 US-09-873-873-9
				Sequence 5, Appli
				Sequence 1, Appli
				Sequence 25, Appl
				Sequence 9, Appli

5	4804.5	76.9	3531	10	US-09-873-873-11	Sequence 11, Appl
6	4804.5	76.9	3531	10	US-09-873-873-13	Sequence 13, Appl
7	4745.5	76.0	3534	10	US-09-873-873-27	Sequence 27, Appl
8	4647.5	74.4	3534	10	US-09-873-873-33	Sequence 33, Appl
9	4313.5	69.1	3579	10	US-09-873-873-29	Sequence 29, Appl
10	4211.5	67.4	4360	10	US-09-756-643-1	Sequence 1, Appli
11	4148	66.4	4300	10	US-09-851-194-1	Sequence 1, Appli
12	4042.5	64.7	3489	10	US-09-826-660-20	Sequence 20, Appl
13	4039	64.7	3468	10	US-09-826-660-12	Sequence 12, Appl
14	4039	64.7	3468	10	US-09-826-660-13	Sequence 13, Appl
15	3629.5	58.1	3558	10	US-09-826-660-14	Sequence 14, Appl
16	3185	51.0	1815	10	US-09-826-660-22	Sequence 22, Appl
17	3185	51.0	1815	10	US-09-826-660-3	Sequence 3, Appli
18	3185	51.0	1815	10	US-09-826-660-7	Sequence 7, Appli
19	3185	51.0	1815	10	US-09-826-660-8	Sequence 8, Appli
20	2708	43.4	1641	10	US-09-826-660-9	Sequence 9, Appli
21	2699	43.2	1635	10	US-09-826-660-10	Sequence 10, Appl
22	2077	33.3	3633	12	US-10-032-717-3	Sequence 3, Appli
23	2077	33.3	6613	12	US-10-032-717-28	Sequence 28, Appl
24	2020	32.4	3621	12	US-10-032-717-1	Sequence 1, Appli
25	2020	32.4	4874	12	US-10-032-717-27	Sequence 27, Appl
26	1769	28.3	6930	10	US-09-756-528A-1	Sequence 1, Appli
27	1597.5	25.6	4896	10	US-09-756-528A-3	Sequence 3, Appli
28	1348.5	21.6	1860	10	US-09-826-660-19	Sequence 19, Appl
29	1345	21.5	1839	10	US-09-826-660-16	Sequence 16, Appl
30	1345	21.5	1839	10	US-09-826-660-17	Sequence 17, Appl
31	1345	21.5	1839	10	US-09-826-660-18	Sequence 18, Appl
32	1001	16.0	2022	12	US-10-032-717-17	Sequence 17, Appl
33	981	15.7	2003	12	US-10-032-717-7	Sequence 7, Appli
34	944	15.1	2010	12	US-10-032-717-9	Sequence 9, Appli
35	944	15.1	2010	12	US-10-032-717-15	Sequence 15, Appl
36	937	15.0	1175	10	US-09-851-194-3	Sequence 3, Appli
37	935.5	15.0	1929	10	US-09-826-660-24	Sequence 24, Appl
38	935	15.0	2003	12	US-10-032-717-5	Sequence 5, Appli
39	933	14.9	2022	12	US-10-032-717-11	Sequence 11, Appl
40	932	14.9	2022	12	US-10-032-717-21	Sequence 21, Appl
41	932	14.9	2022	12	US-10-032-717-39	Sequence 39, Appl
42	925.5	14.8	2013	12	US-10-032-717-23	Sequence 23, Appl
43	925.5	14.8	2013	12	US-10-032-717-43	Sequence 43, Appl
44	923	14.8	1860	12	US-10-032-717-19	Sequence 19, Appl
45	912	14.6	1863	12	US-10-032-717-29	Sequence 29, Appl

#### ALIGNMENTS

RESULT 1  
US-09-826-660-5  
; Sequence 5, Application US/09826660  
; Patent No. US20010026940A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Stelman, Steven J.  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: MA-714XC2D1  
; CURRENT APPLICATION NUMBER: US/09/826,660  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/178,252  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: 60/065,215  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/076,445  
; PRIOR FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 3522  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
US-09-826-660-5

Alignment Scores:

Pred. No.: 0 Length: 3522

Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-09-837-961-8 (1-1174) x US-09-826-660-5 (1-3522)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
 Db 1 ATGGAGATAATATTCARAAATCAATGCGTACCTTACATTCGTTTAAATAATCCTGAGTA 60  
 Qy 21 GluileLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeu 40  
 Db 61 GAAATATTAAATGAGAAAGAAAGTACTGCGAGATTACCGTTAGATATATCCTTATCGGTT 120  
 Qy 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 Db 121 ACACGTTTCCCTTTGAGTGAATTTGTTCCAGGTGTGGAGTTGCCGTTTGGATTATTGAT 180  
 Qy 61 LeuileTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGln 80  
 Db 181 TTAATATGGGGTTTATAACTCCTCTGATTGGAGCTTATTTCTTTTACAGATTCAACAA 240  
 Qy 81 LeuileGluArgIleGlnThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 Db 241 TTGATTGACCAAGATAGAAACATTTGGAAGGAAACCGGGCAATTTACTACATTACGAGG 300  
 Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 Db 301 TTAGCAGATAGCTAGAAATTTATATTGAAGCACCATAAGAGAGTGGGAAGCAATCCTAAT 360  
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuile 140  
 Db 361 AATGCAAAATTAAGGAAAGATGCGTATTCGATTTCGTTAAATACAGACGACGCTTAATA 420  
 Qy 141 ThrAlaileAsnAsnPheThrLeuThrSerPheGluileProLeuLeuSerValTyrVal 160  
 Db 421 ACAGCAATAAATAATTTTACACTTACAACTTTTGAATCCCTCTTTATCGGCTATGTT 480  
 Qy 161 GlnAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 Db 481 CAAGCGCGCAATTTACATTTATCATTATTAAGAGACGCTGTATCGTTTGGGAGGGTTGG 540  
 Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuileAsnLeuileHisArg 200  
 Db 541 GGACTGGATATAGCTACTGTTAATATATCATATTAATAGATTAAATCACTTTATTCATAGA 600  
 Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 Db 601 TATACGAAACATTTGTTGGACACATCAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660  
 Qy 221 ThrArgGluTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240  
 Db 661 ACTCGAATAGGCAAGATTCATCACTAGTTTAGAGAGATTTAACACTTACTGTATTAGAT 720  
 Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 Db 721 ATCGTTGCTCTTTTCCGAACATGAGTGTAGACATATCCAAATCAACAGTCATCCCA 780  
 Qy 261 LeuThrArgGluIleTyrThrSerValIleGluAspSerProValSerAlaAsnIle 280  
 Db 781 TTAACAGGGAATTTATACAGTTCAAGTTAGAGATTTAGAGATTTCCAGTTTCTGCTAATA 840  
 Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProHisLeuMetAspPheMet 300  
 Db 841 CCTAATGGTTTTTAATAGGCGGGAATTTGGAGTTAGACCCGCCCACTTTATGGACTTTAG 900  
 Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
 Db 901 AATTCCTTTGTTGTAAGTGCAGAGACTGTTAGAGTCAAACTGCTGTGGGAGGACACITTA 960  
 Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340

Db 961 GTTAGTTACAGAAATACGGCTGCTAACCCTATTAATTTCCCTAGTTACGGGCTTCAAT 1020  
 Qy 341 ProGlyClyAlaIleTrpIleAlaAsnGluAspProArgProPheTyrArgThrLeuSer 360  
 Db 1021 CCTGGTGGCCCAATTTGGATTGCAGATGAGATCCACGTCCTTTTATCGACATTATCA 1080  
 Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 Db 1081 GATCCTCTTTTCCGAGGAGGATTGGGAATCCTCATTTATCTACTGGGCTTAGGGGA 1140  
 Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
 Db 1141 GTAGCATTTCAACAACTGTGTACGACACACACCGCAACATTTAGAAATAGTGGGACATA 1200  
 Qy 401 AspSerLeuAspGluileProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
 Db 1201 GATTCCTAGATGAATCCCACTCAGGATTAATAGTGGGSCACCTTGGAAATGATTAGT 1260  
 Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluileSerGlySerAspSer 440  
 Db 1261 CATGTATTAATCATGTGTACATTTGTACGATGGCCAGTGAGATTTTCAGGAAGTGATCA 1320  
 Qy 441 TrpArgAlaProMetPheSerTyrThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 Db 1321 TGGAGACCTCAATGTTTCTTGGACGACCGTAGTGCAACCCCTACAAATACAAATGAT 1380  
 Qy 461 ProGluArgIleThrGlnIleProLeuValIleAlaHisThrLeuGlnSerGlyThrThr 480  
 Db 1381 CCGGAGAGGATTACTCAATACCATTTGTTAAAGACATACACTTCAGTCAGTACTACT 1440  
 Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
 Db 1441 GTTGTAGAGGGCCCGGTTTACGGGAGGAGATATTTCTTCGACGACACAGTGGAGGCCA 1500  
 Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
 Db 1501 TTTGCTTATACTATTGTTAATATAATGGCAATATCCCAAGGTATCGTGAAGAATA 1560  
 Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
 Db 1561 CGCTATCCCTCTACTCAAAATCTAAGAAATTTACGTACGTTTGCAGGTGAACGATTTT 1620  
 Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
 Db 1621 GCTGGTCAATTTAACAACAAATGATACCGGTGACCCATTAAACATTTCCAAATCTTTAGT 1680  
 Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
 Db 1681 TACGCAACTATTATACAGCTTTTACATTTCCCAATGAGCCAGAGTAGTTTTCACAGTAGT 1740  
 Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
 Db 1741 GCTGATACTTTTATGTCAGGAATGAAGATTTATATAGACAGATTTGAATTTGATTCAGT 1800  
 Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
 Db 1801 ACTGCAACATTTGAAGCAGAAATATGATTTAGAAAGAGACAAAGGCGGTGAATGCGCTG 1860  
 Qy 621 PheThrSerIleAsnGlnIleGlyIleIleThrAspValThrAspTyrHisIleAspGln 640  
 Db 1861 TTTACTTCTATAAACCAATAGGGATAAACAGATGTGACGGATATCATATTGATTCAA 1920  
 Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGlyLysArgGluLeu 660  
 Db 1921 GTATCCCAATTTAGTGGATTGTTTATCAGATGAATTTTGTCTGGATGAAGACGAGATTG 1980  
 Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
 Db 1981 TCCGAGAAAGTCAACATCGGAGCGACTCAGTGTAGCGGAATTTTACTTCAAGATCCA 2040  
 Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700



Db 2041 AACTCAAGGCATCAATAGGCACTAGACCGTGTGGAGAGGAAGTACCGATATATACC 2100  
 Qy 701 ileGlnArgGlyAspValPheLysGluAsnThrValThrLeuProGlyThrPheAsp 720  
 Db 2101 ATCCAAAGGAGATGAGCTATTCAAGAAATATATGTCACATACAGGTACCTTGAT 2160  
 Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
 Db 2161 GAGTCTATCCAACTATTTATATCAAAAAATAGATGAGTGAATTAACCCCTATACT 2220  
 Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
 Db 2221 CGTTATCAATTAAGAGGGTATATCGAGATAGTCAAGACTTAGAATCTATTGATCCGC 2280  
 Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780  
 Db 2281 TATAATGCAAAACACGAAACAGATAATGTCTAGTACCGGTCTCTTTATGCGCGTTTCA 2340  
 Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyrP 800  
 Db 2341 GTCCAAAGTCCCAATCAGAAAGTGTGGAAACCGAATCCGATGCGCCACACCTTGAATGG 2400  
 Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHis 820  
 Db 2401 AATCTGTATCTAGATTGTCTCTGACAGACGGGGAATAATGTGCACATCATCTCGCATCAT 2460  
 Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840  
 Db 2461 TTCTCTCTGGACATTTGATGTCGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG 2520  
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 Db 2521 ATATTCAAGATTAAACGCAAGATGCCATCGCAACGTAGGAATCTAGATTTCTCGAA 2580  
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 Db 2641 GATAACGTGGAATTTGGAATTTGGAACAAATATTTGTTTAAAGAGCAAAAGAACT 2700  
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 Db 2701 GTAGATGCTTTATTGTTAAACTCTCAATATGATCAATTACAAAGCGSATACGAATATGCC 2760  
 Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
 Db 2761 ATGATTCATCGCGCAGATAAAGCTTTTCATAGAAATTCGGGAAGCGTATCTTCCAGAGTTA 2820  
 Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
 Db 2821 TCTGTGATTCGGGTGTAATGTAGACATTTTCGAAGAAATTAAGGGCGTATTTTCACT 2880  
 Qy 961 AlaPheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
 Db 2881 GCATTTCTCTATATGATCGGAAATGTCAATAAAGCGGTATTCATTAATATGCTTA 2940  
 Qy 981 SerCysTyrAsnValLysGlyHisValAspValGluGluAsnHisArgSerVal 1000  
 Db 2941 TCATGCTGGAACGTGAAGGGGATGTAGATGTAGAGAAACAAACCAACCCGTTCCGGTC 3000  
 Qy 1001 LeuValValProGluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
 Db 3001 CTGTGTTCTCCGAATGGGAAGCAGAGGTCTCACAGAAGTTCTGTCTGTCTCGGGTCT 3060  
 Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
 Db 3061 GGTATATCTCTGTCTCAGCGTACAGAGGGGATATGGAGAGGTTTGGTAACCAATT 3120  
 Qy 1041 HisGluIleGluAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
 Db 3121 CATGACATCGAGAACATACAGACGACGAGATTTAGCAACTGCGTAGAAGAGGAGTC 3180

Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluLutyrGlyGly 1080  
 Db 3181 TATCCAAACACACGCTAACGCTGATTAATGATTACTGCAAAATCAAGAAGAAATACGGGGT 3240  
 Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100  
 Db 3241 CGCTACACTTCCCGTATATCGTGATATGAGAACTATATGGAAGCAATCTTCTGTACCA 3300  
 Qy 1101 AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
 Db 3301 GCTGATTTATCGTCAGCTCTATGAGAAATCTATACAGATGGACGAGACAATCTCT 3360  
 Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
 Db 3361 TGTGAATCTTACAGAGGATATGGGATTACACACCACTACCACTGGCTATGTGACAAA 3420  
 Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160  
 Db 3421 GAATTAGATCTTCCAGAAACCGATAAGTATGATGATGAGATCGGAGAAACGGAAGGA 3480  
 Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
 Db 3481 ACATTCATCTGGACACGCGGAATTACTCTTATGAGGAA 3522

## RESULT 2

US-09-826-660-1  
 ; Sequence 1, Application US/09826660  
 ; Patent No. US20010026940A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cardineau, Guy A.  
 ; APPLICANT: Stelman, Steven J.  
 ; APPLICANT: Narva, Kenneth E.  
 ; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
 ; FILE REFERENCE: MA-714XC2D1  
 ; CURRENT APPLICATION NUMBER: US/09/826,660  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 09/178,252  
 ; PRIOR FILING DATE: 1998-10-23  
 ; PRIOR APPLICATION NUMBER: 60/065,215  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/076,445  
 ; PRIOR FILING DATE: 1998-03-02  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 3444  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic B.t. toxin gene  
 US-09-826-660-1

Alignment Scores:  
 Pred. No.: 0 Length: 3444  
 Score: 5879.00 Matches: 1117  
 Percent Similarity: 95.83% Conservative: 8  
 Best Local Similarity: 95.14% Mismatches: 23  
 Query Match: 94.15% Indels: 26  
 DB: 10 Gaps: 1

US-09-837-961-8 (1-1174) x US-09-826-660-1 (1-3444)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
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 Qy 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 Db 61 GAGATTTCTCAACGAGAGAGGTGCTGACTGGCAGTATGCGGTAGACATCTCCCTGCTCCT 120  
 Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60

Db 121 ACACGTTTCCTGCTGAGTTTGTTCACAGGTGTGGAGTTGGCTTGGCTCTTCGAC 180  
Qy 61 LeuiletrpGlyPheileThrProSerAspTrpSerLeuPheLeuLeuGlnleGluGln 80  
Db 181 CTCATCTGGGGCTCATCTCACTCCATCTGATGTGGAGCTCTTCTCTCCAGATTGAACAG 240  
Qy 81 LeuileGlnArgileGluThrLeuGluArgAsnArgAlaileThrThrLeuArgGly 100  
Db 241 TTGATTGACAAAGGATTGAGACTTGGAAAGGAATCGGGCCCATCTACCTCTCGTGGC 300  
Qy 101 LeuAlaAspSerTyrGluileTyrileGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
Db 301 TTACACAGACGATGATGAGATCTACATGTAGACACTTGAAGAGGTGGAGCCCATCTTAC 360  
Qy 121 AsnAlaGlnLeuArgGluAspValArgileArgPheAlaAsnThrAspAspAlaLeuile 140  
Db 361 AATGCCCACTGAGAGAAGATGTCGTATACGCTTTGCTTAACACAGATGATCTTTGATC 420  
Qy 141 ThrAlaileAsnAsnPhethrLeuThrSerPheGluileProLeuLeuSerValTyrVal 160  
Db 421 ACAGCCATCAACAACTTACCCCTTACAGCTTCGAGATCCCTCTCTCTCGGCTCTATGT 480  
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
Db 481 CAAGCTGCTTAACCTGCATCTGCTACTTCTCGCGACGCTGTCTCTTGGCAAGGTTGG 540  
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuileAsnLeuileHisarg 200  
Db 541 GGACTGGACATGCTACTGTCAACAATCACTCAACAGACTCATCAATCTGATTCATCGA 600  
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
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Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
Db 661 ACTCGCAATGGCCAGGTTCAATCACTAGTTTCAGGAGAGACCTTACACTTACTGTGTAG 720  
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
Db 721 ATAGTTGCTCTCTTCGAACTACGATGTTGCTGATCTATCCGATTCAAACGTCATCCCAA 780  
Qy 261 LeuThrArgGluileTyrThrSerSerValIleGluAspSerProValSerAlaAsnle 280  
Db 781 CTTACAGGGAGATCTACACAGTTTCACTGATTCAGTGAAGACTCTCCAGTTTCTCGCAACA 840  
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProHisLeuMetAspPheMet 300  
Db 841 CCCATGGTTTCAACAGGCTGAGTTTGGAGTCAGACCCACCCCATCTCATGAGCTTCATG 900  
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
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Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPhethrLeuThrValPheAsn 340  
Db 961 GTTAGCTCAGCAGACAGGCTGGCAATCGATCACTTTCCTAGTTACGGGGTCTTCAAT 1020  
Qy 341 ProGlyGlyAlaileTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
Db 1021 CCCGGGGGCCCATCTGGATTGAGATGAGATCCACGCTCTTCTTATCGGACCTTGTC 1080  
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
Db 1081 GATCCTCTCTCGTCGAGAGGCTTGGCAATCCCTCACTATGATCTACTCGTCTTGGGGA 1140  
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrile 400  
Db 1141 GTGGCTTTTCAACAACACTGTAGATATCACACCCGGCACATTCAGGAACCTCCGGGACCAT 1200  
Qy 401 AspSerLeuAspGluileProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
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Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluileSerGlySerAspSer 440  
Db 1361 CATCTGCTGANTCATGTTACTTGTGCGTGGCCAGGTGAGATCTCAGGTTCGACTCA 1320  
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
Db 1321 TGGAGACACCAATGTTCTCTTGGAGCATCTAGTGGCTACCCCAACCAACACCATGTAT 1380  
Qy 461 ProGluArgileThrGlnleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
Db 1381 CCAGAGAGATCACTCASATTCCTTGGTGAAGCACACACACTTCAGTCAAGAACTACA 1440  
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgThrSerGlyGlyPro 500  
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Qy 501 PheAlaThrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgile 520  
Db 1501 TTCGGGTACACCATGTCAACATCAATGGCACTTCCCAAGGATCTGTCAGGATA 1560  
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgilePhe 540  
Db 1561 GGCATGCTCTACTACCAATCTAAGAATCTACGTTACGTTGCGAGTGAACGATCTTT 1620  
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
Db 1621 GCTGGTCAGTTCAACAAGACAATGGATACCGGTGATCCACTTACATTCCTCTCTCC 1680  
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
Db 1681 TACGCCACTATCAACACCGGTTCACTTCCCAATGAGCCAGACAGTTCACAGTAGGT 1740  
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Db 1741 GCTGATACCTTCACTCAGCAAGAACTGTACATTCACAGGTTTGAGTTGATTCAGTT 1800  
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Db 1801 ACTGCCACACTCGAGGAGAGTCTGACTTGGAAAGACACAGAGGGGTAAGTCTCTG 1860  
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
Db 1861 TTCACTCTGCTCAATCAGATTGGGCTCAAGACAGATGTGACTGACTATCACATCTGATCG 1920  
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Db 1921 GTTCCCAACCTTGTGAGTGCTCTCTGATGAGTTCGTGTTGGATGAGAGAAGAGTGG 1980  
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
Db 1981 TCCGAGAGAGTCAACATGCTTAGCGACTTAGTGATGAGCGGAACCTGCTTCAAGATCC 2040  
Qy 681 AsnPhelyGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700  
Db 2041 AACCTTCCGGGATCAACAGCACTAGTCTGATGAGGGGAGAGTACGACATCAC 2100  
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
Db 2101 ATTCAAGAGAGTGTATGATGTTTCAAGGAGAACTATGTTACGCTCTTGGTACCTTTGAT 2160  
Qy 721 GlucyTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
Db 2161 GAGTGTATCCCAATACCTTACCAAGATAGATAGTGAATCGAAACTCAAGAGCTACACA 2220  
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
Db 2221 AGATACCACTGTGAGAGTTCATCGAGACAGTCAAGACCTTCAGATCTACCTCATCAGA 2280  
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780  
Db 2281 TACAACGCCAAACATGAGACAGTCAATGTGCTGGGAGGGTTCACCTGCGCCACTTCA 2340

QY 781 ValGlnSerProileArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800  
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Db 2341 GCCCAAGTCCATC----- 2355  
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHis 820  
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Db 2356 -----GCCAAGTGGCCCATCACTCACACAC 2382  
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
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Db 2383 TTCTCCTTGGACATAGAGCTTGGCTGTACCGACCTGACGAGACCTCGGTGTGGGTG 2442  
QY 841 IlePheLysIleLysThrClnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
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Db 2443 ATCTTCAAGATCAAGACTCAAGATGCCATGCCAGCTAGGCAATCTGGAGTTTCTAGAA 2502  
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880  
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Db 2503 GAGAAACCACTTGTGGAGAACCTCGTAGTGAGAGAGGCTGAGAAGAGTGGAGG 2562  
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysSer 900  
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Db 2563 GACAGAGAGAGAGTGGAAATGGGAACAAACATTTGTACAAAGAAAGCCAAAGAAAGC 2622  
QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920  
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Db 2623 GTTGACGCTCTGTGTGAACTCTCAGTATGATAGCTCCAGCTGATACCAACATAGCT 2682  
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
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Db 2683 ATGATTCATGCTGCAGACAAACCGCTTCATAGCATTCGGAAGCTTACCTCTGAACTT 2742  
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
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Db 2743 ACGTGATTCGGGTGCAATCGCTATCTTTGAGAGTTAGAGGGCGCATCTCACT 2802  
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
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Db 2803 GCATTCCTCTGTATGATCGGAGGATGTCATCAGAATGGTGACTTCAACATGGCCTA 2862  
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000  
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Db 2863 TCCTGTGGAATGTGAAGGGCAGCTAGATGTAGAGAAGACAGCAATCACCGCTCTGTC 2922  
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
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Db 2923 CTGTGTGCTCCTGAGTGGGAGCAGAGTTTACAGAAGATTCGTCTGTCTCTGCTGCT 2982  
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
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Db 2983 GGCTACATTCCTCGTGTACCGGCTACAAAGAGGATAGGAGAGGTTGCGCTCACCAT 3042  
QY 1041 HisGluIleGluAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
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Db 3043 CAGAGATTGAGAACACACCGGAGGCTGAGTTTACAGAACCTGCTGAGGAGGAGTGC 3102  
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080  
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Db 3103 TACCCAAACACACCGTACTTGCATGACTACACTGCGACTCAAGAGGAGTATGAGGT 3162  
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100  
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Db 3163 ACTTACACTTCTCGCAATCGAGGATAGGATGAGGCTATGAGAGCAACTCTTCTGTACCC 3222  
QY 1101 AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
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Db 3223 GCTGACTATCATCAGCCTATGAGGAGGCTTACACCGATGAGCTAGGAGCAATCT 3282  
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
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Db 3283 TGCGAACTTAACAGAGGCTATGGGACTACACCGCTTACACCGGCTATGTCACCAA 3342  
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160

Db 3343 GAGTTAGTACTTTCAGAAACCGACAGGTTTGGATTGAGATTGAGAAACGGAGGA 3402  
QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
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Db 3403 ACAFTCATTTGTATAGCGTGGAGTTACTTCTGATGGAGAA 3444  
RESULT 3  
US-09-873-873-25  
; Sequence 25, Application US/09873873  
; Patent No. US20020064865A1  
; GENERAL INFORMATION:  
; APPLICANT: Malivar, Thomas  
; APPLICANT: Gilmer, Amy Jelen  
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxin  
; FILE REFERENCE: MEMO:210--2  
; CURRENT APPLICATION NUMBER: US/09/873,873  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: US 09/253,341  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: US 08/922,505  
; PRIOR FILING DATE: 1997-09-03  
; PRIOR APPLICATION NUMBER: US 08/754,490  
; PRIOR FILING DATE: 1996-11-20  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 3534  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hybrid Delta-Endotoxin  
; NAME/KEY: CDS  
; LOCATION: (1)..(3531)  
US-09-873-873-25  
Alignment Scores:  
Pred. No.: 0 Length: 3534  
Score: 4812.50 Matches: 933  
Percent Similarity: 84.16% Conservative: 66  
Best Local Similarity: 78.60% Mismatches: 165  
Query Match: 77.07% Indels: 23  
DB: 10 Gaps: 9  
US-09-837-961-8 (1-1174) x US-09-873-873-25 (1-3534)  
QY 1 MetGluAsnAsnIleGln--AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu 19  
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Db 1 ATGGATAACAATCCGACATCAATGAATGCATCTCTATAATTGTTAAGTAACCTGAA 60  
QY 20 ValGluIleLeuAsnGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38  
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Db 61 GTAGAAGTATTAGTGGAGAAAGAAATAGAAACTGGTTACACCCCAATCGATATTCCTTG 120  
QY 39 SerLeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58  
|||||  
Db 121 TCGCTTAACGCAATTTCTTTTGTAGTGAATTTGTCGCGTGTGATTTGCTTAGGACTA 180  
QY 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78  
|||||  
Db 181 GTGTATATATATGGGAATTTTGGTCCCTCTCAATGGGAGCGATTTCTGTACAAAT 240  
QY 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu 98  
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Db 241 GAACAGTTAATTAACCAAGAAATAGAAATTCGCTAGGAACCAAGCCATTTCTAGATA 300  
QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118  
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Db 301 GAAGGACTTAAGCAATCTTTATCAAAATTTACGCAATCTTTTAGAGATGGGAGAGAT 360  
QY 119 ProAsnAsnAlaGlnLeuLeuArgGluAspValArgIleArgPheAlaAsnThrAspAla 138  
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Db 361 CCTACTATCCAGCATTAAGAGAGAGATGCGTATTCATTCATGACATGACATGACAGTGC 420

Qy 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158  
 Db 421 CTTACACCGCTATTCCTCTTTTGGCAGTTCAAAATATCAAGTCTCTTTATCAGTA 480  
 Qy 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln 178  
 Db 481 TATGTTCAAGTCGCAATTTACATTTTATCAGTTTTCAGTATTTGAGAGATGTTTCAGTGTGTGGACAA 540  
 Qy 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIle 198  
 Db 541 AGTGGGATTTGATGCGGACATCATCAATAGTCGTTATATTAATTAAGTACGCTTAT 600  
 Qy 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218  
 Db 601 GCGAACTATACAGATCATGCTGACGCTGCTACAAATACGGGATTAGAGCGGTATGGGA 660  
 Qy 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrVal 238  
 Db 661 CCGATTTCTAGAGATTGGATAAGATATAATCAATTTAGAAGAAATTAACACTAACTGTA 720  
 Qy 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258  
 Db 721 TTAGATATCGTTCTCTATTTCGCACTATGATAGTAGAAGCAATCCAAATTCGACAGTT 780  
 Qy 259 SerGlnHisThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278  
 Db 781 TCCCAATTAACAAGAGAAATTTATACAAACCCAGATTAGAA-----822  
 Qy 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294  
 Db 823 AATTTGATGTAGTTTCGAGGCTCGCTCAGGCGCATAGAAAGAGATATTAGAGTCCA 882  
 Qy 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314  
 Db 883 CATTTGATGGATATACTATAACAGATATAACCACTATACCGATGCTCATAGGGGTTATTAT 942  
 Qy 315 ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332  
 Db 943 TATGGTCAGGCGATCAAAATATGGCTTCCTGTAGGCTTTTCGGGGCCAGATTCAC 1002  
 Qy 333 PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTrpIleAlaAspGluAsp 351  
 Db 1003 TTTCCGCTATATGAACTATGGAATATCCAGCTCCACAAACAGATATTTGTGCTCACTA 1062  
 Qy 352 ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368  
 Db 1063 GGTACGGCGTATAGACATTTATGCTCCACTTATATAGAGACCTTTATATATAGGG 1122  
 Qy 369 PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387  
 Db 1123 ATAAATATCAACAACTATCTGTTCTTCAGGGACAGAAATTTGCTTATGGAACCTCTCA 1182  
 Qy 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407  
 Db 1183 AATTGGCATCCGCTGATATACAGAAAGCGGACGATAGATTCGCTGGATGAATACCG 1242  
 Qy 408 ProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr 427  
 Db 1243 CCACAGATAACACAGTCCACCTAGGCAAGGATTTATGATCATCGATTAAGCCATGTTTCA 1302  
 Qy 428 PheValArgTyrProGlyGluIleSerGlySerAspSerIrrpArgAlaProMetPheSer 447  
 Db 1303 ATGTTTCGTCAGGCTTTAGTAATAGTAGTCTAAGTATAATAGAGCTCCAAATGTTTCT 1362  
 Qy 448 TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle 467  
 Db 1363 TGGACGCGCGGTAGTGAACCCCTACAAATACAAATGATCGGAGAGGATTAACATA 1422  
 Qy 468 ProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe 487  
 Db 1423 CCAATTCGTTAAAGCAGCATACACTTACGTAGTCTACTGTTGTGAAGGGCCCGGGTTT 1482

Qy 488 ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaIleThrIleValAsn 507  
 Db 1483 ACGGGAGAGATATTCCTCGAGCAACAAAGTGGAGGACCAATTCCTTATCTATATGTTAAT 1542  
 Qy 508 IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsn 527  
 Db 1543 ATAAATGGGCAATTTACCCAAAGGTATCGTGCAGAAATACGCTATGCTCTACTACAAAT 1602  
 Qy 528 LeuArgIleTyrValThrValAlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr 547  
 Db 1603 CTAGCAATTTACGTAAACGTTGACAGTGAACGGATTTTCTGGTCAATTTAACAAACA 1662  
 Qy 548 MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla 567  
 Db 1663 ATGGATACCGGTGACCAATTAACATTCCAATCTTTTACGCACTATTAATACAGCT 1722  
 Qy 568 PheThrPheProMetSerGlnSerSerPheThrValGlyAlaAspThrPheSerSerGly 587  
 Db 1723 TTTACATTTCCCAATGACGACAGATGTTTCCAGTAGTGTGATACCTTTTAGTTCAGGG 1782  
 Qy 588 AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu 607  
 Db 1783 AATGAAGTTTATATAGACAGATTTGAATGATTCCAGTTTACTGCAACATTTGAAGCAGAA 1842  
 Qy 608 TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle 627  
 Db 1843 TATGATTTAGAAAGACGACAAAGCGGTGAATCGCTGTTTACTCTATAAACCAATA 1902  
 Qy 628 GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys 647  
 Db 1903 GSGATAAAACAGATGTGACGGATTAATCATATTGATCAAGTATCCAAATTTAGTGGATTGT 1962  
 Qy 648 LeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysValLysHisAla 667  
 Db 1963 TTATCAGATGAATTTGTCTGGATGAAAGCGAGATTTGTCGAGAAAGTCAACATGCG 2022  
 Qy 668 LysArgLeuSerAspGluArgAsnLeuLeuLeuAspProAsnPheLysGlyIleAsnArg 687  
 Db 2023 AAGCCACTCAGTGTGACGGAAATTTACTTCAAGTCCAACTTCAAGGSCATCAATAGG 2082  
 Qy 688 GlnLeuAspArgGlyTrpArgGlySerThrAspIleThrIleGlnArgGlyAspAspVal 707  
 Db 2083 CAACVAGACCTGTGTGGAGAGAGTACGGATATTACCATCCAAAGAGGAGATGACGTA 2142  
 Qy 708 PheLysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu 727  
 Db 2143 TTCAAGAAATATATGTCACACTACCGATACCTTTGATGAGTGTCTATCCAAATATTG 2202  
 Qy 728 TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr 747  
 Db 2203 TATCAAAAATCGATGAATCAAAATTAAGAGCTTTACCCGTTTATCAATTAAGAGGSTAT 2262  
 Qy 748 IleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr 767  
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 Db 2323 GTAAATGTGCCAGSPACGGGTCTCTATGCGCGCTTTTACGCCAAAGTCCAAATCGGAAAG 2382  
 Qy 788 CysGlyGluProAsnArgCysAlaProHisIleLeuGluTrpAsnProAspLeuAspCysSer 807  
 Db 2383 TGTGGAGAGCGCAATCGATGCGCGCCACACCTTGAATGGAATCTCTGACTTAGATTGTTCG 2442  
 Qy 808 CysArgAspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAspIleAspVal 827  
 Db 2443 TGTAGGATGGAGAAAGTGTGCCATCATTCGCGATCATTTCTCTTAGACATTGATGTA 2502  
 Qy 828 GlyCysThrAspLeuAsnGluAspValIrrpValIlePheLysIleLysThrGln 847  
 Db 2503 GGATGTACAGACTTAAATGAGAGACCTAGGTGTATGGGTGATCTTTAAGATTAAAGCCAA 2562  
 Qy 848 AspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluLysProLeuValGlyGlu 867

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Db 2563 CATGGCGCAGCACTAGGGAATCTAGAGTTCTTCGAGAGAAACCATAGTAGAGAA 2622  
Qy 868 AlaLeuAlaArgValIysArgAlaGluLysLysTTPAqAspLysArgGluLysLeuGlu 887  
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Db 2623 GCGCTAGCTCGTGGAAAGACGGAGAAAATGGAGAGACAAACGGTGAATAATGGAA 2682  
Qy 888 LeuGluThrAsnIleValIysGluAlaLysGluSerValAspAlaLeuPheValAsn 907  
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Db 2683 TGGGAACAATAATCGTTATAAGAGGCACAAAGAAATCTGTAGATGCTTTATTTGTAAC 2742  
Qy 908 SerGlnItyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAlaAlaAspLys 927  
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Db 2743 TCTCAATATGATCAATTAACAACGGATACGAATATTCGATGATTCATCGGCGACATAAA 2802  
Qy 928 ArgValHisArgIleArgGluAlaItyrLeuProGluLeuSerValIleProGlyValAsn 947  
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Db 2803 CGTGTTCATAGCATTCGAGAAGCTTATCTGCCTGAGCTGCTGTGATTCGGGTGTCAT 2862  
Qy 948 ValAspIlePheGluGluLeuLysGlyArgIlePheThrAlaPhePheLeuTyrAspAla 967  
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Db 2863 GCGGCTATTTTGAACAATTAGAAGGGCGTATTTTCACTGCAATTCCTCCTATATCATGCG 2922  
Qy 968 ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnValLysGly 987  
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Db 2923 AGAATGTCTATAAATGGTATTTTAAATGCGTTTATCTGCTGGAACGTGAAGCG 2982  
Qy 988 HisValAspValGluGluGlnAsnAsnHisArgSerValLeuValValProGluTrpGlu 1007  
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Db 2983 CATGTAGATGTAGAAGAACAAACCAACCGTTCGGTCTGTTGTTCCGGGAATGGAA 3042  
Qy 1008 AlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeuArgValThr 1027  
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Db 3043 GCGAAGTGTCAACAAGTCTGCTGCTCCGGGTGGTGTATATCTTCTGCTGCACA 3102  
Qy 1028 AlaTyrLysGluGlyTyrGlyGluGlyCysValThrIleHisGluIleGluAsnAsnThr 1047  
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Db 3103 GCGTACAAGGAGGATATGGAAGGTTCCGTAACCATTCATGAGATCAGAACAAATACA 3162  
Qy 1048 AspGluLeuLysPheSerAsnCysValGluGluGluValTyrProAsnAsnThrValThr 1067  
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Db 3163 GAGCAACTGAAGTTTASCAACTGCGTGAAGAGGAAATCTATCCAAATTAACACGCTAAG 3222  
Qy 1068 CysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyValTyrThrSerArgAsnArg 1087  
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Db 3223 TGTAAATGATTAATCTAATCAGAGAGATACGGAGGTGCGTACACTTCTGTAATCGA 3282  
Qy 1088 GlyTyrAspGluThrTyrGlySerAsnSerSerValProAlaAspTyrAlaSerValTyr 1107  
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Db 3283 GGATAACAAGACT-----CCTTCGTACCAGCTGATTATCGCTCAGTCTAT 3330  
Qy 1108 GluGluLysSerTyrThrAspGlyArgArgAspAsnProCysGluSerAsnArgGlyTyr 1127  
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Db 3331 GAAGAAAATCGTATACAGATGACGAGAGAGAAATCCTTGTGAATTAACAGAGGGTAT 3390  
Qy 1128 GlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyrPheProGlu 1147  
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Db 3391 AGGATTACAGCCACTACCACTGCTGTATGTGACAAAGAAATTAAGAACTCCAGAA 3450  
Qy 1148 ThrAspLysValTrpIleGluIleGlyGluThrGluGlyThrPheIleValAspSerVal 1167  
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Db 3451 ACCGAAGGATGATGGATTGAGATTGGAGAACGGAAGCAACATTTATCTGTCGACACGGT 3510  
Qy 1168 GluLeuLeuMetGlnGlu 1174  
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Db 3511 GAATTACTCTTATGGAGAA 3531

## RESULT 4

US-09-873-873-9

: Sequence 9, Application US/09873873

: Patent No. US20020064865A1

: GENERAL INFORMATION:

: APPLICANT: Malvar, Thomas

: APPLICANT: Gilmer, Amy Jelen  
: TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxin  
: FILE REFERENCE: MECO:210-2  
: CURRENT APPLICATION NUMBER: US/09/873,873  
: PRIOR FILING DATE: 2001-08-20  
: PRIOR APPLICATION NUMBER: US 09/253,341  
: PRIOR FILING DATE: 1999-02-19  
: PRIOR APPLICATION NUMBER: US 08/922,505  
: PRIOR FILING DATE: 1997-09-03  
: PRIOR APPLICATION NUMBER: US 08/754,490  
: PRIOR FILING DATE: 1996-11-20  
: NUMBER OF SEQ ID NOS: 35  
: SOFTWARE: Patentin version 3.0  
: SEQ ID NO 9  
: LENGTH: 3531  
: TYPE: DNA  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: Hybrid Delta-Endotoxin  
: NAME/KEY: CDS  
: LOCATION: (1)..(3531)  
US-09-873-873-9

Alignment Scores:  
Pred. No.: 0 Length: 3531  
Score: 4804.50 Matches: 932  
Percent Similarity: 84.08% Conservative: 66  
Best Local Similarity: 78.52% Mismatches: 166  
Query Match: 76.95% Indels: 23  
DB: Gaps: 9

US-09-837-961-8 (1-1174) x US-09-873-873-9 (1-3531)  
Qy 1 MetGluAsnAsnIleGln---AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu 19  
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Db 1 ATGATAACAATCGCAACATCAATGAATGATCTCTTATAATGTTTAACTAACCCGAA 60  
Qy 20 ValGluIleLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38  
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Db 61 GTAGAAGTATTAGTGGGAGAAAGAAATAGAACTGGTACACCCCAATCGATATTCTCTG 120  
Qy 39 SerLeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58  
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Db 121 TCGTAAACCAATTTCTTTTTCAGTGAATTTTCCCGGTGCTGATTTGCTTAGGACTA 180  
Qy 59 PheAspLeuIleTyrGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78  
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Db 181 GTTGATAATAATGGGAAATTTTGGTCCCTCTCAATGGGACGCATTTCTGTACAAAT 240  
Qy 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu 98  
|||||  
Db 241 GAACAGTTAATATACCAAGAATAAGAAATTCGCTAGGAACCAAGCAATTTCTAGATTA 300  
Qy 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118  
|||||  
Db 301 GAAGACTTAAGCAATTTTATCAAAATTTACCGAATTTTATAGAGATGGGAAGCAGAT 360  
Qy 119 ProAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAla 138  
|||||  
Db 361 CCTACTAATCAGCATTAAGAGAGATGCGTATTCATTCATCAATGACATGACAGTGC 420  
Qy 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158  
|||||  
Db 421 CTTACAACCGCTATTCCTCTTTTTCAGTTCCAAATTTATCAAGTCTCTTTTATCATGA 480  
Qy 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln 178  
|||||  
Db 481 TATGTTCAAGTCGAAATTTTACATTTTATCAGTTTTTGAGAGATGTTTCAGTGTGTCG 540  
Qy 179 GlyTyrGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeu 198  
|||||  
Db 541 AGGTGGGATTTGATGCGCGACATCATCAATAGCTGTTAATGATTAATCACTAGCTTATT 600

Qy	199	HisArgTyrThrTyrHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly	218
Db	601	GGCAACTATACAGATTCTCTACGCTGGTACCAATACGGGATTAGAACGTGATTGGGA	660
Qy	219	ThrAsnThrArgTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrVal	238
Db	661	CCGGATTCTAGAGATTGGTAGGTATATCAATTTAGAGAGAAATTAACACATACTGA	720
Qy	239	LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrPheGlnThrSer	258
Db	721	TTAGATATCGTTCTCTGTTCCGAATATGATAGTAGTAGAAGATATCAATTCGAACAGT	780
Qy	259	SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla	278
Db	781	TCCCAATTACAGAGAAATTTATACAAACCCAGTATTAGAA-----	832
Qy	279	AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro	294
Db	823	AATTTTCAGTGTAGTTTTCGAGGCTCGGCTCAGGSCATAGAGAAGATATTAGAGTCCA	882
Qy	295	HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr	314
Db	883	CAITTCATGATATACTTAAACAGTATAACATCTATACGGATGCTCATAGGGGTATTAT	942
Qy	315	ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn	332
Db	943	TATGTCAGGGCATCAATATATGCTCTCTCTAGGGTTTCGGGCCAGAAATTCAC	1002
Qy	333	PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTrpIleAlaAspGluAsp	351
Db	1003	TTTCCGCTATATGGAATCTATGGGAATGCGCTCCACAAACACATGATTGTGCTCACTA	1062
Qy	352	ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly	368
Db	1063	GGTCAGGGCGTGATAGACATTTATCGTCCACTTTATATAGAGACCTTTTAAATATAGG	1122
Qy	369	PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly	387
Db	1123	ATAAATTAATCAACAACATATCTGTCTTGACGGGACAGAAATTGCTTATAGAACTCTCA	1182
Qy	388	ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro	407
Db	1183	AATTGGCATCCGCTGATACAGAAAGCGAAGCGTAGATTCTCGTGGATGAATACCG	1242
Qy	408	ProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr	427
Db	1243	CCACAGAATAACAACGTGCCACCTCAGGCAAGGATTTAGTCATCGAATTAAGCCATGTTCA	1302
Qy	428	PheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProPheSer	447
Db	1303	ATGTTTCTGTCAGGCTTAGTATAGTAGTGAAGTAAATAGAGAGCTCCCAATGTTTCT	1362
Qy	448	TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle	467
Db	1363	TGGACGCACCGTAGTCAACCCCTACAAATACAAATTGATCCGAGAGGATTACTCAATA	1422
Qy	468	ProLeuValIysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe	487
Db	1423	CCATGGTAAAGCACATACATTCAGTCAGGTACTCTGTTGTAAAGAGGCGCCGGGTTT	1482
Qy	488	ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn	507
Db	1483	ACGGGAGAGATATCTCCACGACAAAGTGGAGGACCATTTGCTTATACTATTGTTAAT	1542
Qy	508	IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsn	527
Db	1543	ATAAATGGCAATTTACCCCAAGGATATCGTGCAGAAATACGCTATGCTCTACTACAAAT	1602
Qy	528	LeuArgIleTyrValThrValAlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr	547
Db	1603	CTAAGAAATTTACGTTAAGGTTGACGGTGAACGGATTTTTCCTGGTCAATTTAACAAACA	1662
Qy	548	MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla	567

Db	1663	ATGGATACCGGTGAACCATTAACATTCCAACTCTTTAGTTACGCAACTATTAATACAGCT	1722
Qy	568	PhetThrPheProMetSerGlnSerSerPheThrValGlyAlaAspThrPheSerSerGly	587
Db	1723	TTTACATTTCCCAATGAGCCAGAGTAGTTTTCACAGTAGGTGCTGATACTTTAGTTAGG	1782
Qy	588	AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu	607
Db	1783	AATGAAGTTTATATAGACAGATTTGAATTTGATTCAGTTACTGCAACATTTGAAGCAGAA	1842
Qy	608	TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle	627
Db	1843	TATGATTTAGAAAGACACAAAGCGGTGAATGCCTGTTTACTTCTATPAACCAATA	1902
Qy	628	GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys	647
Db	1903	GGGATATAAACACAGATGTGACGAGATTATCATATGATCAAGTATCCAATTTAGTGGATTGT	1962
Qy	648	LeuSerAspGluPheCysLeuAspGlnLysArgGluLeuSerGluLysValLysHisAla	667
Db	1963	TTTATCAGATGAATTTTGTCTGGATGAAGAAGCAGAAATGTCCGGAGAAGTCARACATGCG	2022
Qy	668	LysArgLeuSerAspGluArgAsnLeuLeuGlnAspProAsnPheLysGlyIleAsnArg	687
Db	2023	AAGCGACTCAGTCATGACGGGAATTTACTTCAAGATCCAAACTTCAAAAGCATCAATAGG	2082
Qy	688	GlnLeuAspArgGlyTrpArgGlySerThrAspIleThrIleGlnArgGlyAspAspVal	707
Db	2083	CAACTAGACCGTGGTGGAGAGAGTAGTAGGATATTACATCCAAAGAGGAGATGACGTA	2142
Qy	708	PheLysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu	727
Db	2143	TTCAAGAAATTAATGTCACACTACAGGTACCTTTGATGAGTGTATCCCAACATAATTG	2202
Qy	728	TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr	747
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Qy	748	IleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr	767
Db	2263	ATCGAAGATAGTCCAGACTTAGAAATCATTAATTCGTACATGCAAAACATCAACA	2322
Qy	768	ValAsnValLeuGlyThrGlySerLeuTrpProLeuSerValGlnSerProIleArgLys	787
Db	2323	GTAATGTGCAGGTACGGGTTCCCTATGCGCGCTTCAGCCCAAGTCCCAATCGGAAG	2382
Qy	788	CysGlyGluProAsnArgCysAlaProHisLeuGluTyrAsnProAspLeuAspCysSer	807
Db	2383	TGTGAGAGCGGAATCGATGCGCGCCACACCTTGAATGGAATCCTGACTAGATTGTTGG	2442
Qy	808	CysArgAspGlyGluLysCysAlaHisSerHisHisPheSerLeuAspIleAspVal	827
Db	2443	TGTAGGATGAGAAAAGTGTGCCATCATCTGCCATCATTTCTCTTACAGCATTTGATGA	2502
Qy	828	GlyCysThrAspLeuAsnGlnAspLeuAspValTyrValIlePheLysIleLysThrGln	847
Db	2503	CGATGTACACACTTAATGAGGACCTAGGTGTATGGGTGATCTTTAAGATTAAGACGCAA	2562
Qy	848	AspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluGluLysProLeuValGlyGlu	867
Db	2563	GATGGCACCAAGACTAGGGAATCTAGAGTTCTTCGAAGAGAAACCACTTATAGTAGGAA	2622
Qy	868	AlaLeuAlaArgValLysArgAlaGluLysLysTrpArgAspLysArgGluLysLeuGlu	887
Db	2623	CGCTAGTCTGCTGAAAAGCGGAGAAAAAATGGAGAGCAACCGTGAATAATTGGAA	2682
Qy	888	LeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeuPheValAsn	907
Db	2683	TGGAAACAAATATCGTTTATAAAGAGGCAAAAGATCTGTAGATGCTTTATTGTAAC	2742
Qy	908	SerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAlaAspLys	927

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Db 2743 TCTCAATATGATCAATAACAGCGGATACCAATATTCGCCATGATTCATCGCGCAGATAAA 2802
Qy 928 ArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValAsn 947
Db 2803 CGTGTCATAGCATTCGGAAGCTTATCTGCTGAGCTGCTGTGATTCGGGTGTCAAT 2862
Qy 948 ValAspIlePheGluLeuLeuLysGlyArgIlePheThrAlaPhePheLeuTyrAspAla 967
Db 2863 GCGGCTATTTTGAAGAANTAGAGGGCGTATTTTCACATGCAATCTCCCTATATGATGCG 2922
Qy 968 ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnValLysGly 987
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Qy 988 HisValAspValGluGluGlnAsnAsnHisArgSerValLeuValValProGluTrpGlu 1007
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Qy 1008 AlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeuArgValThr 1027
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Qy 1048 AspGluLeuLysPheSerAsnCysValGluGluValTyrProAsnAsnThrValThr 1067
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Qy 1068 CysAsnAspTyrThrAlaAsnGlnGluTyrGlyGlyAlaTyrThrSerArgAsnArg 1087
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Qy 1088 GlyTyrAspGluThrTyrGlySerAsnSerSerValProAlaAspTyrAlaSerValTyr 1107
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Qy 1108 GluGluLysSerTyrThrAspGlyArgArgAspAsnProCysGluSerAsnArgGlyTyr 1127
Db 3331 GAAGAAATATCGTATACAGATGGACGACGAGAGAAATCCTGTGTGAATTTACAGAGGTAT 3390
Qy 1128 GlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyrPheProGlu 1147
Db 3391 AGGGATTACACGCCCATACCACTGCTGTTATGTACAAAAGAAATAGAACTCCCCAGAA 3450
Qy 1148 ThrAspLysValTrpIleGluIleGlyGluThrGluGlyThrPheIleValAspSerVal 1167
Db 3451 ACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGAACATTTATCGTGGACACGGT 3510
Qy 1168 GluLeuLeuMetGluGlu 1174
Db 3511 GAATTACTCTTATGGAGAA 3531

RESULT 5
US-09-873-873-11
; Sequence 11, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 11
; LENGTH: 3531
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-09-873-873-11

Alignment Scores:
Pred. No.: 0 Length: 3531
Score: 4804.50 Matches: 932
Percent Similarity: 84.08% Conservative: 66
Best Local Similarity: 78.52% Mismatches: 166
Query Match: 76.95% Indels: 23
DB: 10 Gaps: 9

US-09-837-961-8 (1-1174) x US-09-873-873-11 (1-3531)
Qy 1 MetGluAsnAsnIleGln---AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu 19
Db 1 ATGGATAACAATCCCGAACATCAATGAATGATTCCTTATATATTTGTTAAGTAACCCCTGAA 60
Qy 20 ValGluIleLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38
Db 61 GTAGAGATATTAGCTGGAGAGAAGAAATAGAACTGGTTACACCCCATCGATATTTCTTGG 120
Qy 39 SerLeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58
Db 121 TCGCTAACCAATTTCTTTTGTAGTGAATTTGTCGGGTCTGGATTTGTGTAGGACTA 180
Qy 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78
Db 181 GTTGATATATATGGGAATTTTGTGCTCCTCTCAATGGGACCATTTCTTTGTACAAAT 240
Qy 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu 98
Db 241 GAACACTTAATTAACCAAGAGATAGAGAAATTCGCTAGGAACCAAGCCATTTCTAGATTA 300
Qy 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118
Db 301 GAAGSACTAAGCAATCTTTATCAAAATTTACGAGAAATCTTTTAGAGAGTGGAGAGCAT 360
Qy 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAla 138
Db 361 CCTACTAATCCAGCATTAAGAGAGAGATCGGTATTCAATTAATCAATGACATGACATGCC 420
Qy 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158
Db 421 CTTACAACCGCTATTCTCTTTTTCAGTTCAAAATATATCAAGTTCTCTTTTATCAGTA 480
Qy 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln 178
Db 481 TATGTTCAAGCTGCAAAATTTACATTTATCAGTTTTCAGATTTTTCAGATGTTTGGACAA 540
Qy 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgGluLeuLeuLeuIle 198
Db 541 AGGTGGGATTTGATCCCGGACTATCAATATAGTTCGTTATTAATGATTAACTAGGCTTATT 600
Qy 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218
Db 601 GCAACTATACAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrVal 238
Db 661 CCGGATTCAGAGATTTGGGTAAAGTATAATCAATTTAGAAGAGAAATTAACACTAAGTGA 720
Qy 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258
Db 721 TTAGATATCGTTCTGTTCCCGAATTTATGATAGTAAAGATATCAATTCGAATCGACAGTT 780
Qy 259 SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278

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781 TCCCAATTACAGAGAAATTTATACAAACCCAGTATTAGAA----- 822  
QY AsnIleProAsnGlyPheAsnArgAla-----GlupheGlyValArgProPro 294  
Db APTTTTGATGGTAGTTTCGAGCTCGGCTCAGGGCATAGAAAGATATTAGAGTCCA 882  
QY HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314  
Db CATTTTGATGATATATTACAGTATACCATCTATACGATCTCATAGGGGTTATTAT 942  
QY ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332  
Db TATTTGCTCAGGGCATCAATAATAGGCTTCTCTGTAGGTTTTCGGGGCCAGAAATCACT 1002  
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Db TTTCCGCTATATGGAACATATGGGAATTCAGCTCCCAACAACAGTATTGTGTCTCAACTA 1062  
QY ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368  
Db GTTCAGGGCGGTATAGAACATTTATCGTCACCTTTATATAGAGACCTTTTATATAGGG 1122  
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QY PheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProMetPheSer 447  
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QY TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGluIle 467  
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QY ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn 507  
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QY LeuArgIleTyrValThrValAlaGlyArgIlePheAlaGlyGlnPheAsnLysThr 547  
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QY MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla 567  
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QY AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu 607  
Db ATGCAAGCTTTTATATAGACAGATTTGAATTTGATTCACGTTACTGCAACATTTTGAAGCAGAA 1842  
QY TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle 627

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QY GlnLeuAspArgGlyTrpArgGlySerThrAspIleThrIleGlnArgGlyAspAspVal 707  
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QY ValAsnValLeuGluThrGlySerLeuTrpProLeuSerValGlnSerProIleArgLys 787  
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QY 988 HisValAspValGluGluGlnAsnHisArgSerValLeuValValProGluTrpGlu 1007  
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 DB 3103 GCGTACAGAGGAGGATATGGAGAGGTTCCGTACCACTCATGATGAGATCGAGAACATACA 3162  
 QY 1048 AspGluLeuLysPheSerAsnCysValGluGluGluValTyrProAsnAsnThrValThr 1067  
 DB 3163 GACCAACTGAGTTAGCAACTCGGTAGAAGAGGAATCTATCCAAATAACACGGTAACG 3222  
 QY 1068 CysAsnAspTyrThrAlaAsnGlnGluGlyTyrGlyAlaTyrThrSerArgAsnArg 1087  
 DB 3223 TGTAAATGATTATCTGTAATCAAGAGATACGAGGTGGGTACACTTCTCGTAATCGA 3282  
 QY 1088 GlyTyrAspGluThrTyrGlySerAsnSerValProAlaAspTyrAlaSerValTyr 1107  
 DB 3283 GGATATAACGAGCT-----CCITCCGTACAGCTGATTATGCGTCACTCTAT 3330  
 QY 1108 GluGluLysSerTyrThrAspGlyArgAspAsnProCysGluSerAsnArgGlyTyr 1127  
 DB 3331 GAAGAAAAATCGTATACAGATGGAGAGAGAGAAATCCTTGTGAATTTACAGAGGGTAT 3390  
 QY 1128 GlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyrPheProGlu 1147  
 DB 3391 AGGATTACAGCGCACCTACCACTGGTGTATGTGACAAAGAAATAGAAATCTTCCCGAG 3450  
 QY 1148 ThrAspLysValTrpIleGluIleGlyGluThrGluGlyThrPheIleValAspSerVal 1167  
 DB 3451 ACCGATAAGGTATGGATTGAGATTGGAGAACGAGAGACATTTATCGTGGACAGCGTG 3510  
 QY 1168 GluLeuLeuLeuMetGluGlu 1174  
 DB 3511 GAATTACTCTCTTATGGAGAA 3531

RESULT 6

US-09-873-873-13  
 ; Sequence 13, Application US/09873873  
 ; Patent No. US20020064865A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Malvar, Thomas  
 ; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins  
 ; FILE REFERENCE: MECO:210--2  
 ; CURRENT APPLICATION NUMBER: US/09/873,873  
 ; PRIOR FILING DATE: 2001-08-20  
 ; PRIOR APPLICATION NUMBER: US 09/253,341  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: US 08/922,505  
 ; PRIOR FILING DATE: 1997-09-03  
 ; PRIOR APPLICATION NUMBER: US 08/754,490  
 ; PRIOR FILING DATE: 1996-11-20  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 13  
 ; LENGTH: 3531  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybrid Delta-Endotoxin  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(3531)  
 US-09-873-873-13

Alignment Scores:  
 Pred. No.: 0 Length: 3531  
 Score: 4804.50 Matches: 932

Percent Similarity: 84.08% Conservative: 66  
 Best Local Similarity: 78.52% Mismatches: 166  
 Query Match: 76.95% Indels: 23  
 DB: 10 Gaps: 9  
 US-09-837-961-8 (1-1174) x US-09-873-873-13 (1-3531)  
 QY 1 MetGluAsnAsnIleGln---AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu 19  
 DB 1 ATGGATACAAATCCGAACATCAATGAATTCCTTATAATTTGTTAAGTAACCTGAA 60  
 QY 20 ValGluIleLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38  
 DB 61 GTAGAAGTATTAGTGGGAGAAAGATAGAACTGTTACACCCCAATGATATTTCCTTG 120  
 QY 39 SerLeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58  
 DB 121 TCGCTAACGCAATTTCTTTTTCAGTGAATTTCTCCCGTGTGGATTGTCTTAGGACTA 180  
 QY 59 PheAspLeuIleTyrGlyPheIleThrProSerAspTyrPheSerLeuPheLeuGlnIle 78  
 DB 181 GTTGATATAATATGGGAATTTTGGTCCCTCTCAATGGGACGATTTCTGTACAAAT 240  
 QY 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeu 98  
 DB 241 GAACAGTTAATTACCAAGAAATAGAGAATTCCTAGAACCAAGCAATTTCTAGATT 300  
 QY 99 ArgGlyLeuAlaAspSerTyrGluIleGluAlaLeuArgGluTrpGluAlaAsn 118  
 DB 301 GAAGACTAAGCAATCTTATCAAAATTTACGACAATCTTTTACAGAGTGGAGACGAT 360  
 QY 119 ProAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAla 138  
 DB 361 CCTACTAATCCAGCATTAAGAGAGATCGTATTCATTCATGACATGAACAGTGC 420  
 QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158  
 DB 421 CTTACAACCGCTATTCCTCTTTTTCAGTTCAAAATTTATCAAGTCTCTTTTATCAGTA 480  
 QY 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln 178  
 DB 481 TATGTTCAAGCTGCAAAATTTACATTTTATCAGTTTGTAGAGATGTTTCAGTGTGGCAA 540  
 QY 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAspLeu 198  
 DB 541 AGTGGGATTTGATGCCGCGACTATCAATAGTGGTATATTAATGATTAACTAGCTTATT 600  
 QY 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218  
 DB 601 GGCAACTATACAGATTATGCTGCTACGCTGCTACAAATACGGGATAGAACGTATGGGA 660  
 QY 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrVal 238  
 DB 661 CCGGATCTAGAGATTGGGTAAGTATAATCAATTTAGAAGAAATTAACACTAAGTGA 720  
 QY 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258  
 DB 721 TTAGATATCTGCTGCTGTTCCCGAATATGATAGTAGAAGATATCCAAATCGAACAGTT 780  
 QY 259 SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278  
 DB 781 TCCCAATTACAGAGAAATTTATACAAACCCAGTATTAGAA-----822  
 QY 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294  
 DB 823 AATTTTGATGGTAGTTTTCGAGGCTCGGCTACGGGCATAGAAAGAGTATTAGAGTCCA 882  
 QY 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314  
 DB 883 CATTGTGATGATATACCTTAACAGTATACCATCTATACGATGCTCATAGGGGTTATTAT 942  
 QY 315 ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332

Db	943	TATTGGTCAGCGCATCAAAATAATGGCTTCCTGTAGGGTTTTTCGGGGCCAGAAATTCAC	1002
Qy	333	PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTrpIleAlaaspCluasp	351
Db	1003	TTTTTGGCTATATGAAGACTATGGGAATGAGCTCCACAACAAGTATTTGTTGCTCAACTA	1052
Qy	332	ProArgPropheTyrArgThrLeuSerAspProValPheValArgGly-----Gly	368
Db	1063	GGTCAGGCGGTGTATAGCAACATTATCGTCCACTTTATATAGAGACCTTTTAAATATAGG	1122
Qy	369	PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly	387
Db	1123	ATAAATAATCAACAACATATCTGTCTTGACGGGACAGAAATTTGCTATATGGAACCTCCTCA	1182
Qy	388	ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerIleuaspGluIlePro	407
Db	1183	AATTGGCAATCCGCTGTATACAGAAAGCGGACGGTAGATTCGCTGGATGAATACCG	1242
Qy	408	ProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAspHisValThr	427
Db	1243	CCACAGAATAACAAGTCGCACCTAGCGAAGGATTAGTCATCGATTAAAGCCATGTTTCA	1302
Qy	428	PheValargTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProMetPheSer	447
Db	1303	ATGTTTCGTTCCAGGCTTTAGTAATAGTACTGTAAAGTAAATAAGAGCTCCCAATGTTTCT	1362
Qy	448	TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle	467
Db	1363	TGGAGCAGCCGTAGTCGACCCCTCAAAATACAAITGATCCGGAGAGGATTACTCAATA	1422
Qy	468	ProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe	487
Db	1423	CCATTGGTAAAGCACATACATCTCAGTCAGTACTACTGTTGTTAAAGGGCCCGGGTTT	1482
Qy	488	ThrGlyClyAspIleLeuargArgThrSerGlyGlyProPheAlaTyrThrIleValAsn	507
Db	1483	ACGGGAGCAGATATCTTCGACCAACAGTGGAGGACCATTTGCTTATACTATTGTAAAT	1542
Qy	508	IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleAargTyrAlaSerThrThrAsn	527
Db	1543	ATAATGGGCAATTACCCAAAGGTATGTCGCAAGATACGCTATGCTCTACTACAAAT	1602
Qy	528	LeuArgIleTyrValThrValAlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr	547
Db	1603	CTAAGAATTTACGTAAACGGTTGCAGGTGAACGGATTTTGCTGCTCAATTTACAAAACA	1662
Qy	548	MetAspThrClyAspProLeuthrPheGlnSerPheSerTyrAlaThrIleAsnThrAla	567
Db	1663	ATGGATACGGTGACCCATTAACATTCCAATCTTTAGTTACGCAACTATTAAATACAGCT	1722
Qy	568	PheThrPheProMetSerGlnSerSerPheThrValGlyAlaAspThrPheSerSerGly	587
Db	1723	TTTACATTCCCAATGACCCAGAGTAGTTTCACAGTAGTGCTGATACTTTTAGTTCAGGG	1782
Qy	588	AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu	607
Db	1783	AATCAAGTTTATATAGACAGATTCAATTTGATTCAGTAGTGCTGATACTTTAGTTCAGGG	1842
Qy	608	TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle	627
Db	1843	TATGATTTAGAAGAGCACAAAGCGGTGAATCGCTGTTTACTTCTATAAACCAAAATA	1902
Qy	628	GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys	647
Db	1903	GGGATAAAACAGATGTGACGATTATCATATTCAATCAAGTATCCCAATTTAGTGTGATTGT	1962
Qy	648	LeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysValLysHisAla	667
Db	1963	TTATCAGATCAATTTTGTCTGATGAAAAGCGAATTTGTCGAGAGAGTCARACATGGC	2022
Qy	668	LysArgLeuSerAspGluArgAsnLeuLeuGlnAspProAsnPheLysGlyIleAsnArg	687
Db	2023	AAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAACTTCAAGGCAATCAATAGG	2082

QY	688	GlnLeuAspArgGlyTrpArgGlySerThrAspIleThrIleGlnArgGlyAspVal	707
Db	2083	CAACTAGACCGTGGTTGGAGAGGAAGTACGGATATTACCATCCAAAGGAGATGACGTA	2142
QY	708	PheIysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu	727
Db	2143	TTCAAGAAATATTGTACACTACCAAGTACCTTTGATGAGTGCTATCCAACATATTG	2202
QY	728	TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr	747
Db	2203	TATCAAAAATCGATGAATCAAAATTAAGAAGCTTTACCCGTTATCAATTAAGAGGTTAT	2262
QY	748	IleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr	767
Db	2263	ATCGAAGATAGTCAAGACTTAGAAATCTATTAAATTCGCTTACAATGCAAAACATGAACA	2322
QY	768	ValAsnValLeuGlyThrGlySerLeuTrpProLeuSerValGlnSerProIleArgLys	787
Db	2323	GTAATATGTCAGAGTACGGGTCTCTTATGCGCCGCTTACGCCAAAGTCCAATCGGAAG	2382
QY	788	CysGlyGluProAsnArgCysAlaProHisLeuGluTrpAsnProAspLeuAspCysSer	807
Db	2383	TGTGGAGACCGGAATCGATCGCGCCACACCTTGAATGGAAATCCTGACTTAGATTTGTCG	2442
QY	808	CysArgAspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAspIleAspVal	827
Db	2443	TGTAGGATGGAGAAAGTGTGCCATCATTCGCATCAATTCCTCTAGACATTGATGTA	2502
QY	828	GlyCysThrAspLeuAsnGluAspLeuAspValIrpValIlePheLysIleLysThrGln	847
Db	2503	GGATGTACAGACTTAATAGGACCTTAGGTGTATGGTGATCTTTAAGATTAAGACGCAA	2562
QY	848	AspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluGluLysProLeuValGlyGlu	867
Db	2563	GATGGCAGCAAGACTAGGAATCTAGAGTTTCTCGAAGAGAAACCATTTAGTAGGAA	2622
QY	868	AlaLeuAlaArgValLysArgAlaGluLysLysTrpArgAspLysArgGluLysLeuGlu	887
Db	2623	GGCGTAGCTCGTGTGAAGACGGAGAAATAATGGAGAGACAAACGTGAAAATTTGGAA	2682
QY	888	LeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeuPheValAsn	907
Db	2683	TGGGAAACAAATATCGTTTATAAGAGGCAAAAGAAATCTGTAGATCGTTTATTGTAAAC	2742
QY	908	SerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAlaAspLys	927
Db	2743	TCTCAATATGATCAATTACAAGCGATGCAATATTGCCATGATTCATCGGCAGATAAA	2802
QY	928	ArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValAsn	947
Db	2803	CGTGTTATAGCATTCGAGAACTTATCTGCTGAGCTGTCTGTGTGATTCGGGTGTCAAT	2862
QY	948	ValAspIlePheGluGluLeuLysGlyIlePheThrAlaPhePheLeuTyrAspAla	967
Db	2863	GGGGCTATTTTTGAAGAATTAGAAGGCGTATTTTCACTGCAATCTCCCTATATGATGCG	2922
QY	968	ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnValLysGly	987
Db	2923	AGAAATGTCAATTPAAANATGGTGATTTTAATATGGCTTATCTGCTGGAACTGAAGGG	2982
QY	988	HisValAspValGluGluGlnAsnAsnHisArgSerValLeuValIrpGluTrpGlu	1007
Db	2983	CATGTAGATGTAGAAGAACAAACCAACCGTTCCGTCCTTGTGTTCCCGAATGGGNA	3042
QY	1008	AlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeuArgValThr	1027
Db	3043	CGTAAAGTGTCAAGAAAGTTGCGTACCACTTCAATGATGAGATCGAACAATACA	3102
QY	1028	AlaTyrLysGluGlyTyrGlyGluGlyCysValThrIleHisGluIleGluAsnAsnThr	1047
Db	3103	CGTACAAGGAGGATATGGAGAGGTTGCGTACCACTTCAATGATGAGATCGAACAATACA	3162



Qy	388	ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro	407
Db	1183	AATTTGCCAATCCGCTGTATACAGAAACCGGACGGTAGATTGCTGGATGAATACCG	1242
Qy	408	ProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr	427
Db	1243	CCACAGAATAACAACGTGCCACCTAGCGAAGGATTTAGTCATCGATTAGCCATGTTTCA	1302
Qy	428	PheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProMetPheSer	447
Db	1303	ATGTTTCGTTCAGGCTTTAGTAATACTAGTGAAGTATAATAAGAGCTCCGTATCTCT	1362
Qy	448	TrpHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle	467
Db	1363	TGGATACATCGTAGTCTGAATTAATAATAATAATGTCATCGGATAGTATTACTCAATA	1422
Qy	468	ProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe	487
Db	1423	CCATTGGTAAGACATACACTTCAGTCAGGTACTACTGTGTGAAGAGGCCCGGGTTT	1482
Qy	488	ThrGlyGlyAspIleLeuArgThrSerGlyGlyProPheAlaTyrThrIleValAsn	507
Db	1483	ACGGAGGAGATATCTTCGACAACTCGAGGACCATTGCTTATACTATTGTTAAT	1542
Qy	508	IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleAargTyrAlaSerThrThrAsn	527
Db	1543	ATAAATGGGCAATTACCCAAAGGTATCGTCAAGAATACGCTATGCTCTACTACAAAT	1602
Qy	528	LeuArgIleTyrValThrValAlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr	547
Db	1603	CTAAGAATTACGTACGGTTCGCGTGAACGGATTTTGCTGGTCAATTACAAACA	1662
Qy	548	MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla	567
Db	1663	ATGGATACCGGTACCCCATTAACATCCAACTCTTTAGTTACGCAACTATTAAATACAGT	1722
Qy	568	PheThrPheProMetSerGlnSerPheThrValGlyAlaAspThrPheSerSerGly	587
Db	1723	TTTACATTCCAATGACGACAGTAGTTTCACAGTAGGTGCTGATCTTTTAGTTCAGGG	1782
Qy	588	AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu	607
Db	1783	AATCAAGTTTATATACACAGATTGAATTGATTCAGTCTAGTCACACATTTGAAGACAA	1842
Qy	608	TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle	627
Db	1843	TATGATTTAGAAGAGCACAAAGCGGTGAATGGCGTGTTTACTTCTATAAACCAATA	1902
Qy	628	GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys	647
Db	1903	GGGTAAACACAGTGTGACGGATTATCATATTGATCAAGTATCCAAATTAGTGGATTGT	1962
Qy	648	LeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysValLysHisAla	667
Db	1963	TTATCAGATCAATTTGCTGTGATGAAAAGCGAGAAATGTCCGAGAAAGTCAACATGCG	2022
Qy	668	LysArgLeuSerAspGluArgAsnLeuGlnAspProAsnPheLysGlyIleAsnArg	687
Db	2023	ARGCGATCAGTGTATGAGCGGAATTTACTTCAAGATCCAACTTCAAAGGCATCAATAGG	2082
Qy	688	GlnLeuAspArgGlyTrpArgGlySerThrAspIleThrIleGlnArgGlyAspAspVal	707
Db	2083	CAACTAGACCGTGGTGGAGAGGAGTACGGATATTACATCCAAAGAGGACATCAGCTA	2142
Qy	708	PheLysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu	727
Db	2143	TTCAAGAGAAATTTATGTCACACTACACGGTACCTTTGATGCTGCTATCCAACTATTG	2202
Qy	728	TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr	747
Db	2203	TATCAAAAATTCATGAATCAAAATTAAGCGCTTTACCCGTTTATCAATTAAGAGGTAT	2262

Qy	748	lledgluaspserglnaspLeuGlulIleTyrLeuIleArgTyrAsnAlaIyHisIgluThr	767
Db	2263	ATCGAAGATAGTCAAGACTTTAGAAATCTATTAAATTCGTACAAATGCGAAACATGAACA	2322
Qy	766	ValAsnValLeuGlyThrGlySerLeuTTPProLeuSerValGlnSerProIleArgLys	787
Db	2323	GTAATGTGCCAGTAGCGGGTCTCTATGGCGCTTCAGCCCAAGTCCCAATCGGAAG	2382
Qy	788	CysGlyGluProAsnArgCysAlaProHisLeuGluTTPAsnProAspLeuAspCysSer	807
Db	2383	TGTGAGAGCGGAATCGATCGCGGCACACCTTGAATGGAATCCTGACTAGATTGTTGC	2442
Qy	808	CysArgaspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAspIleAspVal	827
Db	2443	TGTAGGATGAGAAAAGTGTGCCATCATTCGCATCATTTCTCCTTAGACATTGATCTA	2502
Qy	828	GlyCysThrAspLeuAsnGluAspValTTPValIlePheLysIleIyThrGln	847
Db	2503	GGATGTACAGACTTAAATGAGGACCTAGGTGTATGGTGATCTTTAAGATTAAAGCGCA	2562
Qy	848	AspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluGluLysProLeuValIcLgLu	867
Db	2563	CATGGCACCGACACTAGGGAATCTAGAGTTCTCGAGAGAAACCATTAAGTAGGAA	2622
Qy	868	AlaLeualaargVallysArgAlaGluLysLysTTPArgAspLysArgGluLysLeuGlu	887
Db	2623	CGCGTAGCTCGTGTGAAAAGAGCGGAGAAAAAATGGAGACAAACGTGAAAAATCGAA	2682
Qy	888	LeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeuPheValAsn	907
Db	2683	TGGGAACAATAATCGTTTATAAGAGGCAAGAAGATCTGAGATGCTTTATTGTAAAC	2742
Qy	908	SerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAlaAlaAspLys	927
Db	2743	TCTCAATATGATCAATTACAAAGCGGATAGCATATTTGCCATGNTTCAGCGGAGATAA	2802
Qy	928	ArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValAsn	947
Db	2803	CGTGTCTATAGCATTCAGAAAGCTTATCTGCCTGAGCTGCTGATTCGCGGTCTCAAT	2862
Qy	948	ValAspIlePheGluGluLeuLysGlyArgIlePheThrAlaPhePheLeuTyrAspAla	967
Db	2863	CGCGCTATTTTGAAGAATTAGSAGGCGGTATTTTCATGCAATTCCTCTATATGATCGG	2922
Qy	968	ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTTPAsnValLysGly	987
Db	2923	AGAAATGTCATTAATAATGGTATTTATATAGCTTATCCTGCTGGAAAGTGAAGGG	2982
Qy	988	HisValAspValGluGluGlnAsnAsnHisArgSerValLeuValProGlyTTPGlu	1007
Db	2983	CATGTAGATGTAGAAGAACAAAAACACCAACGTCGCTGCTTGTTCGGAATGGAA	3042
Qy	1008	AlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeuArgValThr	1027
Db	3043	GCAGAAGTGTACAAGAAGTCTGTCTGTCGGGTGCGGTATATCTCTCGTGTACACA	3102
Qy	1028	AlaTyrLysGluGlyTyrGlyGluGlyCysValThrIleHisGluIleGluAsnAsnThr	1047
Db	3103	CGGTACAAAGGAGGATATGAGAAGGTTCCGTACCATTCATGAGTCGAGAACATACA	3162
Qy	1048	AspGluLeuLysPheSerAsnCysValGluGluValTyrProAsnAsnThrValThr	1067
Db	3163	GACCAACTGAAGTTTAGCAACTCGGTAGAAGAGGAAATCTATCCAATAACACGGTAACG	3222
Qy	1068	CysAsnAspTyrThrAlaAsnGlnGluTyrGlyValaTyrThrSerArgAsnArg	1087
Db	3223	TGTAATGATTATACTGTAATCAAGAAGAAATACGAGAGTGCCTACACTTCCTGTAATCGA	3282
Qy	1088	GlyTyrAspGluThrTyrGlySerAsnSerSerValProAlaAspTyrAlaSerValTyr	1107
Db	3283	GCATATACCAAGACT-----CCTCCGTCAGCAGCTGATATGCGTCACTAT	3330
Qy	1108	GluGluLysSerTyrThrAspGlyArgArgAspAsnProCysGluSerAsnArgGlyTyr	1127

Db 3331 GAAGAAAAATCGTATACAGATGACGAGAGAGAAATCCTGTGTAATTAACAGAGGTAT 3390  
 QY 1128 GlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyrPheProGlu 1147  
 Db 3391 AGGGATTACAGCGCACTACCACTGGTATGTATGTACAAAAGAAATAGAAATCTCCCGAGAA 3450  
 QY 1148 ThrAspLysValTrpIleGluIleGlyGluThrGluGlyThrPheIleValAspSerVal 1167  
 Db 3451 ACCGATAGGTATGGATTGAGATTGAGAAACGAGAAACATTTATCGTGGACAGCGTG 3510  
 QY 1168 GluLeuLeuLeuMetGluGlu 1174  
 Db 3511 GAATTACTCCTTATGGAGAA 3531

RESULT 8

US-09-873-873-33  
 ; Sequence 33, Application US/09873873  
 ; Patent No. US20020064865A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Malvar, Thomas  
 ; APPLICANT: Gilmer, Amy Jelen  
 ; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins  
 ; FILE REFERENCE: MECO:210-2  
 ; CURRENT APPLICATION NUMBER: US/09/873,873  
 ; CURRENT FILING DATE: 2001-08-20  
 ; PRIOR APPLICATION NUMBER: US 09/253,341  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: US 08/922,505  
 ; PRIOR FILING DATE: 1997-09-03  
 ; PRIOR APPLICATION NUMBER: US 08/754,490  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 33  
 ; LENGTH: 3534  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybrid Delta-Endotoxin  
 US-09-873-873-33

Alignment Scores:

Pred. No.: 0 Length: 3534  
 Score: 4647.50 Matches: 907  
 Percent Similarity: 82.48% Conservative: 72  
 Best Local Similarity: 76.41% Mismatches: 185  
 Query Match: 74.43% Indels: 23  
 Gaps: 9

US-09-837-961-8 (1-1174) x US-09-873-873-33 (1-3534)

QY 1 MetGluAsnIleGln---AsnGlnCysValProTyrAsnCysLeuAsnProGlu 19  
 Db 1 ATGGATAACAATCCGAAACATCAATGAATGATCCCTATTAATTTGTTAAGTAACCCCTGAA 60  
 QY 20 ValGluIleLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38  
 Db 61 GTAGAGATTATAGTGGAGAGAAAGAAAGAACTGGTTACACCCCAATCGATTTCTCTTG 120  
 QY 39 SerLeuThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58  
 Db 121 TCAGTAACGCAATTTCTTTTGTAGTGAATTTGTTCCCGGTCTGGATTTGTAGGACTA 180  
 QY 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIle 78  
 Db 181 GTTGATATAATATGGGAATTTTGTGTCCTCTCAATGGGACGCAATTTCTGTACAAAT 240  
 QY 79 GluGluLeuLeuGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeu 98  
 Db 241 GAACAGTTAATTAACCAAGAAATAGAGAAATTCGCTAGGAACCAAGCAATTTCTAGATA 300  
 QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118

Db 301 GAAGGACTAAGCAATCTTTTATCAAAATTTACGCAAGATCTTTTAGAGAGTGGGAGCAGAT 360  
 QY 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAla 138  
 Db 361 CCTACTAATCCAGCAATTAAGAGAGATGCGTATTTCATTAATCAATGACATGAACAGTGCC 420  
 QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158  
 Db 421 CTTACACCCCTATTCTCTTTTGCAGTTCAAAATTTATCAAGTTCTCTTTTATCATGTA 480  
 QY 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln 178  
 Db 481 TATGTTCAAGCTCGAATTTACATTTATCATGTTTGAGAGATGTTTCAGTGTGTGGCAA 540  
 QY 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgIleLeuLeuLeu 198  
 Db 541 AGTGGGGATTTGATGCGCGGACTATCAATAGTCGTTATATGATGATTTAACTAGGCTTATT 600  
 QY 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218  
 Db 601 GGCACATATACAGATTTGCTGACCTGTCACATACGGGATTAGACGTGATGGGGA 660  
 QY 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrVal 238  
 Db 661 CCGGATTTCTAGAGATTGGGTAAAGTATATCAATTTAGAGAGAAATTAACACTGTA 720  
 QY 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258  
 Db 721 TTAGATATCCTGCTCTGTCGCGAATTTATGATAGTAGAAGATATCCATTCGAACAGTT 780  
 QY 259 SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278  
 Db 781 TCCCAATTACAGAGAAATTTATACAAACCCAGTATTAGAA-----822  
 QY 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294  
 Db 823 AATTTGATGCTAGTTTTCGAGGCTCGGCTCAGGCGCATAGAAAGAGTATTAGGAGTCCA 882  
 QY 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGluThr 314  
 Db 883 CATTTGATGATATACTTAACAGTAAACCATCTATACGATGCTCATAGGGGTATTAT 942  
 QY 315 ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332  
 Db 943 TATTTGTCAGGCGCATCAATAATAGCTTCTCTGAGGTTTTCGGGGCCAGAAATTCAC 1002  
 QY 333 PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTrpIleAlaAspGluAsp 351  
 Db 1003 TTTCCGCTATATGGAACTATGGAAATGCGCTCCACCAACAGTATTGTCTCAACTA 1062  
 QY 352 ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368  
 Db 1063 GGTCAAGGCGCTGATAGAACATTTATCGTCCACTTTATATAGAGACCTTTTAATATAGG 1122  
 QY 369 PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387  
 Db 1123 ATAATAATCAACAACATACTGTTCTTGACGGGACAGCAATTTGCTTATGGAACTCTCTCA 1182  
 QY 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407  
 Db 1183 AATTTGCCATCCCTGTATACAGAAAAGCGAAGCGTAGATTCGCTGGATGAATACCG 1242  
 QY 408 ProGluAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr 427  
 Db 1243 CCACAGAAATAACAACGTGCCACCTAGCAAGAGTTAGTCATCGATTAGCCATGTTCA 1302  
 QY 428 PheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProMetPheSer 447  
 Db 1303 ATGTTTCGTTACGCTTTAGTAAATAGTAGTAAATATAGAGCTCTCTATGTTCTCT 1362  
 QY 448 TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGluIle 467

Db 1363 TGGATACATCGTAGTCTGAATTTAATAATAATAATTCATCGGATAGTATTACTCAATA 1422  
QY 468 ProLeuValLysAlaHisThrLeuGlnSerGlyThrValValArgGlyProGlyPhe 487  
Db 1423 CCATTGGTAAAGACATACACTTCAGTCAGTACTACTGTGTGAAGAGGCCGGGTTT 1482  
QY 488 ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn 507  
Db 1483 ACGGAGAGATATCTTCGACGACACAGTAGGAGGACCATTTGCTTACTATTGTTAAT 1542  
QY 508 IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrAsn 527  
Db 1543 ATAAATGGCAATTTACCCCAAGGTATCGTGCAAGAAATACGCTACTACAAAT 1602  
QY 528 LeuArgIleTyrValThrValAlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr 547  
Db 1603 CTAGAATTTACGTAACGGTTTCAGGTGAACGGATTTTGTCTGGTCAATTTAAACAAACA 1662  
QY 548 MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla 567  
Db 1663 ATGGATACCGGTGACCCATTAACATTCATCTTTAGTTACGCACTATTAAATACAGCT 1722  
QY 568 PheThrPheProMetSerGlnSerSerPheThrValGlyAlaAspThrPheSerSerGly 587  
Db 1723 TTTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGGTGCTGATCTTTAGTTTCAGGG 1782  
QY 588 AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu 607  
Db 1783 AATGAGTTTATATAGACAGATTTGAATGATTCAGTTACTGCAACACTCGAGGCTGAA 1842  
QY 608 TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle 627  
Db 1843 TATAATCTGAAAGAGCGCAGAGCGGTGAATCGCGTGTTCAGTCTACAAACCACTA 1902  
QY 628 GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys 647  
Db 1903 GGGCTAAACAAATGAACGGATATCATATTGATCAAGTGTCCAAATTTAGTTACGTAT 1962  
QY 648 LeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysValLysHisAla 667  
Db 1963 TTATCGATGAAATTTGTCTGGATGAAGCGAAGTGTCCGAGAAAGTCAAAACATGCG 2022  
QY 668 LysArgLeuSerAspGluArgAsnLeuGlnLeuAsnProAsnPheLysGlyIleAsnArg 687  
Db 2023 AAGCGACTAGTGAACGCAATTTACTCAAGATTCAAATTTCAAGACATTAATAGG 2082  
QY 688 GlnLeuAspArgGlyTyrArgGlySerThrAspIleThrIleGlnArgGlyAspVal 707  
Db 2083 CAACCAAGACGTGGTGGGCGGAAGTACAGGGATTCACCATCCAAAGGAGGATGAGTA 2142  
QY 708 PheLysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu 727  
Db 2143 TTTAAAGAAAATACGTCACATATCAGTACCTTTGATGAGTGTATCCACAAATTTG 2202  
QY 728 TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr 747  
Db 2203 TATCAAAAATTCGATGAATCAAAATTAAGCCCTTTACCCGCTTATCAATTAAGAGGGTAT 2262  
QY 748 IleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr 767  
Db 2263 ATCGAAGATAGTCAAGACTTAGAAATCTATTTAATTCGCTACAAATGCAAAACATGAACA 2322  
QY 768 ValAsnValLeuGlyThrGlySerLeuTyrProLeuSerValGlnSerProIleArgLys 787  
Db 2323 GTRAAATGCGCAGGTACGGGTTCTTATGCGCGCTTTACGCCCAAAATCCAAATCGGAAG 2382  
QY 788 CysGlyGluProAsnArgCysAlaProHisLeuGluTrpAsnProAspLeuAspCysSer 807  
Db 2383 TGTGAGAGCGGAATCGATCGCGCCACACTTGAATGAATCCTGACTTAGATTGTCG 2442  
QY 808 CysArgAspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAspIleAspVal 827  
Db 2443 TGTAGGATGGAGAAAAGTGTGCCCATTCATTCGCATCTTCTCCTTAGACATTTAGTGA 2502

QY 828 GlyCysThrAspLeuAsnGluAspLeuAspValTrpValIlePheLysIleLysThrGln 847  
Db 2503 GGTATCAGACCTTAAATGAGACCTAGGTGTATGGTGATCTTTAAGATTAAAGACGAA 2562  
QY 848 AspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluLysProLeuValGlyGlu 867  
Db 2563 GATGGCACCGCAAGACTAGGAATCTAGAGTTTCTCGAAGAGAAACCATTTAGTAGAGAA 2622  
QY 868 AlaLeuAlaArgValLysArgAlaGluLysLysTrpArgAspLysArgGluLysLeuGlu 887  
Db 2623 CGCTAGTCTGTGTAAGAGCGGAGAAAATGAGAGACAAACGTTGAAAATTTGGA 2682  
QY 888 LeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeuPheValAsn 907  
Db 2683 TGGGAAACAAATATCGTTTATAAAGAGGCAAAAGAAATCTGTAGATGCTTTTATTGTAAC 2742  
QY 908 SerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAlaAlaAspLys 927  
Db 2743 TCTCAATATGATCAATTTACAAGCGGATACGAATATTGCCATGATTCTCGCGCAGATAA 2802  
QY 928 ArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValAsn 947  
Db 2803 CGTGTTCATGCAATTCGAGAAAGCTTATCTGCTGAGCTGTCTGTGATTCCGGGTGCAAT 2862  
QY 948 ValAspIlePheGluGluLeuLysGlyArgIlePheThrAlaPheLeuTyrAspAla 967  
Db 2863 CGCGCTATTTTGAAGAAATTAGAAGGCGGTATTTTCACTGCAATCTCCCTATATGATGCG 2922  
QY 968 ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnValLysGly 987  
Db 2923 AGAATGTCAATTAATAATGTCATTTTAATTAATGCTTTATCTCTGGAACTGAAAGGG 2982  
QY 988 HisValAspValGluGluGlnAsnAsnHisArgSerValLeuValValProGluTrpGlu 1007  
Db 2983 CATGTAGATGTAGAAGAACAAACAAACACGTTCCGTCCTTGTGTTCCGSAATGGAA 3042  
QY 1008 AlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeuArgValThr 1027  
Db 3043 GCAGAAGTGTACAAAGAGTTCGTGCTGTCCGGGTGCTGCTATATCTTCGTGTGTCACA 3102  
QY 1028 AlaTyrLysGluGlyTyrGlyGluGlyCysValThrIleHisGluIleGluAsnAsnThr 1047  
Db 3103 CGGTACAGAGGAGGATATGAGAAAGTTGCTAACCAATTCATGAGATCGAGAAACATACA 3162  
QY 1048 AspGluLeuLysPheSerAsnCysValGluGluValTyrProAsnAsnThrValThr 1067  
Db 3163 GACGAACCTGAAGTTTAGCAACTGCGTAGAAGAGAAATCTATCCAAATAACACGTAACG 3222  
QY 1068 CysAsnAspTyrThrAlaAsnGlnGluTyrGlyGlyAlaTyrThrSerArgAsnArg 1087  
Db 3223 TGTAAATGATTATCTGTAATCAAGAAAGATACGAGGTCGCTACACTTCTCGTAATCGA 3282  
QY 1088 GlyTyrAspGluThrTyrGlySerAsnSerValProAlaAspTyrAlaSerValTyr 1107  
Db 3283 GGATATAACGAGCT-----CCCTCCGTACCACCTGATTATGCGTCACTCTAT 3330  
QY 1108 GluGluLysSerTyrThrAspGlyArgArgAspAsnProCysGluSerAsnArgGlyTyr 1127  
Db 3331 GAAGAAAATTCGTATACAGATGAGAGAGAGAAATCCTTGTGAATTTAACAGAGGGTAT 3390  
QY 1128 GlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyrPheProGlu 1147  
Db 3391 AGGATTTACAGCCACCTACCATGTTGTTATGTGACAAAAGAAATAGAAATCTTCCCCAGAA 3450  
QY 1148 ThrAspLysValTrpIleGluIleGlyGluThrGluGlyThrPheIleValAspSerVal 1167  
Db 3451 ACCGATAGGTATGGATGAGATTGAGAAACCGAAGAACATTTATCTGTCGACAGCGTG 3510  
QY 1168 GluLeuLeuLeuMetGluGlu 1174  
Db 3511 GAATTACTCCTTATGGAGGAA 3531

## RESULT 9

US-09-873-873-29  
 ; Sequence 29, Application US/09873873  
 ; Patent No. US20020064865A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Malvar, Thomas  
 ; APPLICANT: Gilmer, Amy Jelen  
 ; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins  
 ; FILE REFERENCE: MCO:210--2  
 ; CURRENT APPLICATION NUMBER: US/09/873,873  
 ; CURRENT FILING DATE: 2001-08-20  
 ; PRIOR APPLICATION NUMBER: US 09/253,341  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: US 08/922,505  
 ; PRIOR FILING DATE: 1997-09-03  
 ; PRIOR APPLICATION NUMBER: US 08/754,490  
 ; PRIOR FILING DATE: 1996-11-20  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 29  
 ; LENGTH: 3579  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybrid Delta-Endotoxin  
 US-09-873-873-29

## Alignment Scores:

Pred. No.: 0 Length: 3579  
 Score: 4313.50 Matches: 844  
 Percent Similarity: 78.42% Conservatives: 97  
 Best Local Similarity: 70.33% Mismatches: 226  
 Query Match: 69.08% Indels: 33  
 DB: 10 Gaps: 12

US-09-837-961-8 (1-1174) x US-09-873-873-29 (1-3579)

QY 1 MetGluAsnAlaLeuGln---AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu 19  
 Db 1 ATGGATAACAATCCGAACATCAATGATGATTCCTTATATATTGTTAAAGTAACCCGAA 60  
 QY 20 ValGluLeuLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38  
 Db 61 GTAGAGATATTAGGTGGAGAAGAAATAGAACTGTTACACCCCAATCGATATTTCCTTG 120  
 QY 39 SerLeuThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58  
 Db 121 TCGTACGCAATTTCTTTGAGTGAATTTGTTCCCGGTGCTGGATTGCTTAGGACTA 180  
 QY 59 PheAspLeuLeuTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78  
 Db 181 GTTCATATAATATGGGAATTTTGGTCCCTCTCAATGGGACGATTTCTTGTACAAATT 240  
 QY 79 GluGlnLeuLeuGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeu 98  
 Db 241 GAACAGTAAATTAACCAAGAATAAGAGAATTCGCTAGGACCAAGCCATTCTAGATTA 300  
 QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118  
 Db 301 GAAGACTACGATCTTATCAATTAACCAAGATCTTTAGAGAGTGGGAAGCAGAT 360  
 QY 119 ProAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAla 138  
 Db 361 CCTACTAATCCAGCATTAAGAGAAGAGATGGGTATTCATTAATGACATGAACAGTCC 420  
 QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuSerVal 158  
 Db 421 CTTACAACCGTATTTCCTCTTTTCAGTCAAAATATCAAGTTCCTCTTTTTCAGTA 480  
 QY 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyCln 178  
 Db 481 TATGTTCAAGCTGCAAAATTTACATTTATCAGTTTGTAGAGATGTTTCAGTCTTTGGACA 540

QY 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIle 198  
 Db 541 AGGTGGGATTTGATGCGCGACATCAATAGTCGTTATATAATGATTAACTAGGCTTATT 600  
 QY 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218  
 Db 601 GGCAACTATACAGATTATGCTGTAGCTGTGACAAATAGCGGATTAGAGCTGTATGGGA 660  
 QY 219 ThrAsnThrArgGlnTTPAlaPheAsnGlnPheArgArgAspLeuThrLeuThrVal 238  
 Db 661 CCGATTCTAGAGATTGGTAAAGTATATCAATTTAGAAGAGAAATTAACACTACTACTA 720  
 QY 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258  
 Db 721 TTAGATATCGTGTCTGTTCCCGAATTTATGATAGTAGAAGATATCAATTCGAACAGTT 780  
 QY 259 SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278  
 Db 781 TCCCAATTAACAGAGAAATTTATACAAACCCAGTATTAGAA-----822  
 QY 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294  
 Db 823 AATTTGATGGTAGTTTCGAGGCTCGCTCAGGCATAGAAAGAAAGTATTAGAGATCCA 882  
 QY 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314  
 Db 883 CATTTGATGGATATACTTAACAGTATACCATCTATACGGATGCTCATAGGGGTTATTAT 942  
 QY 315 ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332  
 Db 943 TATTGGTCAGGGCATCAAAATAATGGCTTCTCTCTAGGGTTTTCGGGCCAGAAATTCAC 1002  
 QY 333 PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTyrPheAlaAspGluAsp 351  
 Db 1003 TTTCGCTATATGCAACTATGCGAAATGCGACTCCACAAACAGTATTGTTGCTCACTA 1062  
 QY 352 ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368  
 Db 1063 GGTCAAGCGGTGATAGAACATTATCGCCACTTTATATAGAGACCTTTTAATATAGGG 1122  
 QY 369 PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387  
 Db 1123 ATAAATATCAACAACTATCTGTTCTTGACGGGACAGAAATTTGCTTATGGAACCTCCCA 1182  
 QY 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407  
 Db 1183 AATTGGCATCCGCTGTATACAGAAAGCGAGAGTAGATTGCTGCGATGAATACCG 1242  
 QY 408 ProGlnAspAsnSerGlyAlaProTyrAsnAspTyrSerHisValLeuAsnHisValThr 427  
 Db 1243 CCACAGAATAACAACGTCGCCACCTAGGCCAAGGATTATAGTCATGATTAAAGCATGTTCA 1302  
 QY 428 PheValArgTTPProGlyGluIleSerGlySerAspSerTyrArgAlaProMetPheSer 447  
 Db 1303 ATGTTTCGTCAGCGTTTAGTAATAGTAGTCTAAAGTAAATAGAGCTCCCTATGTTCTCT 1362  
 QY 448 TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle 467  
 Db 1363 TGGTATACATCTGTATGCAACTCTTACAAATCAATGATCCAGAGAGAAATTAATCAATA 1422  
 QY 468 ProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe 487  
 Db 1423 CCTTTAGTGAAGGATTAGAGTTTGGGGGCGACCTCTGTCATTACAGGACCGAGGATTT 1482  
 QY 488 ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn 507  
 Db 1483 ACAGGAGGGATATCCTCGAAGAAATACCTTGGTGTATTTGTATCTCTACAAGTCAAT 1542  
 QY 508 IleAsnGlyGlnLeuProGlnArgThrArgAlaArgIleArgTyrAlaSerThrThrAsn 527  
 Db 1543 ATTAATTCACCAATTTACCAAAAGATACCGTTTAAGATTTCGTTACGCTCCAGGAGAT 1602  
 QY 528 LeuArgIleTyrVal---ThrValAlaGlyGluArgIlePheAlaGlyGln-----543



Db 1603 GCACGAGTTATAGTATTAACAGGAGCGGCATCCACAGGAGTGGGAGGCCAAGTTAGTGA 1662  
Qy 544 -----PheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
Db 1663 AATATGCTCTTCAGAAAACCTATGGAATAGGGAGAACTTAACATCTAGAACATTTAGA 1722  
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrVal--- 579  
Db 1723 TATACCGATTATAGTAAATCCTTTTTCATTTAGAGCTAATCCAGATATATATGGGATAAGT 1782  
Qy 580 -----GlyAlaAspThrPheSerSerGlyAsnGluValTyrIleAspArg 594  
Db 1783 GAACRACCTTATTTGGTCGACGTTCTATTTAGTAGCGGT---GAACCTTATATAGATAAA 1839  
Qy 595 PheGluLeuIleProValThrAlaThrPheGluAlaGluTyrAspLeuGluAlaGln 614  
Db 1840 ATTGAATATTCTACGACATGCAACATTTGAACGAGAATCTGATTTAGAAAGAGACAA 1899  
Qy 615 LysAlaValAsnAlaLeuPheThrSerIleAsnGlnIleGlyIleLysThrAspValThr 634  
Db 1900 AAGCGGTGAATGCCCTGTTTCTTCCAAATCAATCGGTTAAAAACCGATGTGACG 1959  
Qy 635 AspTyrHisIleAspGlnValSerAsnLeuValAspCysLeuSerAspGluPheCysLeu 654  
Db 1960 GATTATCATATTGATCAAGATCAACATTTAGTAGGATGTTTATCAGATGAATTTGTCTG 2019  
Qy 655 AspGluLysArgGluLeuSerGluLysValLysHisAlaLysArgLeuSerAspGluArg 674  
Db 2020 GATGAAGCGAGAAATGTCGAGAAAGTCAACATGCGAAGCGACTCAGTCAATGAGCGG 2079  
Qy 675 AsnLeuLeuGlnAspProAsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArg 694  
Db 2080 AATTACTTCAAGATCCAACTTCAGAGGATCAATAGACACACCGACCGCTGGGAGA 2139  
Qy 695 GlySerThrAspIleThrIleGlnArgGlyAspAspValPheLysGluAsnTyrValThr 714  
Db 2140 GGAAGTACAGATATTACCATCCAGGAGGAGATGACGTATTCAAAGAGAATTACGTCACA 2199  
Qy 715 LeuProGlyThrPheAspGluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSer 734  
Db 2200 CTACCGGGTACCGTGTGATGAGTGTCTTCCAACTGATTTATATCAGAAAATAGATGAGTGC 2259  
Qy 735 LysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeu 754  
Db 2260 AATATRAACCTTATACCCGTTAIGATTAAGAGGATATATCAAGATAGTCAAGACTTA 2319  
Qy 755 GluIleTyrLeuIleArgTyrAsnAlaLysHisGluThrValAsnValLeuGluThrGly 774  
Db 2320 GAAATCTATTGATCCGTTTACAATGCAAAACAGAAATAGTAATGTGCCAGCAGCGGT 2379  
Qy 775 SerLeuTrpProLeuSerValGlnSerProIleArgLysCysGlyGluProAsnArgCys 794  
Db 2380 TCCTATAGCGCGCTTTTCAGCCCAAGTCCCAATCGGAAGGTGGAGAACCGAATCATGTC 2439  
Qy 795 AlaProHisLeuGluTrpAsnProAspLeuAspCysSerCysArgAspGlyGluLysCys 814  
Db 2440 GCGCCACACCTTGAATGGAATCTGATCTAGATTGTTCTTCGACAGACGGGGAATAATGT 2499  
Qy 815 AlaHisSerHisHisPheSerLeuAspIleAspValGlyCysThrAspLeuAsnGlu 834  
Db 2500 GCACATCATTTCCCATCTTTCACCTTGGATTTGATGTTGATGTACAGACTTAAATGAG 2559  
Qy 835 AspLeuAspValTrpValIlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGly 854  
Db 2560 GACTTAGTGTATGGGTGATATTCAAGATTAGACCGAGATGCCATGCCAAGCTAGGG 2619  
Qy 855 AsnLeuGluPheLeuGluGluLysProLeuValIcylGluAlaLeuAlaArgValLysArg 874  
Db 2620 AATCTAGATTTCTCGAAGAGAAACCATTTATAGGGGAAGCACTAGTCTGTGCAAAAGA 2679  
Qy 875 AlaGluLysTyrTrpArgAspLysArgGluLysLeuGluLeuGluThrAsnIleValTyr 894

Db 2680 GCGGAGAGAGAGTGGAGAGACAAACGAGAGAACTCCAGTTGGAAAAACAATATTGTTTAT 2739  
Qy 895 LysGluAlaLysGluSerValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGln 914  
Db 2740 AAGAGCGAAAGAAATCTGTAGATGCTTTATTTGTAACTCTCAATATGATAGATTACAA 2799  
Qy 915 AlaAspThrAsnIleAlaMetIleHisAlaAlaAspLysArgValHisArgIleArgGlu 934  
Db 2800 GTGGATCAGCAACATCGCAATGATTCATCGCGAGATAAAGCGCTTCATAGAATCCGGGAA 2859  
Qy 935 AlaTyrLeuProGluLeuSerValIleProGlyValAsnValAspIlePheGluLeu 954  
Db 2860 GCGTATCTGCCAGAGTTGTCTGTGATTCAGAGTGTCAATCGGCCCATTTTCGAGAAATTA 2919  
Qy 955 LysGlyArgIlePheThrAlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGly 974  
Db 2920 GAGGACGATTTTACAGCGTATTCCTTATATGATCGGAGAAATGTCATATAAATGGC 2979  
Qy 975 AspPheAsnAsnGlyLeuSerCysTrpAsnValLysGlyHisValAspValGluGln 994  
Db 2980 GATTTCATAATGCTTATTATGCTGGAAGTGAAGGTCTAGATGTAGAGAGACAA 3039  
Qy 995 AsnAsnHisArgSerValLeuValValProGluTrpGluAlaGluValSerGlnGluVal 1014  
Db 3040 AACACCCACCGTTCGCTCTTATCCAGATGGGAGCAGAGGTGTCAAGAGGTT 3099  
Qy 1015 ArgValCysProGlyArgGlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGly 1034  
Db 3100 CGTCTCTTCAGGTCGTGCTATCTCTGTCACAGCATATAAAGAGGGATATGGA 3159  
Qy 1035 GluGlyCysValThrIleHisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsn 1054  
Db 3160 GAGGCTCGCTAACATCCATCAGATCGAGACAATACAGCAGACTGAAATTCAGCAAC 3219  
Qy 1055 CysValGluGluGluValTyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsn 1074  
Db 3220 TGTGTAGAGAGAGATATATCCAAACACACAGTACGTGTAATAATATATCTGCGACT 3279  
Qy 1075 GlnGluGluTyrGlyGlyAlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGly 1094  
Db 3280 CAAGAAGATATGAGGGTACGTACACTCTCTGTAATCAAGGATATGACAGACCTATGGT 3339  
Qy 1095 SerAsnSerValProAlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAsp 1114  
Db 3340 AATAACCTTCCTCGTACAGCTGATTACGCTTCAGTCTATGAGAAAAAATCGTATACAGAT 3399  
Qy 1115 GlyArgArgAspAsnProCysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuPro 1134  
Db 3400 GGACGAGAGAGAAATCCCTTGTGAATCTAACAGAGGCTATGGGGATTACACACCTACCG 3459  
Qy 1135 AlaGlyTyrValThrLysGluLeuGluTyrPheProGluThrAspLysValTrpIleGlu 1154  
Db 3460 GCTGTTATGTAACAAGGATTTAGAGTACTTCCAGAGACCGATAAGGTATGATTGAG 3519  
Qy 1155 IleGlyGluThrGluGlyThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174  
Db 3520 ATCGGAGAGACAGAGGAACATTCATCTGTGATAGCTGGAATTAATCTCTTATGAGGAA 3579

## RESULT 10

US-09-756-643-1

; Sequence 1, Application US/09756643

; Patent No. US2001002639A1

; GENERAL INFORMATION:

; APPLICANT: Rice, Douglas

; APPLICANT: Carozzi, Nadine

; APPLICANT: Anderson, David

; APPLICANT: Rajasekaran, Kanniah

; APPLICANT: Rangan, Thirumale

; APPLICANT: Yemofsky, Richard

; APPLICANT: Lotstein, Richard

; APPLICANT: De Framond, Annick

; TITLE OF INVENTION: Insecticidal Cotton Plant Cells

; FILE REFERENCE: S-16768E



; CURRENT APPLICATION NUMBER: US/09/756,643  
 ; CURRENT FILING DATE: 2001-01-08  
 ; PRIOR APPLICATION NUMBER: 08/218,697  
 ; PRIOR FILING DATE: 1994-03-28  
 ; PRIOR APPLICATION NUMBER: 07/759,969  
 ; PRIOR FILING DATE: 1991-09-16  
 ; PRIOR APPLICATION NUMBER: 07/274,452  
 ; PRIOR FILING DATE: 1988-11-18  
 ; PRIOR APPLICATION NUMBER: 07/122,109  
 ; PRIOR FILING DATE: 1987-11-18  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4360  
 ; TYPE: DNA  
 ; ORGANISM: Bacillus thuringiensis  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (156)..(3623)  
 US-09-756-643-1

## Alignment Scores:

Pred. No.: 0 Length: 4360  
 Score: 4211.50 Matches: 831  
 Percent Similarity: 77.00% Conservative: 83  
 Best Local Similarity: 70.01% Mismatches: 228  
 Query Match: 67.45% Indels: 45  
 DB: 10 Gaps: 9

US-09-837-961-8 (1-1174) x US-09-756-643-1 (1-4360)

Db	756	GGCAACTATACAGATCATGCTGTACGCTGCTACAAATACGGGATTAGAGCGTGTAGGGGA	815
Qy	219	ThrAsnThrArgGlnTrpAlaAargPheAsnGlnPheArgAspLeuThrLeuThrVal	238
Db	816	CGGATTCTAGAGATTGGATAAGATAATACTAATTTAGAAGAGAAATTAACACTACTGTA	875
Qy	239	LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer	258
Db	876	TTAGATATCGTTCTCTATTCCGAAGTATAGTAGTAGACGATATCAATTCGACACAGTT	935
Qy	259	SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla	278
Db	936	TCCCAATTAACAAGAGAAATTTATACAAACCCAGTATTAGAA	977
Qy	279	AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro	294
Db	978	AAUTTTGATGTTAGTTTTCGAGGCTCGGCATAGAGGAGGAGTATTAGAGTCCA	1037
Qy	295	HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr	314
Db	1038	CATTGATGATATATTAACAGTATTAACCATCTATACGGATGCTCATAGAGGAATAT	1097
Qy	315	ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn	332
Db	1098	TATTGGTCAGGGCATCAATAAATGGCTTCTCCTAGGGTTTCGGGGCCAGAAATTCAC	1157
Qy	333	PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTrpIleAlaAspGluAsp	351
Db	1158	TTTCCGCTATATGGAACTATGGAAATGCAGCTCCACAAACATATTGTTGCTCAACTA	1217
Qy	352	ProArgProPheThrArgThrLeuSerAspProValPheValArgGly-----Gly	368
Db	1218	GGTCAGGGCGGTATAGAACATTAATCCTCCACTTATATAGAACCTTTAATATAGGG	1277
Qy	369	PheGlyAsnProHistyr---ValLeuGlyLeuArgGlyValAlaPheGlnThrGly	387
Db	1278	ATAAATAATCAACAACATATCTGTTCTTGACGGGACAGAAATTTGCTTATGGAACCTCTCA	1337
Qy	388	ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro	407
Db	1338	AATTGGCATCCGCTGATACAGAAAAGCGGACGGTAGATTGCTGGATGAATAACCG	1397
Qy	408	ProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr	427
Db	1398	CCACAGATTAACACGTCGCCACCTAGCAAGGATTTAGTCATCGATTAAGCAATTTCA	1457
Qy	428	PheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaPrometPheSer	447
Db	1458	ATGTTTCGTTTCAGGCTTTAGTAATAGTAGTAGTAATAATAAGAGCTCTATGTTCTCT	1517
Qy	448	TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGluIle	467
Db	1518	TGATACATCGTAGTCTGAATTAATAATAATAATTCCTTCATCACAAATTAACAAATA	1577
Qy	468	ProLeuValIleAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe	487
Db	1578	CCTTTACAAAATCTACTAATCTTGGCTCTGGACACTCTGCTGTTAAGGACACAGATTT	1637
Qy	488	ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn	507
Db	1638	ACAGGAGGAGATATCTTCGAAGAAGCTTCACCTGGCCAGATTTCAACCTTAAGAGTAAT	1697
Qy	508	IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsn	527
Db	1698	ATTACTGCACCATTTATCACAAAGATATCGGGTAGAATTCGCTACGCTTCTACCAAAAT	1757
Qy	528	LeuArgIleThrValAlaAlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr	547
Db	1758	TTACAAATTCATACATCAATTCGAGGAAGACCTATTAAATCAGGGGAATTTTTCAGCAAT	1817
Qy	548	MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla	567
Db	1818	ATCAGTAGTGGGAGTAATTACAGTCCGGAGAGCTTAGGACTCTAGGTTTACTACTCCG	1877

Qy	1	MetGluAsnAsnIleGln---AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu	19
Db	156	ATGGATAACATCCGACATCATGATGATCCCTATATATGTTTAAAGTAACCCGAA	215
Qy	20	ValGluIleLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu	38
Db	216	GTAGAAGTATTAGTGGAGAAAGAAATAGAACTGGTTACACCCCAATCGATATTTCTCTG	275
Qy	39	SerLeuThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu	58
Db	276	TCGCTACCGCAATTTCTTTGAGTGAAATTTGTTCCCGGCTGCTGGATTGTTAGGACTA	335
Qy	59	PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle	78
Db	336	GTGATATATATAGGGAAATTTTGTCCCTCTCAATGGACCAATTTCTGTACAAAT	395
Qy	79	GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu	98
Db	396	GAACAGTTAATTAAACCAAGAAGATAGAGAATTCGCTAGGAACCAAGCCATTTCTAGATTA	455
Qy	99	ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn	118
Db	456	GAAGGACTAAGCAATCTTTAICAAATTTACGAGAAATCTTTTAGAGAGTGGGAGCAGAT	515
Qy	119	ProAsnAsnAlaGlnLeuArgGluAspValArgPheAlaAsnThrAspAspAla	138
Db	516	CCCTACTAATCCACATTAAGAGAAGATCGGTATTCAATTCATGACATGAACAGTGCC	575
Qy	139	LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal	158
Db	576	CTTACAAACCGCTATTCCTCTTTTGGAGTTTCAAAATATATCAAGTCTCTTTTATCAGTA	635
Qy	159	TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln	178
Db	636	TATGTTCAAGCTGCAATTTACATATTATCATCTAGTTTGGAGATGTTTCAGTGTGTGGCAA	695
Qy	179	GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIle	198
Db	696	AGGTGGGATTTGATCCCGGCACTATCAATAGTCGTATATATGATTAATTAATAGCTTATT	755
Qy	199	HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly	218



; PRIOR FILING DATE: 2000-07-10  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 4300  
 ; TYPE: DNA  
 ; ORGANISM: Bacillus thuringiensis  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (388)..(3924)  
 ; OTHER INFORMATION:  
 ; US-09-851-194-1

## Alignment Scores:

Pred. No.: 0 Length: 4300  
 Score: 4148.00 Matches: 828  
 Percent Similarity: 76.21% Conservatives: 85  
 Best Local Similarity: 69.12% Mismatches: 241  
 Query Match: 66.43% Indels: 44  
 DB: 10 Gaps: 14

US-09-837-961-8 (1-1174) x US-09-851-194-1 (1-4300)

QY 1 MetGluAsnAsnLeuGln---AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu 19  
 Db 388 ATGGATAACAATCCGAACATCAATGAATGCAATCCTTATAATTTGTTAAGTAACCCGTAA 447  
 QY 20 ValClnLeuLeuAsnGluGluArg--SerThrGlyArgLeuProLeuAspIleSerLeu 38  
 Db 448 GTAGAAGTATTAGGTGGGAGAAAGATAGAACTGGTTACACCCCAATCGATATTTCTCTG 507  
 QY 39 SerLeuThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58  
 Db 508 TCGCTAACGCAATTCCTTTGAGTGAATTTGCTCCGGTGTGGATTGTTAGGACTA 567  
 QY 59 PheAspLeuLeuTrpGlyPheLeuThrProSerAspTrpSerLeuPheLeuGlnIle 78  
 Db 568 GTTGATATAATATGGGAATTTTGGTCCCTCTCAATGGGACGCAATTTCTGTACAAAT 627  
 QY 79 GluClnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeu 98  
 Db 628 GAACAGTTAATTAACCAAGAAATAGAGAATTCGCTAGGAACCAAGCCATTCTAGATTA 687  
 QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118  
 Db 688 GAAGGACTAAGCAATCTTTATCAAAATTTACGCAATCTTTTACAGAGTGGGAGACGAT 747  
 QY 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAla 138  
 Db 748 CCACTAATCCAGCAATTAAGAGAAGATGCGTATCAATTCATCAATGACATGACAGTCC 807  
 QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuSerVal 158  
 Db 808 CTTACACCGCTATCTCTTTTTCAGTCAAAATTAATCAAGTTCCTCTTTTATCAGTA 867  
 QY 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyCln 178  
 Db 868 TATGTTCAAGCTGCAATTTACATTTATCAGTTTGTGAGATGTTTCAAGTCTTTGGCAA 927  
 QY 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIle 198  
 Db 928 AGTGGGGATTGATGCGCGGACACTCAATAGTCTTATATGATTTAAGTATGAGCTTAT 987  
 QY 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218  
 Db 988 GGCACATATACAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047  
 QY 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrVal 238  
 Db 1048 CCGGATCTAGAGATGGGTAAAGTAAATCAATTTAGAGAGAAATTAACACTAACGTGA 1107  
 QY 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258

Db 1108 TTAGATATCGTCTGCTCTCCGCAATATATAGTAGTAAAGATATCCAAATTCGAACAGTT 1167  
 QY 259 SerClnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278  
 Db 1168 TCCCAATTAACAGAGAAATTTATACAAACCCAGTATTAGAA-----1209  
 QY 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294  
 Db 1210 AATTTTCATGAGTATTTTCGAGGCTCGCTCAGGCGCATAGAAAGAGTATTAGGAGTCCA 1269  
 QY 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314  
 Db 1270 CATTTGATGATATACCTAAACAGTATACCATCTATACGATGCTCATAGGGGTATTAT 1329  
 QY 315 ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332  
 Db 1330 TATTTGGTCAAGGATCAAAATAATGGCTTCCTCTAGGGTTTCGGGGCCAGAAATTCAT 1389  
 QY 333 PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTyrIleAlaAspGluAsp 351  
 Db 1390 TTCCGCTATATGGAATGGAATGCGCTCCACACCAACGATTTGTGTCTCAACTA 1449  
 QY 352 ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368  
 Db 1450 GGTACGGCGCTGTATAGAACATTTATCTCCACTTTATATAGAACCTTTTAAATATAGG 1509  
 QY 369 PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387  
 Db 1510 ATAATAATCAACAACTATCTGTTCTTACAGGGGACAGAAATTTGCTTATGGAACTCTCTCA 1569  
 QY 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407  
 Db 1570 AATTTGCCATCCGCTGTATACAGAAAGCGGACGCTAGATTTCGCTGGATGAAATACCG 1629  
 QY 408 ProGlnAspAsnSerGlyAlaProTyrAsnAspTyrSerHisValLeuAsnHisValThr 427  
 Db 1630 CCACAGATAACAAACGTCGCCACTAGGACAGGATTTATGCTATGATTAAGCCATGTTTCA 1689  
 QY 428 PheValArgTrpProGlyGluIleSerGlySerAspSerTyrArgAlaProMetPheSer 447  
 Db 1690 ATGTTTCGTCAGGCTTTAGTAATAGTAGTAAAGTAAATAAGAGCTCCTATGTTCTCT 1749  
 QY 448 TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle 467  
 Db 1750 TGGATACATCGTAGTCTGTAATTAATAATAATAATGCTCGGATAGTATTACTCAAAATC 1809  
 QY 468 ProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe 487  
 Db 1810 CCTGCACTGAAGGAAACCTTTCTTTTAAATGTT---TCTGTAATTTCCAGGACCGAGATT 1866  
 QY 488 ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn 507  
 Db 1867 ACTGCTGGGACCTTAGTATTAAATAGTAGTGAAT-----AAC 1908  
 QY 508 IleAsnGly-----GlnLeuPro-----GlnArgTyr 516  
 Db 1909 ATTCAGATAGAGGTTATTTGAGTTCCTCAATTCCTCCATCGACATCTACCATGAT 1968  
 QY 517 ArgAlaArgIleArgTyrAlaSerThrThrAsnLeuArgIleTyrValValAlaGly 536  
 Db 1969 CGAGTCTGTGACGGTATGCTTCTGTAACCCGATTCACCTCAACGTTAATTTGGGTAAT 2028  
 QY 537 GluArgPheAlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPhe 556  
 Db 2029 TCAPCCATTTTTCCTCAATACAGTACCAGCTACAGCTACGCTACGCTATAGTAAATCTCAATCA 2088  
 QY 557 GlnSerPheSerTyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSer 576  
 Db 2089 AGTGATTTGGTATTTTGAAGTGCACATGCTTTTACA-----TCTCATATTAGT 2139  
 QY 577 PheThrValGlyAlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGlu 596  
 Db 2140 AATATAGTGGTGTAGAAATTTTAGTGGGACTCCAGGAGTGATTAATAGACAGATTTCGA 2199

Qy	597	LeuIleProValThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAla	616
Db	2200	TTTATTCCAGTTACTGCACACCTCGAGGCTGAATAATAATCTGGAAGAGCCGCAGAAGCGC	2259
Qy	617	ValAsnAlaLeuPheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyr	636
Db	2260	GTGAATCGCTGTTTACGTCCTCAACACCAACACTAGGGCTAAACAAACAAATGTAACGGATTAT	2319
Qy	637	HisIleAspGlnValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGlu	656
Db	2320	CATATTGATCAAGTGTCCCAATTTAGTTAGCTATTATTCGATGAATTTTGTCTGATCAA	2379
Qy	657	LysArgGluLeuSerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeu	676
Db	2380	AAGCGAGAAATTTCCGAGAAAGTCAACCATCGAAGCGACTCAGTGTAGTAACCGCAATTTA	2439
Qy	677	LeuGlnAspProAsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySer	696
Db	2440	CTCCAAGATTCAAAATTCAAAGACATTAATAGCAACAGACGTTGGTGGCGCGAAGT	2499
Qy	697	ThrAspIleThrIleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuPro	716
Db	2500	ACAGGGATTTACCATCCAAAGAGGGGATGACGTATTATAAGAAAAATTAGTCCACACTTCA	2559
Qy	717	GlyThrPheAspGluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeu	736
Db	2560	GGTACCTTTGATCAGTGCCTATCCACATATTTGTATCAAAAAATCGATGAATCAAAATTA	2619
Qy	737	LysProTyrThrArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIle	756
Db	2620	AAAGCCTTTACCGCTTATCAATTAAGAGGTTATATCGAAGATAGTCAAGACTTGAATC	2679
Qy	757	TyrLeuIleArgTyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeu	776
Db	2680	TATTTAATTCGGCTACAAATCGAAACATGAACAGATAAATGTGCCAGGTACGGGTTCCTTA	2739
Qy	777	TrpProLeuSerValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaPro	796
Db	2740	TGCGCGCTTTCAGCCCAAGTCCATCGAAAGTGTGGAGAGCCGATCGATGCGCGCCA	2799
Qy	797	HisLeuGluTrpAsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHis	816
Db	2800	CACCTTGAATGGAAATCCTGACTTAGATTGTCCTGCTAGGATGGAGAAAAGTGTGCCCAT	2859
Qy	817	HisSerHisHisPheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeu	836
Db	2860	CATTCGCATATTTCCTTTAGACATTGATGTAGATGTACAGACTTAAATGAGCACTTA	2919
Qy	837	AspValTrpValIlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeu	856
Db	2920	GGTGTATGGTGATCTTTAAGATTAAAGCGCAAGATGGGCACGACAGCTAGGGAATCTTA	2979
Qy	857	GluPheLeuGluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGlu	876
Db	2980	GAGTTTCTCGAAGAGAAACCATTAGTAGAAGCGCTAGCTCGTGTGAAAGAGCGGAG	3039
Qy	877	LysLysTrpArgAspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGlu	896
Db	3040	AAAAATGAGAGACAAACCTGAAAATTTGGAATGGGAAACAAATATCGTTTATAAGAG	3099
Qy	897	AlaLysGluSerValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAsp	916
Db	3100	GCAAAAGAAATCTGTAGATGCTTTATTTGTAACTCTCAATATGATCAATTACRANGCGGAT	3159
Qy	917	ThrAsnIleAlaMetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyr	936
Db	3160	ACGAATATTGCCATTGATTATCGGCAGATAAAGCTGTTCATACCATTCGAGAAGCTTAT	3219
Qy	937	LeuProGluLeuSerValIleProGlyValAsnValAspIlePheGluGluLeuLysGly	956
Db	3220	CTGCCCTGACTGTGTGTGATCCCGGTTGTCATCCGGCTATTTTGAAGAAATTAGAAGG	3279

Alignment Scores:

QY	957	ArgIlePheThrAlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPhe	976
DB	3280	CGTATTTTCTACTGCATCTCCCTATATGATGCAGAAATGCTCATATAAAATGGTGATTTT	3339
QY	977	AsnAspGlyLeuSerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsn	996
DB	3340	AATAATGGCTTATCCYTGCTGGACAGTGAAGGCCATGTAGATGTAGAAGAACAAACAC	3399
QY	997	HisArgSerValLeuValValProGluTyrGpLuAlaGluValSerGlnGluValArgVal	1016
DB	3400	CAACGTTTCGGTCTTGTGTTCGGAAATGGAAGCAGACAGTGTACAAAGAAGTTCGTGTC	3459
QY	1017	CysProGlyArgGlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGly	1036
DB	3460	TGTCGGGGCGTGGCTATATPCTTCTGTGTACACGCGTACAGAGGAGGATATGAGAAAGGT	3519
QY	1037	CysValThrIleHisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysVal	1056
DB	3520	TGCGTAAACCATTCATCAGATCGAAGAACATACAGACGAACTGAAGTTTACCAACTGCGTA	3579
QY	1057	GluGluGluValTyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGlu	1076
DB	3580	GAAGAGGAATCTATCCAATAACACGGTAACGTGAATGATTATATCTGTAAATCAAGAA	3639
QY	1077	GluTyrGlyGlyAlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsn	1096
DB	3640	GAATACGGAGGTCGTAACCTCTCTGTAATCGAGGATATAACGAGCT-----	3687
QY	1097	SerSerValProAlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArg	1116
DB	3688	CCTTCGGTACCAGCTGATTATGCGTCAGTCTATGAAGAAAAATCGTATACAGATGACGA	3747
QY	1117	ArgAspAsnProCysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGly	1136
DB	3748	AGAGAGAATCCTTGTGAAATTTACAGAGGGTATAGGGATTACAGCCATPACCAGTTGGT	3807
QY	1137	TyrValThrLysGluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGly	1156
DB	3808	TATGTGACAAAAAGATTAGAATACTTCCACAGAAACCGATAAGGTATGGATTGAGATTGA	3867
QY	1157	GluThrGluGlyThrPheIleValAspSerValGluLeuLeuMetGluGlu	1174
DB	3868	GAACGGGAAGAACATTTATCTGCGACGCGTGAATTTACTCCTTATGGAGGAA	3921

RESULT 12  
US-09-826-660-20

Sequence 20, Application US/09826660  
Patent No. US20010026940A1

; GENERAL INFORMATION:

; APPLICANT: Cardineau, Guy A.  
 ; APPLICANT: Stelman, Steven J.

; APPLICANT: Narva, Kenneth E.

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; TITLE OF INVENTION: Plant-Optimized Genes
; FILE REFERENCE: MA-714XC2D1

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; CURRENT APPLICATION NUMBER: US/09/826,660  
 ; CURRENT FILING DATE: 2009-04-05

; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 00-0370-050

; PRIOR APPLICATION NUMBER: 09/178,252  
 : PRIOR FILING DATE: 1008-10-23

; PRIOR FILING DATE: 1998-10-23  
 : PRIOR APPLICATION NUMBER: 60/066 315

; PRIOR APPLICATION NUMBER: 60/065,215  
 : PRIOR FILING DATE: 1997-11-12

; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/076445

; ERROR AFFILIATION NUMBER: 60/0/6,443  
 ; PRIOR FILING DATE: 1998-03-02

; NUMBER OF SEO ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 3489

; TYPE: DNA

; ORGANISM: Artificial Sequence

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; COMMENT: the character sequence
; FEATURE:

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OTHER INFORMATION: Synthetic B.t. toxin

US-09-826-660-20

Alignment Scores:

Qy	314	ThrValTrpGlyGlyHisLeuValSerSerArgAsnThrAlaGlyAsnArgIleAsnPhe	333
Db	958	TTCTACTGGGGTGGACATCGTGTGATCTCTAGCTTAGGTGGAGGTAAACATCACATCT	1017
Qy	334	ProSerTyrGlyValPheAsnProGlyGlyAlaIleTrpIleAlaAspGluAsPro---	352
Db	1018	CCATCTATGGT-----AGGAGGCCAAATCAGAGCGCTCCA	1053
Qy	353	-----ArgProPheTyrArgThrLeuSerAspProVal-----Phe	364
Db	1054	AGATCCTTCATTTCAATGGACCGCTTCAGAGACTTGTCTCCATCCPACTTGGGATTG	1113
Qy	365	ValargGlyGlyPheGlyAsnProHisTyrValLeu---GlyLeuArgGlyValAlaPhe	383
Db	1114	TTACAACAACATGGCGCTGCTCCACCATCAACTTACGTGGTGTGTTGAAGAGTAGAGTTC	1173
Qy	384	GlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeu	403
Db	1174	---TCACACCCCAACAC---AGCTTCAGCTATCGTGAAGAGGTCAAGTTGATTCGCTG	1227
Qy	404	AspGlnIleProGlnAsnAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeu	423
Db	1228	ACTGAGTTACCGCTCAGGACAACTCAGTCCACTCGCGAAGGCTACAGTACGCTCTC	1287
Qy	424	AsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAla	443
Db	1288	TGTCACGCAACCTTTGTTCAAAGTCTGCA-----ACA	1320
Qy	444	Pro-----MetPheSerTrpThrHisArgSerAlaThrProThrAsn	457
Db	1321	CGGTCTCTGACAACTGGTGTGCTTCTCTCGACTCATCGTAGCGCAACTCTTACCAAC	1380
Qy	458	ThrIleAspProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSer	477
Db	1381	ACCAATTGATCCAGAGGATCAATCAGATACCTCTTGGAAGGCTTCAGAGTTGGGG	1440
Qy	478	GlyThrThrValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSer	497
Db	1441	GGCACTTCTGTGATCCCGCTCAGGATTCACAGAGGGGACATTTCTCGACGCAACACC	1500
Qy	498	GlyGlyProPheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArg	517
Db	1501	TTTGGTGACTTTGTATCTCTCAAGTCAACATCAACTCACCATCACCAAGATACCGT	1560
Qy	518	AlaArgIleArgTyrAlaSerThrAsnLeuArgIleTyrVal---ThrValAlaGly	536
Db	1561	CTAAGGTTCTGTTACGCTTCCAGTAGAGATGACCGTGTGATGACTACAGAGGCTGCA	1620
Qy	537	GluArgIlePheAlaGlyGln-----PheAsnLysThrMetAspThr	550
Db	1621	TCCACAGAGTTGGAGGCCAAGTTAGTGTCAACATGCTCTTTCAGAAGACTATGAGATA	1680
Qy	551	GlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAlaPheThrPhe	570
Db	1681	GGGAGAACTTGACCTCTAGAACCCTTCGTACACCGACTTCAGCAAPCCCTTCTCATTC	1740
Qy	571	ProMetSerGlnSerSerPheThrVal-----GlyValaAspThrPhe	584
Db	1741	AGACCCNATCCACACATCATTTGGGATCATGACAAACCTCTCTTTGGTGCAGGTTCCATC	1800
Qy	585	SerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPhe	604
Db	1801	AGTAGCGGT---CAACTGTATACATAGACAAGATTGAGATCATCTAGCTGATGCAACACTC	1857
Qy	605	GluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIle	624
Db	1858	GAGCGAGAGTCTGACTTGGAAAGACACAGAAGCGGTGAATGCTGCTGTCACTTCGCTCC	1917
Qy	625	AsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeu	644
Db	1918	ATCAGATTGGGCTCAAGACAGATGTGACTGACTATCATCGATCGATCGCGTTTCCAACCTT	1977
Qy	645	ValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysVal	664

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Db 1978 GTTGAGTSCCTCTCTGATGAGTTCTGTTGGATGAGAGAGGAGTTCTCCGAGAGGTC 2037
QY 565 LysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspProAsnPhelLysGly 684
Db 2038 AAAATGCTAAGCAGCTTAGTGTATGAGCGGAGCTTGTCTTCAAGATCCCAACTTTCGCGGG 2097
QY 685 IleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThrIleGlnArgGly 704
Db 2098 ATCAACAGGCAACTAGATCTGTTGGATGGAGGAGATGACGACATCACCATTCAAGGAGGT 2157
QY 705 AspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrPro 724
Db 2158 GATGATGTGTTCAAGGAGAACTATGTTACGCTCTGGGTACCTTTGATGAGTGCTATCCA 2217
QY 725 ThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeu 744
Db 2218 ACATACCTGTACCAAGAGATAGATGAAATCGAAACTCAAGCCTACACAAAGATACCAAGTTG 2277
QY 745 ArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLys 764
Db 2278 AGAGTTACATCGAGGACAGTCACAGCCTTGAGATCTACCTTCATCAGATACACGCCCAA 2337
QY 765 HisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSerValGlnSerPro 784
Db 2338 CATGAGACAGTCAATGTGCTCGGCGGGTTCACCTGTGCCCACTTTCAGCCCAAGTCCC 2397
QY 785 IleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyrAsnProAspLeu 804
Db 2398 ATC----- 2400
QY 805 AspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAsp 824
Db 2401 -----GGCAAGTGTGCCCATCATCTACACCCACTTCTCCTTGAC 2439
QY 825 IleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrValIlePheLysIle 844
Db 2440 ATAGACGTTGGCTGTACCGACCTCAACAGACCTCGGTGTGTGGTGATCTTCAAGATC 2499
QY 845 LysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluGluLysProLeu 864
Db 2500 AAGACTCAAGATGGCCATGCCAGGCTAGGCAATCTGGAGTTCTAGAAGAAACCACTT 2559
QY 865 ValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArgAspLysArgGlu 884
Db 2560 GTTGGAGAAGCCCTCGCTAGAGTGAAGAGGCTGAGAGAGAGTGGAGGCAACAGAGAG 2619
QY 885 LysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeu 904
Db 2620 AAGTTGGAATGGGAACAACAACATTGTGTACAAAGAAAGCCAAAGAAAGCGTTGACGCTCG 2679
QY 905 PheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAla 924
Db 2680 TTTGTGAACTCTAGTATGATGAGCTCCAGCTGATACCAATGATGATGATGATGATGCT 2739
QY 925 AlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIlePro 944
Db 2740 GCAGACAACCGTTATAGCATTCGGAAGCTTACCTTCTGAACTTAGCGTGATTCG 2799
QY 945 GlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThrAlaPhePheLeu 964
Db 2800 GGTGTCAATGCTGCTATCTTTGAAGAGTTAGAAGGGCGCATCTTCACTGCAATCTCCTTG 2859
QY 965 TyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTyrAsn 984
Db 2860 TATGATCGGAGGATGTCATCAAGAATGGTGACTTCAACAATGGCCCTATCTGCTGGAAT 2919
QY 985 ValLysGlyHisValAspValGluGlnAsnAsnHisArgSerValLeuValValPro 1004
Db 2920 GTGAAGGGCACGTAGATGTAGAGAGACAGAACCAATCACCCTCTGTCTTGTGTTCTCT 2979
QY 1005 GluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeu 1024

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Db 2980 GASTGGGAGCAGAGTTTTCACAGAAAGTTCTGTCTCTGCTGGTCTGCTGCTACATTCTT 3039
QY 1025 ArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIleHisGluLeuGlu 1044
Db 3040 CGTGTACCGCGTACAAAGAAAGATACGGAAGAGTTGCGTCACCATACACGAGATTGAG 3099
QY 1045 AsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluGluValTyrProAsnAsn 1064
Db 3100 AACACACCGGAGAGTGAAGTTGAGCAACTGCGTCGAGGAGGAAGTCTACCCAAACAC 3159
QY 1065 ThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyTyrGlyGlyValTyrThrSer 1084
Db 3160 ACCGTAACCTGCAATGACTACACTGCGACTCAAGAGGAGTATGAGGGTACTTACACTTCT 3219
QY 1085 ArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValProAlaAspTyrAla 1104
Db 3220 CGCAATCGAGATACGATGAGCCCTATGAGAGCAACTCTTCTGTACCCGCTGACTATGCA 3279
QY 1105 SerValTyrGluLysSerTyrThrAspGlyArgArgAspAsnProCysGluSerAsn 1124
Db 3280 TCAGCCTATGAGAGAGGCTTACCCGATGAGCTAGGAGCAATCTTGGATCTGAATCTAAC 3339
QY 1125 ArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyr 1144
Db 3340 AGAGCTATGGGACTACACACCGTTACCGCGGCTATGTCAACAAAGAGTTAGAGTAC 3399
QY 1145 PheProGluThrAspLysValTyrIleGluLeuGlyGluThrGlyGlyPheIleVal 1164
Db 3400 TTCCAGAAACCGACAGGTTTGGATTGAGATTGGAGAAACCGAAGGAACATTCAATGTT 3459
QY 1165 AspSerValGluLeuLeuMetGluGlu 1174
Db 3460 GATACGCTGGAGTTACTTCTGATGGAGAA 3489

RESULT 13
US-09-826-660-12
; Sequence 12, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: WA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-12

Alignment Scores:
Pred. No.: 0 Length: 3468
Score: 4039.00 Matches: 813
Percent Similarity: 74.79% Conservative: 83
Best Local Similarity: 67.86% Mismatches: 236
Query Match: 64.69% Indels: 66
DB: 10 Gaps: 14

US-09-837-961-8 (1-1174) x US-09-826-660-12 (1-3468)
QY 1 MetGluAsnAsnIleGln---AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu 19

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QY 717 GlyThrPheAspGluCysTyrProThrTyrLeuTyrGluLysIleAspGluSerLysLeu 736  
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QY 737 LysProTyrThrArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIle 756  
DB 2233 AAAGGCTATPACCGGTACCAATTAAGAGGTATATCGAAGATAGTCAAGACTTAGAATC 2292  
QY 757 TyrLeuIleArgTyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeu 776  
DB 2293 TATTATTCGTACATCCCAACACGAACAGTAATGTCCAGGTACGGGTCCCTTA 2352  
QY 777 TrpProLeuSerValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaPro 796  
DB 2353 TGGCGCTTTCAGCCCAAGTCCCAATC----- 2379  
QY 797 HisLeuGluTrpAsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHis 816  
DB 2380 -----GGAAAATGTGCCCAT 2394  
QY 817 HisSerHisPheSerLeuAspPileAspValGlyCysThrAspLeuAsnGluAspLeu 836  
DB 2395 CATTCCTCATCTCTCTGGACATGTATGTGGATGTACAGACTTAATAGGACTTA 2454  
QY 837 AspValTrpValIlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeu 856  
DB 2455 GGTGTATGGTGATATTCAAGATTAAAGACCAAGATGGCCATGCAAGACTAGAAATCTA 2514  
QY 857 GluPheLeuGluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGlu 876  
DB 2515 GAATTCGGAAGAAACCATTAGTAGAGAGCACTAGCTCGTGTGAAAGAGCGGAG 2574  
QY 877 LysLysTrpArgAspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGlu 896  
DB 2575 AAAAAATGGAGACAAAGCTGAANAATTGGAATGGAAACAAATATCTTTTATAAGAG 2634  
QY 897 AlaLysGluSerValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAsp 916  
DB 2635 GCAAAAGAATCTGTAGATCTTATTGTAACTCTCAATATGATAGATTACAAGCGAT 2694  
QY 917 ThrAsnIleAlaMetIleHisAlaLysArgValHisArgIleArgGluAlaTyr 936  
DB 2695 ACCACATCGCGATGATTCATCGGCAGATAAACCGTTCATAGATTTCGAGAAGCTTAT 2754  
QY 937 LeuProGluLeuSerValIleProGlyValAsnValAspIlePheGluGluLeuLysGly 956  
DB 2755 CTGCGTGAGCTGCTGTGATTCGGGTGTCATGCGGCTATTTTCAAGAATTAGAAGG 2814  
QY 957 ArgIlePheThrAlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPhe 976  
DB 2815 COTATTTTCACTGCATTTCTCCCTATATGATGCGAGAAATGTCTATTAATAATGGTGATTT 2874  
QY 977 AsnAsnGlyLeuSerCysTrpAsnValLysGlyHisValAspValGluGluLysAsn 996  
DB 2875 AATAATGGCTTATCTCTGCGAAGCGTGAAGGCGATGTAGATGTAGAAGAACAAACAAAC 2934  
QY 997 HisArgSerValLeuValProGluTrpGluAlaGluValSerGlnGluValArgVal 1016  
DB 2935 CACCGTTCGGTCTTGTGTTCCGAAATGGGAGCAGAGTGTCAAGAAAGTTCGTGTC 2994  
QY 1017 CysProGlyArgGlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGly 1036  
DB 2995 TGTCGGGTGCGTGGTATATCTCTGTGTCACAGCGTCAACAGGAGGATATGAGAAGGT 3054  
QY 1037 CysValThrIleHisGluIleGluAsnThrAspGluLeuLysPheSerAsnCysVal 1056  
DB 3055 TCGTAACCATTCATGAGATCGAGAACCAATACAGACGAACACTGAAGTTTAGCAACTGTGA 3114  
QY 1057 GluGluGluValTyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGlu 1076  
DB 3115 GNAGAGGAAGTATATCCAAACACACGGAAGTAACTGTAATGATTATCTCGGACTCAAGAA 3174

QY 1077 GluTyrGlyGlyAlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsn 1096  
DB 3175 GAATATGAGGTACGTACACTTCTCGTAATCGAGGATATGACGGAGCCCTATGAAGCAAT 3234  
QY 1097 SerSerValProAlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArg 1116  
DB 3235 TCTTCTGTACCAAGCTGATTATGCATCAGCCTATGAAGAAAAGCATATACAGATGCGCA 3294  
QY 1117 ArgAspAsnProCysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGly 1136  
DB 3295 AGAGCAATTCCTGTGAATCTAACAGAGGATATGGGATTACACACCACTACACAGTGC 3354  
QY 1137 TyrValThrLysGluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGly 1156  
DB 3355 TATGTGACAAAAGATTAGACTCTCCAGAAACCGATAGGTATGGATTGAGATCGGA 3414  
QY 1157 GluThrGluGlyThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174  
DB 3415 GAACGGAAGGAACATTCATCGTGACAGCGTGAATTACTTCTTATGGAGAA 3468

## RESULT 14

US-09-826-660-13  
; Sequence 13, Application US/09826660  
; Patent No. US20010026940A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Stelman, Steven J.  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: MA-714XC2D1  
; CURRENT APPLICATION NUMBER: US/09/826,660  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/178,252  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: 60/065,215  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/076,445  
; PRIOR FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 3468  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic B.t. toxin gene  
US-09-826-660-13

## Alignment Scores:

Pred. No.:	0	Length:	3468
Score:	4039.00	Matches:	813
Percent Similarity:	74.79%	Conservative:	83
Best Local Similarity:	67.86%	Mismatches:	236
Query Match:	64.69%	Indels:	66
DB:	10	Gaps:	14

US-09-837-961-8 (1-1174) x US-09-826-660-13 (1-3468)

QY 1 MetGluAsnAsnIleGln---AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu 19  
DB 1 ATGGACAACAATCCCAACATCAACAGTGCATTCTTACAACTGCTGAGCAACCTGAG 60  
QY 20 ValGluIleLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38  
DB 61 GTTGAGGTGCTGGGTGGAGACGGATTGAGACTGGTTACACACTTATCGACATCTCGTTG 120  
QY 39 SerLeuThrArgPhePheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58  
DB 121 TCACATTACCAATTCCTTTTGTACAGTTCGTGCCGCTGCGGATTCGTGCTGCACTT 180  
QY 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78  
DB 181 GTCGATATCATTTGGGGAATCTTTGGTCCCTCTCAATGGGACGCTTCTTCTGTACAGATA 240



QY 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu 98  
 DB 241 GAGCACTATCAACCAAGAGATGAGAGTTCGCTAGGAAACCAAGCACTCAAGGTTA 300  
 QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrGluAlaAsn 118  
 DB 301 GAAGGCCTCAGCAACCTTTACAGATTACGAGAACTCTTTCCAGAGTGGGAGCAGAC 360  
 QY 119 ProAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAla 138  
 DB 361 CCAGCAATCCTCCCTTAAGAGAGAGATGCGCATTCATATCAATGATGATGAGATCC 420  
 QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158  
 DB 421 CTGACGACCCCAATTCGCGCTTCGCGGTTGAGAAATACCAAGTCTCTTTATCCGTTG 480  
 QY 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln 178  
 DB 481 TACGTGCAGGCTGCCAACCTGCCTTGTGCGTGTCTCGCGCATGCTCCGTTGTCGGACAA 540  
 QY 179 GlyTyrGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeu 198  
 DB 541 CGTGGGGTTTCATGCCCACTATCAATAGCTGTTATATGATGATGATGATGATGATG 600  
 QY 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218  
 DB 601 GGCACATATACCATATGCTGTTCGTTGATACACACGCGGCTCTCGAACGTGCTCGGGGA 660  
 QY 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrVal 238  
 DB 661 CCGGATTCAGAGATTGGGTTCAGGTACACCACTTCCAGCGAGAGTTGACATACTGTC 720  
 QY 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258  
 DB 721 CTAGCATTTGCTCTCTTTCCCACTAGCACTAGCGGCTAGCGGCTACCCAACTCCGTTACT 780  
 QY 259 SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278  
 DB 781 TCACATTAAGCCGGGAAATCTACANAACCCAGTCTCTCGAG----- 822  
 QY 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294  
 DB 823 AACTTCGAGGTAGCTTCGAGGCTCGGCTCAGGCGATAGAGAAAGCACTGCTCCA 882  
 QY 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314  
 DB 883 CACCTGATGACATATTGAACAGATATCACCATCTACCCGATCGGACCGCGGTATTAC 942  
 QY 315 ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332  
 DB 943 TACTGTGTCAGGCGATCAGATCATGGCATCACCGTGGGTCTCTGGACCAAGATTCACT 1002  
 QY 333 PheProSerTyrGlyValPhe-----AsnProGlyGlyAlaIleTrpIleAlaAspGluAsp 351  
 DB 1003 TTCCCACTTTACGGGACTATGGCAATGCGAGCTCCCAACAAGATATTGTTGCTCAACTC 1062  
 QY 352 ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368  
 DB 1063 GGTACGGGCTGTATAGAACCTTGTCCAGCACTCTATATAGGAGACCTTTCAACATCGGC 1122  
 QY 369 PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387  
 DB 1123 ATCAACAATCAACAATTTCTGTGCTGTGCGGACAGCAAAATTCCTATGGAACCTCTCA 1182  
 QY 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407  
 DB 1183 AATCTGCCATCCGCTGTCTACAGAAAGCGGAACAGTTGATAGCTTGATGATGATCCCT 1242  
 QY 408 ProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr 427  
 DB 1243 CCACAGAAACAACACGTTCCACCTGAGGAGGTTAGCCATGCGCTTAGCCATGCTGTC 1302

QY 428 PheValArgTrpProGlyGluIleSerGlySerAspSerTyrArgAlaProMetPheSer 447  
 DB 1303 ATGTTCCGTTCAGGCTTTAGTAATAGCAGCGTTAGTATCATCAGAGCTCCGATTTCTCT 1362  
 QY 448 TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle 467  
 DB 1363 TGGATACATCGTAGTCTGAGTTTAAACAACATAATTCATCCGATGATCATCTACTCAGATC 1422  
 QY 468 ProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe 487  
 DB 1423 CCAGCTCTCAAGGGAAGCTTTCTCTTTAATAGT---TCTGTCAATTCAGGACAGGATTC 1479  
 QY 488 ThrGlyClyAspIleLeuArgArgThrSerGlyClyProPheAlaTyrThrIleValAsn 507  
 DB 1480 ACTGGAGGCGACTTGGTAGCTGAATCTTCCGGCAAC-----AAC 1521  
 QY 508 IleAsnGly-----GlnLeuPro-----GlnArgTyr 516  
 DB 1522 ATCCAGATAGAGGATATATTGAAGTSCCCATTCACCTTCCATCGCATCTACCAGATAT 1581  
 QY 517 ArgAlaArgIleArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGly 536  
 DB 1582 CGGTTCGTCTAAGGTATGCTCTGTTCACCCCTATTCACTCAACGTCATTTGGGGTAAT 1641  
 QY 537 GluArgIlePheAlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPhe 556  
 DB 1642 TCCTCATCTTTTCCCAATACAGTACCGACAGCTACATCTTGGATAATCTCCAATCT 1701  
 QY 557 GlnSerSerTyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSer 576  
 DB 1702 AGCGATTTCGTTACTTCGAAAGTGCCTTCCCTTACC-----TCTCCCTAGGT 1752  
 QY 577 PheThrValGlyAlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGlu 596  
 DB 1753 AACATAGTAGTGTAGAAATTTCTCCGGAACCGCGAGTGAATAATCGACCGCTCGAA 1812  
 QY 597 LeuIleProValThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAla 616  
 DB 1813 TTCATTCCCGTTTACTGCACAGCTCGAGGCGAGTCTGACTTGGAAAGAGCACAAAGCG 1872  
 QY 617 ValAsnAlaLeuPheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyr 636  
 DB 1873 GTCAATGCTCTGTTACTTCTCCATCAGATGCGGCTCAAGCAGATGAGTACTGACTAT 1932  
 QY 637 HisIleAspGlnValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGlu 656  
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 QY 657 LysArgGluLeuSerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeu 676  
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 QY 777 TrpProLeuSerValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaPro 796

Db 2353 TGGCCACTTTTCAGCCCAAGTCCCATC----- 2379  
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 QY 857 GluPheLeuGluGluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGlu 876  
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 Db 2755 CTTCCTGAACCTAGCGTGAATCCGGGTGTCATCTGCTATCTTTGAAGAGTTAGAAGG 2814  
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Db 3355 TATGTCACCAAGAGTTAGAGTACTTTCCAGAAACCGACARAGTTTGGATTGAGATTGGA 3414  
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 RESULT 15  
 ; Sequence 14, Application US/09826660  
 ; Patent No. US20010026940A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cardineau, Guy A.  
 ; APPLICANT: Stelman, Steven J.  
 ; APPLICANT: Narva, Kenneth E.  
 ; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
 ; FILE REFERENCE: MA-714XC2D1  
 ; CURRENT APPLICATION NUMBER: US/09/826,660  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 09/178,252  
 ; PRIOR FILING DATE: 1998-10-23  
 ; PRIOR APPLICATION NUMBER: 60/065,215  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/076,445  
 ; PRIOR FILING DATE: 1998-03-02  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 14  
 ; LENGTH: 3468  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic B.t. toxin gene  
 US-09-826-660-14  
 Alignment Scores:  
 Pred. No.: 0 Length: 3468  
 Score: 4039.00 Matches: 813  
 Percent Similarity: 74.79% Conservative: 83  
 Best Local Similarity: 67.86% Mismatches: 236  
 Query Match: 66 Indels: 66  
 DB: 14 Gaps: 14  
 US-09-837-961-8 (1-1174) x US-09-826-660-14 (1-3468)  
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 QY 20 ValGluIleLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38  
 Db 61 GTTGAGTGTGTTGGTGAGAACGGATTGAGACTGGTTACACACCTATCGACATCTCGTTG 120  
 QY 39 SerLeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58  
 Db 121 TCAGTTACCAAAATTCCTTTTGTCTGAGAGTTCGTGCCGCTGCTGGATTCTGTGGACTT 180  
 QY 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIle 78  
 Db 181 GTGATATCATPTTGGGAATCTTTGGTCCCTCTCAATGGGAGCGCTTCTGTACAGATA 240  
 QY 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu 98  
 Db 241 GAGCAGTTAATTAACCAAGAATAAGAAATTCGCTAGGAAACCAAGCATCTCAAGTTA 300  
 QY 99 ArgGlyLeuAlaAspSerTyrlGluIleTyrlIleGluAlaLeuArgGluTrpGluAlaAsn 118  
 Db 301 GAAGGCTCAGCAACCTTTACCAGATTTCAGCAGAAATCTTTTCGAGAGTGGAGAGCAGAC 360  
 QY 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAla 138  
 Db 361 CCGACCAATCTCTCCCTTAAGAGAGGAGATGCGCATTCATTCATTCAATGACATGAACGCGC 420  
 QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuSerVal 158

Db 421 CTGACGACCGCAATTCGGCTTCGGCGTTTCAGAAATACCAAGTTCCTCTTTATCCGTG 480  
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Db 481 TACGTGAGGCTGCAACCTGCATCTGTCGGTGTCTCGCGAGTCTCCGTGTCGGCAA 540  
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Db 541 CGGTGGGGCTTTGATGCGCGCAACATCAATAGTGTATATGATGATGACTAGGCTTATT 600  
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Db 601 GGCAACTATACCGATTATGCTTTCGGTGTACACACCGGTCTCGAAGCGTCTCGGGA 660  
QY ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrVal 238  
Db 661 CGGATTCCTAGAGATTGGTCAGGTACCAACAGTTCAGGGAGAGTTGACACTAAGTTC 720  
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Db 721 CTAGACATTGTCGCTCTCTTCCCACTACGACTTAGGCCCTACCCAATCCGTACTGTG 780  
QY SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278  
Db 781 TCACAATGACCCGGGAATCTACACAAACCCAGTCTCCGAG----- 822  
QY AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294  
Db 823 AACTTCACCGTAGCTTCGAGGCTCGGCTCAGGCGATAGAGAAACATCAGGCTCCCA 882  
QY HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314  
Db 883 CACCTGATGACATATTGAACAGTATCACGATCTACCCGATCGCACCCTGTTATAC 942  
QY ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332  
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QY ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368  
Db 1063 GGTACGGCGTGTATAGAACCTTCCAGCACCTATATAGGAGAACCTTTCAACATCGC 1122  
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QY ProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr 427  
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QY TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle 467  
Db 1363 TGGATACATCGTAGCTGAGTTTAAACAACATAATTCATCCGATACATACATCAGATC 1422  
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QY ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn 507  
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QY IleAsnGly-----GlnLeuPro-----GlnArgTyr 516  
Db 1522 ATCCAGAAATAGAGGATATATTAAAGTGGCCATTCACITCCCATCGACATCTACCATAT 1581  
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Db 1582 CGTGTCTGTGAGGTATGCTCTGTACCCCTATTACCTCAACGCTCAATGGGGTAAAT 1641  
QY GluArgIlePheAlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPhe 556  
Db 1642 TCCCTCCATCTTTCCCAATACAGTACCAGGACAGCTACATCCTTGGATAATCTCAACT 1701  
QY GlnSerPheSerTyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSer 576  
Db 1702 AGCGATTTCGGTTACTTCCGAAAGTCCCAATGCCTTCACC-----TCCTCCCTAGGT 1752  
QY PheThrValGlyAlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGlu 596  
Db 1753 AACATAGTAGGTGTAGAAATTTCTCCGGAACCCCGAGGTGATAATCGACCGCTCGAA 1812  
QY LeuIleProValThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAla 616  
Db 1813 TTCATTCCCGTTACTGCAACGCTCGAGGACAGTCTGACTTTGGAAGACACAGAGCGG 1872  
QY ValAsnAlaLeuPheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyr 636  
Db 1873 GTSAATCTCTGTTCACCTTCTCCCAATCAGATTGGGCTCAAGACAGATGTGACTGACTAT 1932  
QY HistLeuAspGlnValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGlu 656  
Db 1933 CACATCATCGCTTCCCAACCTTTGAGTGCCCTCTCTGAGAGTCTCTGTGTTGGATGAG 1992  
QY LysArgGluLeuSerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeu 676  
Db 1993 AAGAAGAGTGTTCGAGAGAGTCAACATGCTAAGCGACTTAGTGATGACGCGAATTG 2052  
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Db 2053 CTTCAGATCCCACTTTCCGCGGATCAACAGGCACTAGATCTGATGAGGAGGAAGT 2112  
QY ThrAspIleThrIleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuPro 716  
Db 2113 ACGGACATCACCATTCAAGAGGTGATGATGTGTCAAGGAGAACTATGTTACCTCTTG 2172  
QY GlyThrPheAspGluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeu 736  
Db 2173 GGTACCTTTGATGAGTGTCTCCAACTACCTGTACCAGAAAGATAGATGAATCGAAACTC 2232  
QY LysProThrThrArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIle 756  
Db 2233 AAGCCTACACAGATACCACTTGAGAGGTATACATGAGGACAGCTCAAGACCTTGAGATC 2292  
QY TyrLeuIleArgTyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeu 776  
Db 2293 TACCTCATCAGATACACGCCCAACATGACAGCTCAATGTGCTGGGCGGTTCACTC 2352  
QY TrpProLeuSerValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaPro 796  
Db 2353 TGGCCACTTTTCAGCCCCCAAGTCCCATC----- 2379  
QY HisLeuGluTrpAsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHis 816  
Db 2380 -----GGCAAGTGTGCCCAT 2394  
QY HisSerHisPheSerLeuAspIleAspValcylCysThrAspLeuAsnGluAspLeu 836  
Db 2395 CACTCACACACCTTCTCTTGGACATAGAGCTTGGCTGTACCCAGCTGAAGAGACCTC 2454  
QY AspValTrpValIlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeu 856  
Db 2455 GGTGTGGGTGATCTTCAAGATCAAGACTCAAGATGGCCATGCCAGGCTAGGCCATCTG 2514

Db 1480 ACTGAGGCGAGCTTGGTTAGGCTGAAATTCCTCCGGCAAC-----AAC 1521  
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DB 2695 ACCAATAGCTATGATTTCATGCTGAGACAAACCGGTTTCATAGCATTCGGGAAGCTTAC 2754  
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DB 2755 CTTCCTCAACTTAGCGTGATTCGGGTGTCAATGCTGCTATCTTTGAGAGTTAGAGGG 2814  
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DB 3055 TGGGTACCATACACAGAGATTGAGACACACCCAGCAGCTGAAGTTACAGCACTGCGTGC 3114  
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DB 3175 GAGTATGAGGGTACTTACACTTCTCGCAATCGAGGATACGATGGAGCCCTATGAGAGCAAC 3234  
QY 1097 SerSerValProAlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArg 1116  
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QY 1117 ArgAspAsnProCysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGly 1136  
DB 3295 AGGACAAATCCCTTGCGAATTAACAGAGGCTATGGGGACTACACACCGTTACCGCGGC 3354  
QY 1137 TyrValThrLysGluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGly 1156  
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QY 1157 GluThrGluGlyThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174  
DB 3415 GAAACGGAAGGAACATTCATTGTTGATAGCTGGAGTTACTTCTGATGGAGGAA 3468

Search completed: November 28, 2002, 02:22:32  
Job time : 315 secs

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 27, 2002, 20:26:25 ; Search time 104 Seconds

(without alignments)  
3461.909 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	6244	100.0	3522	US-07-828-788A-9	Sequence 9, Appl
2	6244	100.0	3522	US-08-349-867-28	Sequence 24, Appl
3	6244	100.0	3522	US-08-239-476-24	Sequence 24, Appl
4	6244	100.0	3522	US-08-356-034-7	Sequence 7, Appl
5	6244	100.0	3522	US-08-598-305A-24	Sequence 24, Appl
6	6244	100.0	3522	US-08-639-923A-24	Sequence 24, Appl
7	6244	100.0	3522	US-08-933-891-7	Sequence 7, Appl
8	6244	100.0	3522	US-09-178-252-5	Sequence 5, Appl
9	6244	100.0	3522	PCT-US92-11337-9	Sequence 9, Appl
10	6244	100.0	3522	PCT-US95-05431-24	Sequence 24, Appl
11	6244	100.0	3522	5188960-7	Patent No. 5188960
12	6244	100.0	4020	PCT-US91-02560-1	Sequence 1, Appl

13	6049	96.9	3522	1	US-08-349-867-28	Sequence 28, Appl
14	6049	96.9	3522	1	US-08-239-476-28	Sequence 28, Appl
15	6049	96.9	3522	1	US-08-598-305A-28	Sequence 28, Appl
16	6049	96.9	3522	2	US-08-639-923A-28	Sequence 28, Appl
17	6049	96.9	3522	5	PCT-US95-05431-28	Sequence 28, Appl
18	5902	94.5	3444	1	US-08-349-867-22	Sequence 22, Appl
19	5902	94.5	3444	1	US-08-349-867-26	Sequence 26, Appl
20	5902	94.5	3444	1	US-08-239-476-22	Sequence 22, Appl
21	5902	94.5	3444	1	US-08-239-476-26	Sequence 26, Appl
22	5902	94.5	3444	1	US-08-598-305A-22	Sequence 22, Appl
23	5902	94.5	3444	1	US-08-598-305A-26	Sequence 26, Appl
24	5902	94.5	3444	2	US-08-639-923A-22	Sequence 22, Appl
25	5902	94.5	3444	2	US-08-639-923A-26	Sequence 26, Appl
26	5902	94.5	3444	5	PCT-US95-05431-22	Sequence 22, Appl
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28	5879	94.2	3444	4	US-09-178-252-1	Sequence 1, Appl
29	5674	90.9	3450	1	US-08-349-867-20	Sequence 20, Appl
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31	5674	90.9	3450	1	US-08-598-305A-20	Sequence 20, Appl
32	5674	90.9	3450	2	US-08-639-923A-20	Sequence 20, Appl
33	5674	90.9	3450	5	PCT-US95-05431-20	Sequence 20, Appl
34	5415	86.7	3504	1	US-08-291-368-3	Sequence 3, Appl
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37	4815.5	77.1	3531	3	US-08-754-490-13	Sequence 13, Appl
38	4815.5	77.1	3531	3	US-08-922-505A-13	Sequence 13, Appl
39	4815.5	77.1	3531	4	US-09-260-952A-13	Sequence 13, Appl
40	4815.5	77.1	3531	4	US-09-253-341-13	Sequence 13, Appl
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42	4815.5	77.1	3531	4	US-09-261-040-13	Sequence 13, Appl
43	4812.5	77.1	3534	3	US-08-754-490-25	Sequence 25, Appl
44	4812.5	77.1	3534	3	US-08-922-505A-25	Sequence 25, Appl
45	4812.5	77.1	3534	4	US-09-260-952A-25	Sequence 25, Appl

#### ALIGNMENTS

#### RESULT 1

US-07-828-788A-9

; Sequence 9, Application US/07828788A

; Patent No. 5273746

; GENERAL INFORMATION:

; APPLICANT: PAYNE, JEWEL M.

; APPLICANT: HICKLE, LESLIE A.

; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES

; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID R. SALIWANCHIK

; STREET: 2421 N.W. 41st STREET, SUITE A-1

; CITY: GAINESVILLE

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/828,788A

; FILING DATE: 19920129

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: SALIWANCHIK, DAVID R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: MA75

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100

; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3522 base pairs

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; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811a
; US-07-828-788A-9

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

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US-09-837-961-8 (1-1174) x US-07-828-788A-9 (1-3522)

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Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheClyLeuPheAsp 60
Db 121 ACACGTTTCCCTTTGAGTGAATTTGTCAGGTGGGAGTTGCGTTGGGATTATTGAT 180
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## RESULT 2

US-08-349-867-24  
: Sequence 24, Application US/08349867  
: Patent No. 5508264  
: GENERAL INFORMATION:  
: APPLICANT: Bradfisth, Gregory A.  
: APPLICANT: Thompson, Mark  
: APPLICANT: Schwab, George E.  
: TITLE OF INVENTION: No. 5508264el Pesticidal Compositions  
: NUMBER OF SEQUENCES: 34  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: David R. Saliwanchik  
: STREET: 2421 N.W. 41st Street, Suite A-1  
: CITY: Gainesville  
: STATE: FL  
: COUNTRY: USA  
: ZIP: 32606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/349,867  
: FILING DATE:  
: CLASSIFICATION: 514  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Saliwanchik, David R.  
: REGISTRATION NUMBER: 31,794  
: REFERENCE/DOCKET NUMBER: MA86  
: TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-349-867-24

Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00 Conservative: 0
Best Local Similarity: 100.00 Mismatches: 0
Query Match: 100.00 Indels: 0
DB: 1 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-349-867-24 (1-3522)

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Db 61 GAAATACATGACGAAGAACGACGACCGCCGCTCGCGCTGGACATCAGCCTGAGCCTT 120
Qy 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheClyLeuPheAsp 60
Db 121 ACACGTTCCCTTTGAGTGAATTTGTTCCAGGTGGAGTTGCGTTTGGATTATTGAT 180
Qy 61 LeuLeuTrpGlyPheLeuThrProSerAspTrpSerLeuPheLeuGlnLeuGln 80
Db 181 TTAATATGGGTTTATACCTCTCTGATTTGGAGCTTATTTCTTTTACAGATTGAACAA 240
Qy 81 LeuLeuGluGlnArgGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100
Db 241 TTGATTAGCAAAAGAAATAGAAACATGTGAAAGAACCGGGCAATTTACATTACGAGGG 300
Qy 101 LeuAlaAspSerTyrGluLeuTrpGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
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Qy 121 AsnAlaGlnLeuArgGluAspValArgGluPheAlaAsnThrAspAspAlaLeuLe 140
Db 361 AATGCACAAATTAAGGAGAGATGCGGTATTCGATTGCTAATACAGACGACGCTTTAATA 420
Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
Db 421 ACAGCAATAAATAATTTTACACTTACAAGTTTGAATCCCTCTTTTATCGGTCTATGTT 480
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
Db 481 CAACGGCGGAATTTACATTTTACATATTAAGAGACGCTGATCGTTTGGCAGGTTGG 540
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Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu 320
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Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
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Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACCTTTTACTCAGGGAATGAAGTTTATATAGACATTTGAATTTGATTCACGATT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAAGCAGAAATATGATTTAGAAAGAGCACAAAGCGGTGAATGCGGTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleThrAspValThrAspTyrHisIleAspGln 640

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Db 1921 GTATCCCAATTTAGTGAGTTGTTATCAGATGAATTTCTCGGATGAAAGCGAAATG 1980  
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Db 2701 GTAGATGCTTTATTTGTAACCTCAATATGATCAATATCAAGCGGATACCAATATTGCC 2760  
Qy MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
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Qy TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080  
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Db 3481 ACATTATCGTGGACAGCGTGAATTAATCTCTTATGGAGGAA 3522

## RESULT 3

US-08-239-476-24

: Sequence 24, Application US/08239476

: Patent No. 5527883

: GENERAL INFORMATION:

: APPLICANT: Thompson, Mark

: APPLICANT: Schwab, George E.

: TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in

: NUMBER OF SEQUENCES: 34

: CORRESPONDENCE ADDRESS:

: ADDRESS: David R. Saliwanchik

: STREET: 2421 N.W. 41st Street, Suite A-1

: CITY: Gainesville

: STATE: Florida

: COUNTRY: USA

: ZIP: 32606

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/239,476

: FILING DATE:

: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:

: NAME: Saliwanchik, David R.

: REGISTRATION NUMBER: 31,794

: REFERENCE/DOCKET NUMBER: MA83

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (904) 375-8100

: TELEFAX: (904) 372-5800

: INFORMATION FOR SEO ID NO: 24:

: SEQUENCE CHARACTERISTICS:

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; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-239-476-24

Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-239-476-24 (1-3522)

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Qy 41 ThrA:gpheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
Db 121 ACACGCTTCCTTTGAGTGAATTTGTTCCAGGTGGGAGTTGCGTTTGGATTTTGTAT 180
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Db 3001 CTTGTGTTTCCGGAATGGGAAGCAGAGAGTGTCAAGAAGTTCTGTCTGTCCGGTGT 3060  
Qy GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGlyCysValThrIle 1040  
Db 3061 GGCTATATCCCTTCCGTGCACAGCGTACAGGAGGATATGGAGAAGTTGCGTAACCAT 3120  
Qy HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
Db 3121 CATGAGATCGAACAATACAGACCACTGAAGTTAGCACTGGTAGAAGGAAGTC 3180  
Qy TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGly 1080  
Db 3181 TATCCAAACACACCGTAACTGATGATTAATGATTAATGCTCAAAATCAAGAAGATACGGGT 3240  
Qy AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100  
Db 3241 GCGTACACTCCGTAATCGTGGATATGCGAACTTATGGAAGCAATCTCTTCTTACCA 3300  
Qy AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
Db 3301 CCGTATTATGCGTCACTATGACAGAAATCGTATACAGATGGACGAGACCAATCCT 3360  
Qy CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
Db 3361 TGTGAATCTAACAGAGGATATGGGATACACACCACTACCACTGGCTATGTGACAAA 3420  
Qy GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyCyluThrGluGly 1160  
Db 3421 GAATTAGAGTACTTCCAGAACCGATAGGTATGATGATGATGATGATGATGATGATG 3480  
Qy ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
Db 3481 ACATTCATCGTGGACAGCGTGGAAATCTCTCTTATGGAGGAA 3522

## RESULT 4

US-08-356-034-7  
; Sequence 7, Application US/08356034  
; Patent No. 5691308

## GENERAL INFORMATION:

; APPLICANT: Payne, Jewel M.  
; APPLICANT: Sick, August J.  
; TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate  
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding  
; TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,034  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/210,110  
; FILING DATE:  
; APPLICATION NUMBER: 07/865,168  
; FILING DATE: 09-APR-92  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/451,261  
; FILING DATE: 14-DEC-89  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/371,955  
; FILING DATE: 27-JUN-89

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, Roman
REGISTRATION NUMBER: 21,023
REFERENCE/DOCKET NUMBER: MA43.C1.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
TELEFAX: (904)372-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3522 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811a
US-08-356-034-7

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Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

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US-09-837-961-8 (1-1174) x US-08-356-034-7 (1-3522)

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QY 1 MetGluAsnAsnIleGlnCysValProTyrAsnCysLeuAsnProGluVal 20
DB 1 ATGGAGAATAATATCAAAATCAATCGGTACCTTCAATTTGTTAAATCCTGAAGTA 60
QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeu 40
DB 61 GAAATATTAAATGAAGAAAGTAGTACTGCGACATTACCGTTAGATATATCCATTATCGCTT 120
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
DB 121 ACACGCTTCCCTTTGAGTGAATTTGTTCCAGGTGGGAGTTGCCGTTTGGATTATTGAT 180
QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
DB 181 TTAATATGGGGTTTATAACTCTCTGATTGAGCTTATTTCTTTACAGATTGAACAA 240
QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
DB 241 TTGATTGAGCAAGAAATGAACAATTGTTAGACCACTAAGAGAGTGGGCAATTTACTACATTACGAGGG 300
QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
DB 301 TTAGCAGATAGCTATGCAATTTATATTGAGCACTAAGAGAGTGGGCAATTTACTACATTACGAGGG 360
QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140
DB 361 AATGCACAATTAAGGAAGATGTGCGTATTCGATTTCGTTAATACAGACCGACCTTTAATA 420
QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
DB 421 ACAGCAATAAATAATTTTACACTTACAGTTTGAATTTGAAATCCCTTTTATCGGTCTATGTT 480
QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
DB 481 CAAAGCGGCAATTTACATTTATCATTATTAAGAGACGCTGTATCTGTTGGGAGGGTTGG 540
QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200

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QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
DB 661 ACTCGACAATGGCAAGATTCAATCAGTTTAGCAGAGATTTAACACTTACTGTATTAGAT 720
QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
DB 721 ATCGTGTGCTCTTTTCCGACATACGATGTAGAACATATCCCAATTCACAGCATCCCCAA 780
QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
DB 781 TTAACAAGGGAAATTTATACAAAGTTCAAGTAATGAGGATTCACAGTTCTGCTAATA 840
QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetaspPheMet 300
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QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
DB 901 AATTCCTTTGTTGTAACCTGACAGACTGTTAGAGTCAACACGTGTGGGGAGACACTTA 960
QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
DB 961 GTTAGTTACGAAATACGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGTCTTCAAT 1020
QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProAspProPheTyrArgThrLeuSer 360
DB 1021 CCTGTGGCGCCATTTGGATTGCAGATGAGATCCACGTCCTTTTATCGGCATTATCA 1080
QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
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QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
DB 1141 GTAGCATTTCAACAACTGGTACGAACCAACCCGCAACATTTAGAAATAGTGGACCATA 1200
QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTrpSer 420
DB 1201 GATTCCTAGATGAATCCCACTCAGGATAATAGTGGGCCACCTTGGGAATGATTATAGT 1260
QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
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QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
DB 1321 TGGAGAGCTCCAATGTTTCTTTGGACCGCACCGTAGTGAACCCCTACAAAATACAATTGAT 1380
QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
DB 1381 CCGGAGAGGATTTACTCAATACCATTTGGTAAAGACACATACACTTCAGTCAGGTACTACT 1440
QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
DB 1441 GTTGTAGAGGGCCCGGGTTTACGGGAGGAGATATCTTCGACGACCAAGTGGAGAGCA 1500
QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
DB 1501 TTTGCTTATACTATTGTTAAATAATAATGGCAATTTACCCAAAGGTATCGTCGAAGAATA 1560
QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
DB 1561 CGCTATGCTCTACTACAAATCTAAGAATTTACGTAAAGGTTGCAAGTGAACGGATTTT 1620
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560

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Db 1621 GCTGGTCAATTTACAAACAAATGGATACCGGTACCCATTAACATCCCAATCTTTTGTAGT 1680  
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Db 1681 TACCACTATTATACAGCTTTTACATTCCTCCATAGCCAGAGTAGTTTCCAGTAGAGT 1740  
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Db 1741 GCTCATCTTTTACTTCCAGGAATGAAGTTTATATAGACAGATTGAATTGATTCACAGTT 1800  
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Db 1801 ACTCCACATTTGAGCAGATATGATTTAGAAAGACACAAAAGCGGTGAATGCGGTG 1860  
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
Db 1861 TTTACTTCTATAAACCAATAGGATATAAACAAGATGTGACGGAATTATCAATATTGATCAA 1920  
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Db 1921 GTATCCAAATTTAGTGGATGTTTATCAGATGAATTTTCTGCGATGAAGACGGAATG 1980  
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluLysArgAsnLeuGlnAspPro 680  
Db 1981 TCCGAGAAAGTCAACATGCCAAGCGACTCAGTATGAGCGGAATTTACTTCAAGATCCA 2040  
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700  
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Qy 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
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Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
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Db 2761 ATGATTTCATCGCGCAGATAAACGTTTCATAGAAATTCGGGAAGCGTATCTTCCAGAGTTA 2820  
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Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
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Db 2941 TCATGCTGACAGCTGAAAGGCGCATGTAGATGTAGAGACAAACAACACCCTGCGTC 3000  
Qy 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
Db 3001 CTTGTGTTTCCGAATGGAAAGCAGAAAGTGTACAAAGAAGTTCGTGTCTGTCGGGTCGT 3060  
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
Db 3061 GGCATATCTCTCGTGTCCAGCGTACAGGAGGATATGGAGAAGTTCGTGTCTGTCGGGTCGT 3120  
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Db 3181 TATCCAAACAAACACGCTAACGTGTAATGATTAATCTGCAAAATCAAGAAGAAATACGGGT 3240  
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Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
Db 3361 TGTGAATCTAACAGAGGATATGGGATTAACACACACTACCACTACCACTGCTATGTGACAAA 3420  
Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160  
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## RESULT 5

US-08-598-305A-24  
; Sequence 24, Application US/08598305A  
; Patent No. 5827514  
; GENERAL INFORMATION:  
; APPLICANT: BRADFISCH, Gregory A.  
; APPLICANT: THOMPSON, Mark  
; APPLICANT: SCHWAB, George E.  
; TITLE OF INVENTION: No. 5827514el Pesticidal Compositions  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/598,305A  
 FILING DATE: 08-FEB-1996  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/349,867  
 FILING DATE: 06-DEC-1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sanders, Jay M.  
 REGISTRATION NUMBER: 39,355  
 REFERENCE/DOCKET NUMBER: MAB6.D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 352-375-8100  
 TELEFAX: 352-372-5800  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3522 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-598-305A-24

Alignment Scores:  
 Pred. No.: 0 Length: 3522  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-598-305A-24 (1-3522)

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QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
DB 1 ATGGAAATAATATTCAAAATCAATCGTACCTTACAAATGTTTAAATAATCCTGAAGTA 60
QY 21 GluIleuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
DB 61 GAAATACGTGAACGAAGAAGAACACCGCGCGCTGCGGTGGACATCAGCCTGAGCCTT 120
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
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QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
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QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
DB 241 TTGATTGCGCAAGAATAGAAACATTGGAAGAAGAACCGGCAATTACTATTACAGGG 300
QY 101 LeuAlaAspSerThrGluIleThrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
DB 301 TTACAGATAGCTATGAAATTTATATTAAGACACTTAAGAGAGTGGGAAGCAATCCTAAT 360
QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140
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QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTrpVal 160
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DB 481 CAACGGCGGAATTTACATTTATCATTATTAAGAGACGCTATCGTTGGCAGGTTGG 540
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DB 541 GGACTGGATATAGTACTGTGTTAATAATCATATAATAGATTAAATCTTATTCATAGA 600
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DB 601 TATACGAACAATTTGTTGGACACATACAACTAGGATTAGAAACCTTAGAGGTACTPAT 660
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DB 781 TTAACAAGGGAAATTTATACAAGTTCAAGTAATTTGAGGATTCTCCAGTTTCTGCTAATA 840
QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
DB 841 CCTAATGTTTAAATAGGGGGAAATTTGGAGTTAGACCGGCCCACTTATGGACTTTATG 900
QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
DB 901 AATCTTTGTTTGAATCGCAGACACTGTTAGAACTCAAACTGTGTGGGAGGACACTTA 960
QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
DB 961 GTTAGTTCCAGAAATACGGCTGGTAACGTATAAAATTTCCCTAGTTACGGGGTCTTCAAT 1020
QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
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DB 1141 GTAGATTTTCAACAACTGGTACGAACCAACCCGACACATTTAGAAATAGTGGGACCATTA 1200
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QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
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DB 1381 CCGGAGAGGATTTACTCAAAATACCATTGTTGTTAAAGACACATACACTTCAGTCAGTACT 1440
QY 481 ValValArgGlyProGlyPheThrGlyAspIleLeuArgArgThrSerGlyGlyPro 500
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QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
DB 1501 TTTGCTTATACTATTGTTAATAATAAAGGGCAATTAACCCAAAGGTATCTGTCAGGATA 1560
QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
DB 1561 CGCTATGCTCTACTACAAATCTAAGAATTTACGTAAAGGTTGCAAGGTGAACGGATTTT 1620
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560

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Db 1621 GCTGGTCAATTTAACAACAATGATACCGGTGACCATTAACATCCAACTCTTTAGT 1680  
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
Db 1681 TAGCAACTATTATACAGCTTTTACATCCCATGACCCAGAGTAGTTTCACAGTAGT 1740  
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Db 1741 GCTGATACTTTTAGTTCAGGGAATGAAGTTTATATAGACAGATTGAATTCATCCAGTT 1800  
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Db 1801 ACTGCACATTTGAAGCAGATATGATTTAGAAAGACACAAAAAGCGGTGAATCGCGTG 1860  
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
Db 1861 TTTACTTCTATAACCAANTAGGATATAAACAAGATGTGACGGATTATCATATTGATCAA 1920  
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Db 1921 GTATCCAAATTTAGTGGATTGTTATCAGATCAATTTTGTCTGGATGAACACGGAATG 1980  
QY 661 SerGlnLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
Db 1981 TCCGAGAAAGTCAACATGCGAAGCGACTCAGTGTATGATGACGGGAATTTACTTCAAGATCCA 2040  
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIlePhe 700  
Db 2041 AACTTCAAGGCATCATAGCCACTAGCCGCTGGTGGAGAGGAATGACGGATATTACC 2100  
QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
Db 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAAAATTTATGTCACACTACACAGTACCTTTGAT 2160  
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
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QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
Db 2221 CGTTATCAATTAAGAGGGTATATCAGGATAGTCAAGACTTAGAANAATTTATGATCCG 2280  
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780  
Db 2281 TATTAATGCAAAACACGAACAGTAAATGTGCTAGTACGGGTTCTTTATGCGCCGTTTCA 2340  
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr 800  
Db 2341 GTCCAAAGTCCAAATCAGAAAGTGGAGAACCGAATCGATCGCGCCACACACTTGAATGG 2400  
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820  
Db 2401 AATCCTCATCTAGATTCTCTGTCAGAGACGGGGAANAATGTGCACATCATTCGCATCAT 2460  
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840  
Db 2461 TTTCTCTTGACATATGATGTGGATGTACAGACTTAATAGGACTTAGATGTATGGGTG 2520  
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
Db 2521 ATATTCAGATTAGACGCAAGATGGCCATCAGACTAGGAATCAGAGTTTCTCGAA 2580  
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880  
Db 2581 GAGAAACCATTTAGTCGGGAGCAGCTAGTCTGTGTAAGAGCAGAGAAAAATGGAGA 2640  
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900  
Db 2641 GATAAAGCTGAAAAAATGGATTTGGAACAAATATTTGTTATATAAGAGCGCAAAAGAACT 2700  
QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920  
Db 2701 GTAGTCTCTTTTGTAAACTCTCAATATGATCAATTAACAAGCGGATACGAATATTGCC 2760

QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
Db 2761 ATGATTTCATGCGGAGATAAAACGGTTCATAGAAATTCGGGAGCGGTATCTTCCAGAGTTA 2820  
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
Db 2821 TCTGTGATTCGGGTGTAATATGTAGACATTTTCGAAGAAATTAAGGCGGTATTTCCTACT 2880  
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
Db 2881 GCATTCTCTTATATGATGCGAGAAATGTCATTAATAACGGTGTATTCATATAATGGCTTA 2940  
QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000  
Db 2941 TCATGCTGGAACGGAAGGCGCATGTAGATGTAGAAGAACAAACACACCGTTCGGTGC 3000  
QY 1001 LeuValValProGluTyrPgluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
Db 3001 CTTCTTGTTCGGGATGGGAAGCAGAGTGTCAAGAAGTTCGTGCTGTCCGGGTGCT 3060  
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
Db 3061 GGCATATATCTCTGTACAGCGTACAAAGGAGGATATGGGAAGGTTCGGTAAACCAT 3120  
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
Db 3121 CATGAGATCGAAGAACATACAGACGAACTGAAGTTTAGCACTGCGTAGAAGAGAGTC 3180  
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080  
Db 3181 TATCCAAACACACGGTAACGTGTAAATGATTATATCTGCAATCAAGAGATACGGGGGT 3240  
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100  
Db 3241 GCGTACACTTCCCTTAATCGTGGATATGACGAAACTATGGAAGCAATTCCTCTGTACCA 3300  
QY 1101 AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
Db 3301 GCTGATTATGCGTCAGTCTATGAAGAAAAATCGTATACAGATGGACGAGACAACTCCT 3360  
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
Db 3361 TGTGAATCTAACAGAGGATATGGGATATACACCACTACCACTGCGTATGTGACAAA 3420  
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160  
Db 3421 GAATTAGAGTACTTCCCGAAGAACCGATAAGGTATGGATTGAGATCGGAGAAACGGAAGA 3480  
QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
Db 3481 ACATTCACTGTCGACACGGTGGAAATTTACTCTCTATGGAGAA 3522

## RESULT 6

US-08-639-923A-24  
: Sequence 24, Application US/08639923A  
: Patent No. 5840554  
: GENERAL INFORMATION:  
: APPLICANT: Thompson, Mark  
: APPLICANT: Schwab, George E.  
: TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in  
: Pseudomonas fluorescens  
: NUMBER OF SEQUENCES: 38  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: David R. Saliwanchik  
: STREET: 2421 N.W. 41st Street, Suite A-1  
: CITY: Gainesville  
: STATE: Florida  
: COUNTRY: USA  
: ZIP: 32606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible



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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,923A
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,476
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Salliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-639-923A-24

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Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

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US-09-837-961-8 (1-1174) x US-08-639-923A-24 (1-3522)

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QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
DB 1 ATGGAATAATATATCAAAATCAATGCGTACCTTACAAATGTTTAAATATCCTGAAGTA 60
QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeu 40
DB 61 GAAATACTGAACGAGAACGACGACCGCGCGCTGCGCTGGACATCAGCGCTGAGCGCTT 120
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
DB 121 ACAGCTTCCCTTTTGAGTCAATTTGTTCCAGGTGTGGAGTGTGCTTTGGATTATTTGAT 180
QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
DB 181 TTAATATGGGGTTTATATACTCTCTGATTGGAGCTTATTTCTTACAGATTGACAA 240
QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
DB 241 TTGATTGAGCAAGAAATAGAAACATTGGAAGAACCGGGCAATTACTACATTACGAGGG 300
QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
DB 301 TTACAGATAGCTATGAAATTTATATTGACACCTAGAGAGTGGGAGCAATCCCTAAT 360
QY 121 AsnAlaGlnLeuArgGluAspValArgPheAlaAsnThrAspAspAlaLeuIle 140
DB 361 AATGCAAAATTAAGGAAGATGTCGGTATTCGATTTCGTAATACAGAGCGCTTTAATA 420
QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
DB 421 ACAGCAATAATAATTTTACACTTTACAAAGTTTGAATCCCTCTTTATCGTCTATGTT 480
QY 161 GlnAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
DB 481 CAACGGCGAATTTACATTTATCTACTATTAGAGACGCTGTATCGTTGGCGAGGTGG 540
QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuHisArg 200

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DB 541 GGACTGGATATAGCTACTGTTTAAATATATATATATATATATATATATATATATATATAGA 600
QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
DB 601 TATACGAAACATTTGTTGGACACATACAAATCAAGGATTAGAAAATTAAGAGGTACTAAT 660
QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
DB 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAACACTTACTGTATTAGAT 720
QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
DB 721 ATCGTGTCTCTTTTCCGAACCTACCATGTTAGAATATATCCAAATCAACACGTCATCCCAA 780
QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
DB 781 TTAACAAGGAAATTTATACAAGTTTCAGTAATTAGGATTCTCCAGTTCTCTTAATATA 840
QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
DB 841 CCTAATGTTTTAATAGGCGGAAATTTGGAGTTAGACGCCCATCTTATGGACTTTATG 900
QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
DB 901 AATCTTTGTTTGAACCTGAGAGACTGTTAGAAGTCAAACTGTGTGGGAGGACACTTA 960
QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
DB 961 GTTAGTTTCCAGAAATACGCGTGGTAACCGTATAAATTTCCCTAGTTACGGGGTCTTCAAT 1020
QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
DB 1021 CCTGTGGCGCAATTTGGATTGCAGATGAGATCCACGCTCTTTTATTCGGACATTATCA 1080
QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
DB 1081 GATCCTGTTTGTTCGAGAGAGGATTGGGAATCTCTATTATGTACTGGGCGTTAGGGGA 1140
QY 391 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
DB 1141 GTAGCATTTCAACAACTGGTACGAAACACACACCGCAACATTAGAAATAGTGGGACCAT 1200
QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
DB 1201 GATTCTCTAGTAAATCCCACTCAGGATAATAGTGGGCGCACCTTGGAAATGATTATAGT 1260
QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
DB 1261 CATGTATTAAATCATGTTACATTGTACGATGGCCAGGTGAGATTTCAGGAAGTGATTCA 1320
QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
DB 1321 TGGAGAGCTCCAATGTTTCTTGGACGCAACCGTAGTGCACCCCTACAAATACAAATTGAT 1380
QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
DB 1381 CCGAGAGGATTACTCAAAATACCATTGGTAAAGCACATACACTTCAGTCAAGGTACTACT 1440
QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
DB 1441 GTTGTAGAGGGCCCGGTTTACGGGAGGAGATATTCTTCGACCAACAGTGGGAGGACCA 1500
QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
DB 1501 TTTCTTATATACTATTGTTAATAAATGGCAATACCCCAAGAGTATCTGTCGAGAGATA 1560
QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
DB 1561 CGTATGCCCTCTACTCAAAATCTAAGAAATTTACGTAACGGTGTGACGTTGAACGGATTTT 1620
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560

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Db 1621 GCTGGTCATTTTAAACAAACATGATGATCCGGTGCACCCATTAACATTCCTTTTGTAGT 1680  
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
Db 1681 TACGCAACATTAATACAGCTTTTACATCCCAATGAGCCAGAGTAGTTTCACAGTAGT 1740  
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Db 1741 GCTGATCTTTTAGTTCAGGGAATCAAGTTTATATAGACAGATTTGAATGATCCAGTT 1800  
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Db 1801 ACTGCAACATTTGAAGCAGATATATGATTAGAAAGACACAAAAGCGGTGAATCGCGTG 1860  
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
Db 1861 TTTACTCTTAACCAATAGGGATAAACAAGATGACGATGACGATTTATCATATTGATCAA 1920  
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Db 1921 GTATCCAAATTTAGTGGATTGTTTATCAGATGAATTTGTCTGGATGAAGCGAATGTG 1980  
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680  
Db 1981 TCCGAGAAAGTCAACATTCGGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCA 2040  
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrAspGlySerThrAspIleThr 700  
Db 2041 AACITCAAGGCATCAATAGGCACTAGACCGTGTGGAGGAAGTAGCGATATTACC 2100  
QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
Db 2101 ATCCAAAGAGGAGATGACGATTCAAGAAATATTATGTCACACTACCAGGTACCTTTGAT 2160  
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
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QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780  
Db 2281 TATATGCAAAACACGAAACAGTAATGTCTAGTACGGGTCTTTATGGCCGCTTTCA 2340  
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyrP 800  
Db 2341 GTCCAAAGTCCCAATCAGAAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTGAATGG 2400  
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820  
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QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840  
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QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
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QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrIleuProGluLeu 940  
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QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
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QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000  
Db 2941 TCATCTGCTGAACGTGAAAGGCGATGTAGATGTAGAGAACAAACACCCGTTCCGGTC 3000  
QY 1001 LeuValValProGluTyrPheAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
Db 3001 CTTGTGTTCCGGAATGGAGACAGAGTGTACAGAAGTTCTGTGTCTCCGGTCTGT 3060  
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
Db 3061 GGCTATATCTTCTGTGTACAGCGTACAAGGAGGATATGGAGAAGGTTGCGTAACCAT 3120  
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
Db 3121 CATGAGATCGAGAACAAATACAGACCACTGAAGTTTAGCACTGCGTAGAGAGGAAGTC 3180  
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080  
Db 3181 TATCCAAACACACGCTAACGTGTAATGATTATATCTGCAAAATCAAGAATAACGGGGT 3240  
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100  
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QY 1101 AlaAspTyrAlaSerValTyrCysGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
Db 3301 GCTGATTATGCTGCTAGTCTATGAGAAAAATCGTATACAGATGGACGAGACAAATCCT 3360  
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QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyLeuThrGluGly 1160  
Db 3421 GAATTAGAGTAGTCTCCAGAAACCGATAAGGTATGGATTGAGATCGGAGAAACGGAAGA 3480  
QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174  
Db 3481 ACATTCATCGTGACGAGCGTGAATTAATCTCTTATGGAGAA 3522

## RESULT 7

US-08-933-891-7

; Sequence 7, Application US/08933891

; Patent No. 6096708

; GENERAL INFORMATION:

; APPLICANT: Payne, Jewel M.

; APPLICANT: Sick, August J.

; TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate

; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding

; TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik &amp; Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: US

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/933,891

## FILING DATE:

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/356,034

FILING DATE: US/08/210,110

FILING DATE: 07/865,168

FILING DATE: 09-APR-92

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/451,261

FILING DATE: 14-DEC-89

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/371,955

FILING DATE: 27-JUN-89

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, Roman

REGISTRATION NUMBER: 21,023

REFERENCE/DOCKET NUMBER: MA43.C1.D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (904)375-8100

TELEFAX: (904)372-5800

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 3522 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: BACILLUS THURINGIENSIS

STRAIN: ATZAWAI

INDIVIDUAL ISOLATE: PS811

IMMEDIATE SOURCE:

LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST STICK

CLONE: 811A

US-08-933-891-7

## Alignment Scores:

Pred. No.: 0 Length: 3522  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-933-891-7 (1-3522)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
 Db 1 ATGGAGAAATAATATCAAAATCAATGCTACCTTACAATTTGTTAAATAATCCGGAAGTA 60  
 Qy 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 Db 61 GAAATATAATGAAGAAGAAGTACTGGCAGATTACCGTTAGATATATCCTTATCGCTT 120  
 Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 Db 121 ACACGTTTCCCTTTGAGTGAATTTGTTCCAGGTGGGAGTTGCGTTGGATTTATGAT 180  
 Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuGlnIleGluGln 80  
 Db 181 TTAATATGGGGTTTATAACTCCCTCTGATTGGAGCTTATTTCTTTACAGATTGAACAA 240  
 Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 Db 1321 TGGAGAGCTCCATGTTTCTTGGAGCGCCAGCTAGTGCACCCCTACAAATCAATGAT 1380

Db 241 TTGATTGAGCAAAAGAAATAGAAACATTTGAAAGGAACCGGGCAATTTACTACATTTACGAGGG 300  
 Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 Db 301 TTAGCAGATAGCTATGAATTTATATTGAAGCACTAAGAGAGTGGGAAGCAATCCCTAAT 360  
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140  
 Db 361 AATGCACAATTAAGGGAAGATGCGTATTGCAATTTGCTAATACAGACAGCGCTTTAATA 420  
 Qy 141 ThrAlaIleAsnAsnProPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 Db 421 ACAGCATATAAATTTTACACTTACAAGTTTGAATCCCTCTTTATCCGCTTATGTT 480  
 Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 Db 481 CAAGCGCGGAATTTACATTTATCACTAATTAAGAGAGCGTATCGTWTGGCAGCGGTTGG 540  
 Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 Db 541 GGACTGGATATAGCTACTGTTAATAATCATTAATAATAGATTAAATAAATCTTTATCATAGA 600  
 Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
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 Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 Db 781 TTAACAAGGGAAATTTATACAAAGTTCAAGTAATTGAGGATTCCTCCAGTTCTGCTAATAATA 840  
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 Db 841 CCTAATGGTTTAAATAGGCGGAATTTGGAGTTAGACCGCCCACTTATGGACATTTATG 900  
 Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
 Db 901 AATTCCTTTGTTAACTGCAGAGACTGTAGAAAGTCAAACTGTGTGGGAGGACACTTA 960  
 Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 Db 961 GTTAGTTCACGAATACGGCTGGTAACCGTATAAAATTTCCCTAGTTACGGGCTCTCAAT 1020  
 Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProCArgProPheTyrArgThrLeuSer 360  
 Db 1021 CCTGGTGGCGCCATTGGATTGCAGATGAGGATCCACGCTCTTTTATCGGACATTAACA 1080  
 Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 Db 1081 GATCCTGTTTGTCCGAGGAGGATTTGGGAATTCCTCATATTATGTACTGGGGCTTAGGGGA 1140  
 Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
 Db 1141 GTAGCATTTCACAAACTGGTAGACACACCCGCAACATTTAGAAAATAGTGGGACCATTA 1200  
 Qy 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
 Db 1201 GATTCCTAGATCAATCCCACTCAGGATAATAGTGGGCACTTGAATGATTATAGT 1260  
 Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
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 Qy 441 TrpArgAlaProMetPheSerThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 Db 1321 TGGAGAGCTCCATGTTTCTTGGAGCGCCAGCTAGTGCACCCCTACAAATCAATGAT 1380

Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
Db 1381 CCGGAGAGGATTACTCAAAATACCAITGGTTAAAGACACATACACTTCAGTCAGTACTACT 1440  
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
Db 1441 GTTGTAAAGAGGCCCGGGTTTACGGAGAGAGATATCTTCGAGCAACAAGTCGAGGAGCA 1500  
Qy 501 PheAlaThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
Db 1501 TTTGCTTATACTATTGTTAATAAATGGCAATTACCCCAAGGTATCGTCAGAATA 1560  
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Db 1561 CGCTATGCTCTACTACAAATCTAAGATTTACGTAAACGGTTGCAGGTGAACGGATTTT 1620  
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
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Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
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Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Db 1741 GCTGATACTTTTAGTTCAGGGAATCAAGTTTATATAGACAGATTTGAATGATCCAGTT 1800  
Qy 601 ThrAlaThrPheGluAlaGlyTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Db 1801 ACTGCCAATTTGAAGCAGATATATGATTAGAAAGACACAAAAGCGGTGAATCGCGTG 1860  
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
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Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Db 1921 GTATCCAATTTAGTGATTTTATACAGATGAATTTTGTCTGATGAAAGCGAATG 1980  
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680  
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Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700  
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Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
Db 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAAATATGTTCACACTACAGGTACCTTTGAT 2160  
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProThrThr 740  
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Db 2281 TATATGCAAAACAGCAACAGTAATGTCTAGTACGGGTTCTTTATGCGCGCTTTCA 2340  
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Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820  
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Db 2701 GTAGATGCTTTATTGTTAAACTCTCAATATGATCAATTACAAGCGGATACGAATATTGCC 2760  
Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
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Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
Db 2821 TCTGTGATTCGGGTGTTAAATGTAGACATTTTCGAAGAATTTAAAGGGCGTATTTCAC 2880  
Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
Db 2881 GCATTCCTTCTATATGATCGGAGAAATGCTATTAACAAACGGTGATTTCATTAATGCTTA 2940  
Qy 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000  
Db 2941 TCATCTGGAAGCTGAAAGGGCATGTAGATGTAGAAGAACAAACACACCGTTCGGTTC 3000  
Qy 1001 LeuValValProGluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
Db 3001 CTTGTGTTCCGGAATGGAGACCAAGTGTCAAGAAGTTCGTGTCGTCCGGGTCTGT 3060  
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGlyGlyCysValThrIle 1040  
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Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
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Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080  
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Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100  
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Qy 1101 AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
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Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
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Db 3421 GAATTAGAGTACTTCCAGAGAAACCGATAGGTATGATGATGATGATGATGATGATGAT 3480  
Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
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RESULT 8

US-09-178-252-5

: Sequence 5, Application US/09178252  
 : Patent No. 6218188  
 : GENERAL INFORMATION:  
 : APPLICANT: Cardineau, Guy A.  
 : APPLICANT: Stelman, Steven J.  
 : APPLICANT: Narva, Kenneth E.  
 : TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
 : FILE REFERENCE: MA-714XC2  
 : CURRENT APPLICATION NUMBER: US/09/178,252  
 : CURRENT FILING DATE: 1998-10-23  
 : EARLIER APPLICATION NUMBER: 60/065,215  
 : EARLIER FILING DATE: 1997-11-12  
 : EARLIER APPLICATION NUMBER: 60/076,445  
 : EARLIER FILING DATE: 1998-03-02  
 : NUMBER OF SEQ ID NOS: 27  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 5  
 : LENGTH: 3522  
 : TYPE: DNA  
 : ORGANISM: Bacillus thuringiensis  
 US-09-178-252-5

## Alignment Scores:

Pred. No.: 0 Length: 3522  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-09-837-961-8 (1-1174) x US-09-178-252-5 (1-3522)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
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 Qy 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
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 Db 121 ACACGTTTCCTTTTGGTGAATTTGTTCCAGGTGTGGAGTTGCGTTTGGATTATTGAT 180  
 Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80  
 Db 181 TTAATATGGGGTTTATTAACCTCTCTGATTGGAGCTTAITTTCTTACAGATTGAACAA 240  
 Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 Db 241 TTGATTGACAAAGATAAGAACATTGGAAGGACCGGGCAATTACTACATTAGAGGG 300  
 Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 Db 301 TTAGCAGATAGCTATGAAATTTATATTGAAGCATTGAAGAGGTGGAAGCAATCCTAAT 360  
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
 Db 361 AATGCACAAATTAAGGAGAGATGTGCGTATTTCGATTGTCTAATACAGACGACCTTAATA 420  
 Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 Db 421 ACAGCAATAAATAATTTTACACTTACAAGTTTGAATCCCTCTTTTATCGGCTATGTT 480  
 Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 Db 481 CAAGCGGCAATTTTACATTTATCACTATTAAAGACGCTGTATCGTTTGGCGAGGGTTGG 540  
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Qy 201 TyrThrIlyHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
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 Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240  
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 Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 Db 721 ATCGTTTCTCTTTTCCGAACCTACGATGTTAGAACATATCCAATTCACAGCTCATCCCA 780  
 Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 Db 781 TTAACAAGGGAATTTATACAGTTCAGTAATTTAGAGATTCTCCAGTTCTGCTGAATATA 840  
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 Db 1141 GTAGCATTTCAACAACCTGTTAGCAACACACCGCAACATTTAGAAATAGTGGGACCATTA 1200  
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 Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 Db 1321 TGGAGAGCTCCAATGTTTCTTGGACGCGCATGTCGCAACCCCTACAAATACAATTGAT 1380  
 Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
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 Db 1501 TTTCGTTTACTATTGTTAATAATGGCAATTTACCCCAAGGTATCGTGCAGGAAGATA 1560  
 Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
 Db 1561 CSCATATGCTCTACTACAAATCTAGAAATTTACGTAAACGGTTGCGAGGTGAACGGATTTT 1620  
 Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
 Db 1621 GCTGGTCAATTTAACAACAATGGATACCGGTGACCCATTAAACATTCATCTTTTAGT 1680  
 Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580

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Db 1681 TACCCAACTATTATACAGCTTTTACATTCACCAATGACCCAGAGTAGTTTCCAGTAGGT 1740
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACTTTTAGTTCAGGGAATGAAGTTATATAGACAGATTGAATTCCAGTT 1800
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAAGCAGAAATGATTTAGAAAGACACAAAAGCGGTGAATGCGCTG 1860
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTACTTTCTATAAACCAAAATAGGGATATAAACACAGATGACGGATTATCATATTGATCAA 1920
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
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QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
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QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
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QY 701 IleGluArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCAAAGAGAGATGACGATTATCAAGAAATATATCATACACTACCAGGTACCTTTGAT 2160
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
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QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
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QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780
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QY 781 ValGlnSerProIleArgLysCysGlyLeuProAsnArgCysAlaProHisLeuGluTrp 800
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Db 2821 TCTGTGATTCGGGTGTAAATGTAGACATTTTCGAAAGAAATTAAGAGCGGTATTTTCACT 2880
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 2881 GCATTCCTCTATATGATCGGAGAAATGTCAATTAACACGGTGATTTCAATTAATGGCTTA 2940
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
Db 2941 TCATGCTGGAAACGTAAGGGCATGTAGATGTAGAAGAACAAAACACCCGTTCCGGTC 3000
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 3001 CTTGTTCTTCGGGAATCGGAAGCAGAGTGTCAAGAAGTTCTGTCTGTCCGGTTCGT 3060
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysIleGlyTyrGlyGluGlyCysValThrIle 1040
Db 3061 GGCTATATCTCTCGTGTACAGCGTCAAGAGGAGATATGGAGAAGGTTCGGTAACCAT 3120
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3121 CATGAGATCGAGAAACAATACAGACGAATGAAGTTTAGCAACTCGTAGAAGAGAAATC 3180
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080
Db 3181 TATCCAAACACACGTAACGTGAATGATTAATATCTCAATCAAGAAATATCGGGGGT 3240
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
Db 3241 GCGTACACTTCCCGTAACTCGTGATATGACGAAACTTATGGAACAATTCCTCTGTACCA 3300
QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
Db 3301 GCTGATTATGCTGCTAGTCTATGAAGAAAAATCGTATACAGATGGACGAAGACAACTCT 3360
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
Db 3361 TGTGAATCTAACAGAGGATATGGGGATTACACACACTTACCAGCTGGCTATGTGACAAA 3420
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
Db 3421 GAATTAGACTATTCACAGAAACCGATAAGGTATGGATGGATCGGAGAAACCGAAGGA 3480
QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCGTGGACAGCGTGAATTAATCTCTTATGGAGGAA 3522
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## RESULT 9

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PCT-US92-11337-9
; Sequence 9, Application PC/TUS9211337
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/11337
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FILED DATE: 19921231  
CLASSIFICATION:  
PRIOR APPLICATION DATA: 97/828,788  
APPLICATION NUMBER: 97/828,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: SALIWANCHIK, DAVID R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MA75  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3522 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: BACILLUS THURINGIENSIS  
STRAIN: AIZAWAI  
INDIVIDUAL ISOLATE: PS811  
IMMEDIATE SOURCE:  
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK  
CLONE: 811A  
PCT-US92-11337-9

Alignment Scores:  
Pred. No.: 0 Length: 3522  
Score: 6244.00 Matches: 1174  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-09-837-961-8 (1-1174) x PCT-US92-11337-9 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
DB 1 ATGAGAGATATATCAAAATCAATGCGTACCTTACAAATGTTTAAATAATCACTGAAGTA 60  
QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
DB 61 GAATATTAATGAGAAAGAGACTGCGAGATACCGTTAGATATATCCTTATCGCTT 120  
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
DB 121 ACACGTTTCCTTTTGGAGTGAATTTGTTCCAGGTGTTGGAGTTTGGATTATTGAT 180  
QY 61 LeuIleArgPheIleThrProSerAspTrpSerLeuPheLeuLeuGlnIleGluGln 80  
DB 181 TTAATATGGGGTTTATAACTCCTTCTGATTGGAGCTATTCTTTACAGATTGAACAA 240  
QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100  
DB 241 TTGATTGAGCAAGATAGAAACATTTGGAAGAACCGGCAATTTACTACATTACGAGGG 300  
QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
DB 301 TTACGATAGCTATGAATTTATATTGAGCACTAAGAGAGTGGAGCAAAATCCCTAAT 360  
QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
DB 361 AATGCACAAATTAAGGAAGATGTCGATTGCTTAAATACAGACGCGCTTTAATA 420  
QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
DB 421 ACAGCAATAATAATTTTACACTTACAAGTTTGAAGTCCCTCTTTATCGGCTCTAGTT 480  
QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180

DB 481 CAACGGCGCAATTTACATTTATCTACTATTAAGACGCTGTATCGTTGGCAGCGTTGG 540  
QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
DB 541 GGACTGGATATAGCTACTGTTTAATAATCATTAATAGATTAAATAAATCTTATTCATAGA 600  
QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
DB 601 TATACGAACCATTTGTTGGACACATACAAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660  
QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
DB 661 ACTGCACATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAACAACCTTACTGTATTAGAT 720  
QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
DB 721 ATCGTTGCTCTTTTCCGAACATGATGTTAGAACATATCAAAATTCAAACGTCATCCCAA 780  
QY 261 LeuThrArgGluIleTyrThrSerValIleGluAspSerProValSerAlaAsnIle 280  
DB 781 TTAACAAGGGAAATTTATACAAGTTCAAGTTCAGTAATTCAGGATTCCTCAGTTTCTGTAATA 840  
QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
DB 841 CCTAATGTTTAAATAGGCGGAAATTTGGAGTTAGACCGCCCATCTTATGGACTTTAAG 900  
QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
DB 901 AATCTTTTGTGTTAACTGCAGAGACTGTTAGAAGTCAAACTGTGGGGAGGACACTTA 960  
QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
DB 961 GTTAGTTACAGAAATACGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGTCTTCAAT 1020  
QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
DB 1021 CCTGSGGGCCATTTGGATTGCAATGAGATCCAGATCCACGCTCTTTTATCGACATTATCA 1080  
QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
DB 1081 GATCCTGTTTGTCCGAGGAGGATTTGGGAATCCTCATTTATGTACTGGGCTTAGGGGA 1140  
QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
DB 1141 GTAGCATTTCAACAACCTGTTACGAACACACACCGACACATTTAGAAAATAGTGGGACCATTA 1200  
QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
DB 1201 GATTCCTAGATGAATCCACCTCAGGATTAATAGTGGGGACCTTGGAAATGATTATAGT 1260  
QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
DB 1261 CATGATTAATCAATCATGTTATCATTTGTACGATGGCCAGGTGAGATTTCAGGAAGTGATTCA 1320  
QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
DB 1321 TGGAGAGCTCCAAATGTTTCTTGGACGACCGTAGTGCACCCCTACAAAATACAAATTGAT 1380  
QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
DB 1381 CCGGAGAGGATTAATCAATACCAATTCGTTAAAGCACATACACTTCAGTACGTTACTACT 1440  
QY 481 ValValArgGlyProGlyPheThrGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
DB 1441 GTTGTAGAGGCGCCGGTTTACGGGAGGAGATATTCTTCGACGACAAAGTGGGAGGACCA 1500  
QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
DB 1501 TTTGCTTATACTATTGTTAATAAATGGGCAATTCACCCCAAGGTATCGTGCAGGAATA 1560  
QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540

Db 1561 CGTATGCCCTCTACTACAAATCTAAGAATTTTACGTAACGGTTGACGGTGAACGGAATTTT 1620  
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
Db 1621 GCTGGTCAATTTTACAAACAATGGATACCGGTGACCCATTAACATTTCCAAATCTTTAGT 1680  
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
Db 1681 TAGCAACTATTATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTCCACAGTAGT 1740  
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Db 1741 GCTGATACTTTTACCTCAGGGAATGAAGTTTATATAGACAGATTGAATTCATCCAGTT 1800  
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Db 1801 ACTGCCAATTTGAAGCAGAAATATGATTTAGAAAGACACAAAAGCGGTGAATCGCGTG 1860  
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
Db 1861 TTTACTTCTATAAACCAAAATAGGATAAAACACAGATGTGCGGATTTATCATATTGATCAA 1920  
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Db 1921 GTATCCAAATTTAGTGGATTGTTTATCAGATGAATTTTGTCTGGATGAAAACCGAGATTG 1980  
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
Db 1981 TCGAGAAATCAACATGCGAAGCACTCAGTGCATGAGCGGAATTTACTTCAAGATCCA 2040  
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIlePhe 700  
Db 2041 AACTTCAAGGCATCATAGCACTAGACCGTGGTGGAGAGAGTACGAGATATTACC 2100  
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
Db 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAAAATTTATGTCACACTACCAAGGTACCTTTGAT 2160  
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
Db 2161 GAGTGCATCCACGATTTTATACAAAATATAGATGATGATCGAATTAACCCCTATACT 2220  
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
Db 2221 CGTTATCAATTAAGAGGTATATCGAGATAGTCAAGACTTAGAAATCTATTGATCCGC 2280  
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780  
Db 2281 TATAATGCAAAACACGAACAGTAAATGTGCTAGTACGGGTTCTTTATGCCCGTTTCA 2340  
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr 800  
Db 2341 GTCCAAAGTCCAAATCAGAAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTCAATGG 2400  
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820  
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Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840  
Db 2461 TTTCTCCTTGGACATGTATGTTGGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG 2520  
Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
Db 2521 ATATTCAAGATTAGACCAAGATGGCCATCAAGACTTAGAAATCTAGAGTTTCTCGAA 2580  
Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrPhe 880  
Db 2581 GAGAAACCATTTAGTCGGGAGCACTAGCTCGTGTGAAAAGAGCAGACAAAAATGGAGA 2640  
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Qy 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920  
Db 2701 GTAGATGCTTTATTGTAAACTCTCAATATGATCAATATACAGCGGATACCAATATTGCC 2760  
Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
Db 2761 ATGATTCATCGGCAGATAAAGGTTCATAGAAATTCGGGAAGCGTATCTTCCAGAGTTA 2820  
Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
Db 2821 TCTGTGATTCGGGTGTAATGTAGACATTTTCGAAGAAATTAAGGCGGTATTTCCTACT 2880  
Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
Db 2881 GCATTCCTCTATATGATGCGAGAAATGTCAATAAACGGTGATTTCAATATATGGCTTA 2940  
Qy 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000  
Db 2941 TCATGCTGGAACTGAAAGGCGCATGTAGATGTAGAAGACAAACACACCGTTCGGTC 3000  
Qy 1001 LeuValValProGluTyrPheGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
Db 3001 CTTGTTGTTCCGGATGGAAGCAGAGTGTCAAGAAGTTCGTGCTGTCCGGGTGCT 3060  
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
Db 3061 GGTATATCTCTGTCACAGCGTACAGGAGGATATGGAGAGGTTGCGTAACCAAT 3120  
Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
Db 3121 CATGAGATCGAACAATACAGACGAACTGAAGTTTAGCACTGCGTAGAAGAGAGTC 3180  
Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyTyrGlyGly 1080  
Db 3181 TATCCAAACAACACGCTAACGTGAATGATTATATCTGCAAAATCAAGAAGAAATACGGGGT 3240  
Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100  
Db 3241 GCGTACACTTCCCGTATPCGTGGATATGACGAAACTTATGGAAGCAATCTCTGTACCA 3300  
Qy 1101 AlaAspTyrAlaSerValTyrGluGlyLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
Db 3301 GCTGATATGCGTCAGTCTATGAGAAAAATCGTATACAGATGGACGAGAGACAATCT 3360  
Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
Db 3361 TGTGAATCTAACAGAGGATATGGGATTTACACCACTACCACTGCGCTATGTGCACAAA 3420  
Qy 1141 GluLeuGluTyrPheProGluThrAspLysValThrIleGluIleGlyGluThrGluGly 1160  
Db 3421 GAATTAGAGTACTTCCCAAGAACCGATGAAGTATGGATTGAGATCGGAGAAACGGAAGA 3480  
Qy 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174  
Db 3481 ACATTCATCGTGGACAGCGTGAATTTACTCTTATGGAGGAA 3522

## RESULT 10

PCT-US95-05431-24

; Sequence 24, Application PC/TUS9505431

; GENERAL INFORMATION:

; APPLICANT: Street address: 5501 Oberlin Drive

; APPLICANT: City: San Diego

; APPLICANT: State/Province: California

; APPLICANT: Country: US

; APPLICANT: Postal code/zip: 92121

; APPLICANT: Phone number: (619) 453-8030

; APPLICANT: Telex number:

; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; Fax number: (619) 453-6991



ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: Florida  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/05431  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: MA83  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (904) 375-8100  
 TELEFAX: (904) 372-5800  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3522 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 PCT-US95-05431-24

Alignment Scores:  
 Pred. No.: 0 Length: 3522  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-09-837-961-8 (1-1174) x PCT-US95-05431-24 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
 DB 1 ATGGAAATAATATCAAAATCAATCGTACCTTACAATTTGTTAAATAATCCTGAAGTA 60  
 QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 DB 61 CAATACTGACGAGAGACGACGACCGCCGCCCTGCGCTGGACATCAGCCTGAGCCTT 120  
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 DB 121 ACAGTTTCCCTTTGAGTGAATTTGTTCCAGGTGTGGAGTTGCGTTGGATTATTGAT 180  
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIleGluGln 80  
 DB 181 TTAATATGGGTTTTATAACTCCCTCTCATTTGGAGCTTATTTCTTTTACAGATTGAACAA 240  
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 DB 241 TTGATTGACCAAGATACAGAACATTTGAAAGGAACCGGGCAATTACTACATTACGAGGG 300  
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 DB 301 TTAGCAGATAGCTATGAATTTATATTGAACACTAAGACAGATGGGAGGACCAATCCCTAAT 360  
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140  
 DB 361 AATCCAAATTAAGGAGAGATGCGTATTCGATTTCGTAATACAGACGACGCTTTAATA 420  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 DB 421 ACAGCAATAATAATTTTACACTTACAAGTTTGAAGTCCCTCTTTATCGTCTATGTT 480

QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 DB 481 CAAGCGCGCAATTTACATTTATCACTATTAAAGAGAGCGCTGATCGTTGGCAGGCTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgIleAsnLeuIleHisArg 200  
 DB 541 GCACGTGATATAGCTACTGTTTAAATATCAATTAATAGATTAAATAATCTTATTCATAGA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 DB 601 TATACCAACATTTGTTGGACACATACAAATCAAGGATTAGAAAACCTTAAGAGTACTAAT 660  
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240  
 DB 661 ACTCCACAATGGCGAAGATTCAATCAGTTTAGAGAGATTAACTTACTTACTATTAGAT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 DB 721 ATCGTTGCTCTTTTCCGAACTACGATGTAGAACATATCCAAATTCAAACGTCATCCCAA 780  
 QY 261 LeuThrArgGluIleTyrThrSerValIleGluAspSerProValSerAlaAsnIle 280  
 DB 781 TTACAAGGGAATTTATACAAGTTTCAGTAATTGAGGATTCCTCAGTTTCTGCTAATAFA 840  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
 DB 841 CCTAATGGTTTTAATAGGCGGAATTTGGAGTTAGACCGCCCTCTTATGGACCTTATG 900  
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
 DB 901 AATCTTTGTTGTAACCTGCAGAGACTGTTAGAATTCAAACTGTGTGGGAGACACITTA 960  
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 DB 961 GTTAGTTTCCAGAAATACGCTGGTAAACCGTATAAATTTCCCTAGTTACGGGCTCTCAAT 1020  
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
 DB 1021 CCTGTGGCGCATTTGGATTGCAGATCAGGATCCACCTCTCTTTTATCGGACATTATCA 1080  
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 DB 1081 GATCCTGTTTTCGCCGAGGAGGATTTGGGAATCTCTATATGTACTGGGGCTTAGGGGA 1140  
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
 DB 1141 GTAGCATTTCAACAACTGGTACGAAACACACCCCAACATTTAGAAATAGTGGGACCATTA 1200  
 QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
 DB 1201 GATTCCTAGATGAATCCACCTCAGGATAATAGTGGGCGCACCTTGGAAATGATTATAGT 1260  
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
 DB 1261 CATGTATTAAATCATGTTTACATTGTACATGGCCAGGTGAGATTTACAGGAGTGATTCA 1320  
 QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 DB 1321 TSGAGCTCCAAATGTTTCTTGGACGCAACCGTAGTGCACCCCTACAAATACAATTGAT 1380  
 QY 461 ProGluArgIleThrGlnIleProLeuValIlyAlaHisThrLeuGlnSerGlyThrThr 480  
 DB 1381 CCGAGAGGATTACTCAAAATACCATTTGGTAAAGACATACACTTCACTAGTACGTTACT 1440  
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
 DB 1441 GTTGTAGAGGCCCGGGTTTACGGGAGGAGATATTCTTCGACCAACAAGTGGGAGGACCA 1500  
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
 DB 1501 TTTGCTTATACTATTGTTAATAATAATGGGCAATTTACCCCAAGATTCGTGCAAGATA 1560  
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540



1561 CGCTATGCGCTCTACTACAAATCTAAGAATTTACGTACGCTTCAGGTGAACGATTTT 1620  
541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
1621 GCTGGTCAATTTAACAAACAATGGATACCGGTGACCCATTAAACATTCCTTAGT 1680  
561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
1681 TAGGCAACTATTATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTTCACAGTAGG 1740  
581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
1741 GCTGATACCTTTAGTTCAGGGAATGAAGTTTATATAGACAGATTGAATTCATCCAGTT 1800  
601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
1801 ACHGCAACATTTCAAGCAGAAATGATTTTGAAGAGACACAAAAGCGGTGAATCGCGTG 1860  
621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
1861 TTTACTTCTATAAACCAATPAGGATAAACAAGATGTCGACGATTTATCATATGATCAA 1920  
641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspCysLeuArgGluLeu 660  
1921 GTATCCAAATTTAGTGAATGTTTATCATCAGATGAATTTTGTCTGCATGAAAAGCAGAAATG 1980  
661 SerGluLysValLysHisAlaLysArgLeuSerAspCysLeuArgAsnLeuGlnAspPro 680  
1981 TCCGAGAAGTCAAAATGCGAAGCAGCTCAGTGTAGCGGAATTTACTTCAAGATCCA 2040  
681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrPheGlySerThrAspIleThr 700  
2041 AACTTCAAGGCATCAATAGGCAACTAGACCGTGGTTGGAGAGAGACTACGGATATACC 2100  
701 IleGluArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
2101 ATCCAAAGAGAGATGACGTATTCAAAGAAATATTGTCTCACATACACAGTACTTTGAT 2160  
721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
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741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
2221 CGTTATCAATTAGAGGTATATCGAGGATAGTCAGACTTAGAATTCATATTTGATCCGC 2280  
761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780  
2281 TATAATGCAAAACACAGAAACAGTAAATGTCTAGGTACGGGTCTTTATGGCGCTTCA 2340  
781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr 800  
2341 GTCCAAAGTCCATCAATCAAGAAGTGTGAGAACCAATCGATGCGCGCACACCTTGAATGG 2400  
801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820  
2401 AATCCTGATCTAGATTGTTCTCTCAGAGAGGGGAAAAATGTCACATCATTTCCATCAT 2460  
821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValIlePhe 840  
2461 TTTCTCTTGGACATTTGATGTTGATGATACAGACTTAATGAGGACTTAGATGGGTG 2520  
841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
2521 ATATTCAGATTTAGACGCAAGATGCGCATGCAAGACTAGGAAATCTAGAGTTTTCGAA 2580  
861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880  
2581 GAGAAACCATTTACTCGGGAGCAGCTAGCTGCTGTGTAAGAGACGACAGAAAAATGGAGA 2640  
881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900

2641 GATAAAGCTGAAAAATTTGGAATTTGGAACAAATATTTTATTAAAGAGCAAAAGATCT 2700  
901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920  
2701 GTAGATGCTTTATTGTAAACTCTCAATATGATCAATTAACAGCGGATACGAATATTGCC 2760  
921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
2761 ATGATTCATCGGCAAGATAAACCGTTTCATAGAAATTCGGGAAGCGTATCTTCAGAGTTA 2820  
941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
2821 TCTGTGATTCGCGGTGTAAATGTAGACATTTTCGAAGAATTAAGAGCGCTATTTCCTACT 2880  
961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
2881 GCATTCCTCTATATGATCGAGAAATGTCATTAATAACGGTGAATTCATAATATGGCTTA 2940  
981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000  
2941 TCATGCTGGAACTGAAAGGCGATGTAGATGTAGAGAACAAACACACCGTTCGGTC 3000  
1001 LeuValValProGluTyrPheGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
3001 CTGTGTTGTTCCGGAATGGGAAGCAGAAAGTGTCAAGAAGTTCTGTGTCCTCCGGTCTG 3060  
1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
3061 GGTATATCTCTGTCACAGCTACAGAGGGATATGGAGAAGGTTTCGCTAAACCAT 3120  
1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
3121 CATGAGATCGAGAACAAATACAGACGAACTGAAGTTTAGCAACTCGGTAGAGAGGAGTC 3180  
1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080  
3181 TATCCAAACAACACGTTAAGTGTATGATTATCTGCAATCAAGAAGAATACGGSGGT 3240  
1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100  
3241 GCGTACACTTCCGTTATCTGTGATATGACGAACCTATGGAAGCAATCTTCTGTACCA 3300  
1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
3301 GCTGATTTGCGTCGCTCTATGAGAAATAATCGTATACAGATGACGAGAGACAACTCT 3360  
1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
3361 TGTGAATCTAACAGAGGATATGGGATTAACACACCACTACCACTGCTGCTATGTGACAAA 3420  
1141 GluLeuGluTyrPheProGluThrAspLysValThrIleGluIleGlyGluThrGluGly 1160  
3421 GAATTAGATGACTTCCAGAAACCGATTAAGGTATGATGATGATGATGATGATGATGATG 3480  
1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
3481 ACATTCATCGTGACAGCGGTGAATTAATCTCTTATGGAGGAA 3522

RESULT 11  
5188960-7  
; Patent No. 5188960  
; APPLICANT: PAYNE, JEWEL-SICK, AUGUST J.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE  
; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL  
; LEPIDOPTERAN-ACTIVE TOXINS  
; NUMBER OF SEQUENCES: 8  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/451,261  
; FILING DATE: 14-DEC-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 371,955  
; FILING DATE: 27-JUN-1989  
; SEQ ID NO:7;

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; LENGTH: 3522
5189960-7

Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-837-961-8 (1-1174) x 5189960-7 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
Db 1 ATGCAGAAATAATATCAAAATCAATGGTACCTTACAAATGCTTTAAATAATCCCTGAGTA 60

QY 21 GlulleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
Db 61 GAAATATTAATGAAGAAGAAGTACTGGCAGATTACCGTTAGATATATCCTTATCGCTT 120

QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
Db 121 ACACGTTTCCTTTTACGTGAATTTGTTCCAGGTGTGGAGTTGCGTTTGGATTATTTGAT 180

QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuGlnIleGluGln 80
Db 181 TTAATATGGSGTTTATAACTCCTCTGATTGGAGCTTATTTCTTTTACAGATTGACAA 240

QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
Db 241 TTGATTGAGCAAAAGAAAGAACATTGGAAGAACCGGCAATTTACTATACGAGG 300

QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
Db 301 TTACAGATAGCTATGAATTTATTTAGACACTAGAGAGTGGGAGCAAAATCCCTAAT 360

QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
Db 361 AATGCACAATTAAGGAAGATGTCGGTATTCGATTGCTTAATACAGACGCGCTTTAATA 420

QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
Db 421 ACAGCAATAATAATTTTACACTTACAAATTTTGAATCCCTCTTTTATCGGCTATGTT 480

QY 161 GlbAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnClyTrp 180
Db 481 CAGCGCGGATTTACATTTATCTATTTAGAGACGCTGTATCGTTTGGCAGGGTTGG 540

QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
Db 541 GGACTGGATATAGTACTGTTAATAATCAATTAATAGATTAATAATCAATTTATTCATAGA 600

QY 201 TyrThrIlyHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
Db 601 TATACGAAACATGTTTGGACATACAATCAAGGATTAGAAGATTAAGAGGTACTAAT 660

QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
Db 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGAGAGATTAAACACTTACTGTATTAGAT 720

QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
Db 721 ATCGTTGCTCTTTTCCGAATACGAGTTTAGAACAATCCAAATTCAAAGCTATCCCAA 780

QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
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QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProHisLeuMetAspPheMet 300
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QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyClyHisLeu 320
Db 901 AATTCCTTTGTTTGAACGAGACTGTTAGAGTCAAACTGTTGGGGAGGACACTTA 960

QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
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QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
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QY 361 AspProValPheValArgGlyGlyPheClyAsnProHisTyrValLeuGlyLeuArgGly 380
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QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
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QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
Db 1201 GATTCTCTAGATGAATCCCACTCAGSATAATAGTGGGCACTTGGCAATCATTAAGT 1260

QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
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QY 461 ProGluArgIleThrGlnIleProLeuValIlyAlaHisThrLeuGlnSerGlyThrThr 480
Db 1381 CCGGAGAGGATTACTAAATACCAATTCGTAAGACACATACACTTCAGTACAGTACTACT 1440

QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
Db 1441 GTGTAGAGGGCCCGGTTTACGGGAGGAGATATTCTTCACCAACAAGTGGAGGACCA 1500

QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
Db 1501 TTTGCTTATACTAATTTAATAAATGGCAATTCGCCAAGATATCGTGCAGAAATA 1560

QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
Db 1561 CGCTATCCCTCTACTACAAATCTAAGAAATTTACGTAAACGTTTGCAGGTGAACGGATTTT 1620

QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGGTCAATTTAACAACAATAGGATACCGGTGACCCATTAACATTCCAATCTTTAGT 1680

QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TAGCCAACTAATAACAGCTTTTACATTCCTCAATGACGAGTACTTTTACAGTAGGT 1740

QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
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QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGACGAGAAATGATTTAGAAAGACACAAAGCGGGAATGGCGTG 1860

QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTACTTCTATAACCAAAATAGGATAAACAAGATGTGACGAGTATCATATTGATCAA 1920

QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAATTTAGTGGATTGTTTATCAGATGAATTTTGTCTGATGAAAGCGAGAATTG 1980

QY 661 SerGluLysValIlyHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
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Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040

Db 3061 GGCTATATCCCTTCGTGTACACCGTACAGAGGAGGATATGGAGAAAGTTGCGTAACCAT 3120  
Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
Db 3121 CATGAGATCGAGAACAAATACAGACGAACCTGAAGTTTAGCAACTGCGTAGAAGAGAGTC 3180  
Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080  
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Db 3421 GAATTAGAGTACTTCCAGAAACCGATAGGTATGATGATGATGATGATGATGATGATG 3480  
Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
Db 3481 ACATTCTATCGTGGACGCGTGAATTACTCTTATGAGGAA 3522

## RESULT 12

PCT-US91-02560-1  
; Sequence 1, Application PC/TUS9102560  
; GENERAL INFORMATION:  
; APPLICANT: Gawron-Burke, Cynthia  
; APPLICANT: Chambers, Judith A.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryIF and cryIX  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze et al, c/o A.S. Nadel  
; STREET: 1601 Market Street, 38th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/02560  
; FILING DATE: 19910415  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/510327  
; FILING DATE: 16-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-27 U1  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4020 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: Gouble  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 478..4002

PCT-US91-02560-1

## Alignment Scores:

Pred. No.: 0 Length: 4020  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-09-837-961-8 (1-1174) x PCT-US91-02560-1 (1-4020)

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 QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 DB 538 GAAATATTAAATGAAGAAGAGTACTGCGCAGATTACCGTTAGATATATCCTTATCGGTT 597  
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
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 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80  
 DB 658 TTAATATGGGTTTATAACTCTCTGATTGAGCTTATTTCTTTTACAGATTGACAA 717  
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 DB 718 TTGATGTAGCAAAAGAAATAGAAACATTGGAAGGAAACCGGGCAATTTACTACATTACGAGGG 777  
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
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 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
 DB 838 AATGCACAAATTAAGGGAAGATGCGCTATTCGATTGTCTAATACAGACGACGCTTTAATA 897  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 DB 898 ACAGCAATTAATAATTTTACACTTACAAGTTTGAAGTTCCTCTTTTATCGGTCATGTT 957  
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyCloglyTrp 180  
 DB 958 CAAGCGGCAATTTACATTTATCACTATTAGAGACGCTGTATCGTTGGCAGGSGTTGG 1017  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 DB 1018 GGACTGGATATAGCTACTGTTAATAATCATTTATATAGATTAAATAATCTTATTCATAGA 1077  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
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 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
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 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 DB 1198 ATCGTGTCTCTTTTCCGAATACGATGTTAGAACATATCCAAATTCAAACGTCATCCAA 1257  
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 DB 1258 TTACAGAGGAAATTTATACAAAGTTCAGTAATTGAGGATTCTCCAGTTTCTGCTAATATA 1317  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
 DB 1318 CCTAATGTTTATAGCGCGGAATTTGGAGTTAGACCGCCCAATCTTATGGACTTTATG 1377  
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu 320

DB 1378 AATCTTTGTTGTTAACTCCAGAGACTGTAGAAGTCAAACTGTGTGGGAGACACTTA 1437  
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 DB 1438 GTTAGTTCACGAATAACGCTGTAAACCGTATAAATTTCCCTAGTTACGGGCTCTCAAT 1497  
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
 DB 1498 CCGTGTGGCGCATTTGGATTGCAGATGAGATCCACGCTCTTTTATCGCAGATTATCA 1557  
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 DB 1558 GATCTGTTTGTCCGAGGAGATTGGGAATCCTCATTTATGTACTGGGGCTTAGGGGA 1617  
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
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 QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
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 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
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 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
 DB 1858 CCGGAGAGGATTAACAAATACCAATGTTGTAAGAACACATACACTTCAGTCAGGTACTACT 1917  
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
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 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
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 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
 DB 2038 CGCATGCGCTCTACTACAAATCTAAGAAATTTACGTAACGGTGCAGGTGAACGGATTTT 2097  
 QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
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 DB 2278 ACTCAACATTTGAAGCAGATATGATTTAGAAAGACACAAAGCGGTGAATGCCGCTG 2337  
 QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
 DB 2338 TTTACTTCTATAAACCAAAATAGGGATAAAAACAGATGTGACGGATTATCATATTGATCAA 2397  
 QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
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 Db 2518 AACPTCAAGGCGATCAATAGCAACTAGACCGTGGTGGAGAGAAATACGGATATTACC 2577  
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 QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080  
 Db 3658 TATCCAAACACACGCGTAACGCTGAATGATATATCTGCAAAATCAAGAAGAAATACGGGGT 3717  
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 RESULT 13  
 US-08-349-867-28  
 ; Sequence 28, Application US/08349867  
 ; Patent No. 5508264  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bradfisch, Gregory A.  
 ; APPLICANT: Thompson, Mark  
 ; APPLICANT: Schwab, George E.  
 ; TITLE OF INVENTION: No. 5508264el Pesticidal Compositions  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: FL  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/349,867  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 31,794  
 ; REFERENCE/DOCKET NUMBER: MA86  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 904-375-8100  
 ; TELEFAX: 904-372-5800  
 ; INFORMATION FOR SEQ ID NO: 28:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3522 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-349-867-28  
 Alignment Scores:  
 Pred. No.: 0 Length: 3522

Score: 6049.00 Matches: 1143  
 Percent Similarity: 97.79% Conservative: 5  
 Best Local Similarity: 97.36% Mismatches: 26  
 Query Match: 96.88% Indels: 0  
 DB: 1 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-349-867-28 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGluCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
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QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 DB 61 GAATACTGAACGAGAACGAGACCGCGCGCTGCGCTGGACATCAGCTTGAGCCCT 120

QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 DB 121 ACACGTTTCCTTTAGAGTGAATTTGTTCCAGTGTGGAGTTGCGTTGGATTATTTCAT 180

QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuGluIleGluIn 80  
 DB 181 TTAATATGGGGTTTATAACCTCTCTGATTGGAGCTTATTCTTTTACAGATTGAACAA 240

QY 81 LeuIleGluInArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
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QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
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QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAsnAlaLeuIle 140  
 DB 361 AATCGCAATTAAGGAGAGATGCGGATTCGATTTCGTAATACAGACGCGCTTTAATA 420

QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 DB 421 ACAGCAATAAATAATTTACACTTACAAGTTTGAAGTTTCCCTCTTTATCGTCTATGTT 480

QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 DB 481 CAAGCGGCGAATTTACATTTATCACTAATAAGACGCGTGTATCGTTTGGCAGGGTTGG 540

QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgIleLeuAsnLeuIleHisArg 200  
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QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
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QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 DB 661 ACTCGCAATGGGCAAGATTCAATCAGTTTATAGGAGAGATTAAACACTTACTGTATTAGAT 720

QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 DB 721 ATCGTGTCTCTTTCCGAACTACGATGTTAGAACATATCCAAATTCAAACGTCATCCAA 780

QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
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QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
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QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu 320  
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DB 1021 CCTGGTGGCGCAATTTGGATTTCAGATGAGGATCCACGCTCTTTTATCGGACATTATCA 1080

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DB 1081 GATCCTGTTTGTTCGAGAGAGATTTCGGGAATCTCTATTTACTGGGCTTAAAGGGA 1140

QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400

DB 1141 GTAGCATTTCAACAACTGGTACGAACCAACCCGAAACATTTAGAAATAGTGGGACCATA 1200

QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420

DB 1201 GATTCCTAGATGAATCCCACTCAGGATAATAGTGGGCACTTGGAAATGATTATAGT 1260

QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440

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DB 1381 CCGGAGAGGATTACTCAAAATACCATTGGTAAAGCACATACACTTCAGTCAGGTACTACT 1440

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QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540

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QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620

DB 1801 ACTCCAACATTTGAAGCAGAAATATGATTAGAAAAGACACAAAAGGGGTGAATGCGCTG 1860

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DB 1861 TTTACTTCTATAAACCAATAGGGATAAACACATGTGACGGATTATCATATCGATCGA 1920

QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660

DB 1921 GTGTCCAATTTAGTTACGTATTTCGGATCAATTTGTTCTGGATGAAGCGGAGATTG 1980

QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680

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Db 2101 ATCCAGGAGGGGATGACGCTATTAAAGAAATACGTCACACTATCAGGTACCTTTGAT 2160  
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Db 3181 TATCCAAACACACCGTACGTGTATGATTAATACGCCACTCAAGAAATATGAGGCT 3240  
Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100  
Db 3241 ACGTACACTCTCGTAATCGAGGATATGACGGAGCCTATGAAAGCAATTTCTTCTGTACCA 3300  
Qy 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgAspAsnPro 1120  
Db 3301 GGTGATTATGTCATCGCCTATGAAGAAAAGCATATACAGATCGGACGAGACAAATCCT 3360  
Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
Db 3361 TGTGATCTAAACAGAGATATGGGATTTACACACACTACCAGCTGGCTATGTGACAAA 3420  
Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160  
Db 3421 GAATTAGACTACTTCCAGAAACCGATAAGGTATGATGATGAGATCGGAGAAACCGAAGA 3480  
Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
Db 3481 ACATTATCTGTGACACGCTGGAATTTACTTCTTATGGAGAA 3522

## RESULT 14

US-08-239-476-28  
; Sequence 28, Application US/08239476  
; Patent No. 5527883

## GENERAL INFORMATION:

; APPLICANT: Thompson, Mark  
; APPLICANT: Schwab, George E.  
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in  
; TITLE OF INVENTION: Pseudomonas fluorescens  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/239,476  
; FILING DATE:

## CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: MA83

## TELECOMMUNICATION INFORMATION:

; TELEPHONE: (904) 375-8100

; TELEFAX: (904) 372-5800

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3522 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-239-476-28

## Alignment Scores:

Pred. No.: 0 Length: 3522  
Score: 6049.00 Matches: 1143  
Percent Similarity: 97.79% Conservative: 5  
Best Local Similarity: 97.36% Mismatches: 26  
Query Match: 96.88% Indels: 0



DB: 1 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-239-476-28 (1-3522)

QY 1 MetClnAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
 DDb 1 ATCGAAATTAATATCAAAATCAATCGGTACCTTACAATTTTAAATAATCCTGAAGTA 60  
 QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 DDb 61 GAATACTGAACAGAACACACCGCGCGCTGCGCTGGACATCAGCCTGAGCCT 120  
 QY 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 DDb 121 ACAGCTTCCCTTTGAGTGAATTTGTCAGGTGTCAGGTGTCGCTTGGATTATTTGAT 180  
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80  
 DDb 181 TTAATATGGGGTTTATAACTCCTCTGATTGGAGCTTATTTCTTTACAGATTGAACA 240  
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 DDb 241 TTGATTGACCAAGATAGAAATTTGGAAGAACCGGCAATTTACTATTACGAGG 300  
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 DDb 301 TTACGAGATAGCTATGAATTTATATTGAAGCACTAAGAGAGTGGGAAGCAATCCTAAT 360  
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
 DDb 361 AATGCAACATTAAGGAAGATGCGTATTCGATTTGCTAATACAGACGCGCTTTAATA 420  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 DDb 421 ACAGCAATAAATAATTTTACACTTACAGTTTGAATCCCTCTTTATCGGCTATGTT 480  
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 DDb 481 CAAGCGCGCAATTTACATTTATCACTATTACATTTAAGAGAGCGCTGATCGTTTGGCGAGGTTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 DDb 541 GGACTGGATATAGCTACTGTATATAATCATATTATTAATAGATTATAAATCTTATTCATAGA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuAsnLeuArgGlyThrAsn 220  
 DDb 601 TATACGAACAATGTTTGGACACATACATCAAGGATTAGAANAATTAAGAGTACTAAT 660  
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240  
 DDb 661 ACTCGACAATGGGCAAGATTCAATCASITTTAGGAGAGATTTACACTTACTGTATTAGAT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 DDb 721 ATCGTTGCTCTTTCCGAACTACGATGTTAGAACATATCCAAATCAACGCTCATCCCA 780  
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 DDb 781 TTAACAAGGGAATTTATACAAGTTCAGTAATTTAGGATTTCCAGATTTCTGCTATATA 840  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
 DDb 841 CCTAATGGTTTAAATAGGCGGAATTTGGAGTTAGACCGCCCATCTTATGGACTTATG 900  
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGluThrValTrpGlyGlyHisLeu 320  
 DDb 901 AATCTTTTGTGTAACGAGACTGTTAGAAGTCAAACTGTGTGGGAGGACACTTA 960  
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 DDb 961 GTTAGTTACGAAATACGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGTCTTCAAT 1020  
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360

Db 1021 CCTGGTGGCCCATTTGGATTGCAGATGCAGATCCACGCTCTTTTATCGGACATTAACA 1080  
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 DDb 1081 GATCCTGTTTTCGCGAGGAGGATTGGGAATCCTCATTATGATGCTACCTGGGCTTAGGGGA 1140  
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
 DDb 1141 GTAGCATTTCAACAACTGGTACGAACACACCCGAACATTTAGAAATAGTGGACCATTA 1200  
 QY 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
 DDb 1201 GATCTCTAGATGAATCCACCTCAGGATATAGTGGGCACCTTGGGAATGATTATAGT 1260  
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
 DDb 1261 CATGTATTAATCATGTTACATTTGTACGATGCCAGGTGAGATTTTCAGGAAGTGATTCA 1320  
 QY 441 TrpArgAlaProMetPheSerTyrThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 DDb 1321 TGGAGAGCTCCAATGTTTCTTGGACGCCAGCTAGTGCACCCCTACAAATACAAATTGAT 1380  
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
 DDb 1381 CCGAGAGGATTTACTCAATACCATTTGGTAAAGACATACACTTCAGTCAGGTACTACT 1440  
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
 DDb 1441 GTTGTAAAGGGCCCGGTTTACGGGAGGAGATATTCTTCGACGAAACAAGTGAGGACCA 1500  
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
 DDb 1501 TTTGCTTATACTATTGTTAATAATAGGCAATTAACCCAAAGGATCGTGCAGAATA 1560  
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
 DDb 1561 CGCTATGCTCTACTACAAATCTAAGAATTTAGTAAAGTTCAGGTTCAGGTGACGATTTT 1620  
 QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
 DDb 1621 GCTGTCAATTTAAACAAACAATGGATACCGGTGACCCATTAACATTTCAATCTTTAGT 1680  
 QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
 DDb 1681 TAGCAACATTAATAACAGCTTTTACATTTCCCAATGAGCCAGAGTAGTTCACAGTAGT 1740  
 QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
 DDb 1741 GCTGATACCTTTTAGTTCAGGAATGAAGTTTATATAGACAGATTTTGAATTTGATCCAGTT 1800  
 QY 601 ThrAlaThrPheGluAlaGluIleThrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
 DDb 1801 ACTGCAACATTTGAAGCAGATATGATTTAGAAAGAGCACAAAAGCGGTGAATGGCTG 1860  
 QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
 DDb 1861 TTTACTTCTATAACCAATAGGATAAAACAGATGTGACGATTTATCATATCGATCGA 1920  
 QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
 DDb 1921 GTGTCCAATTTAGTTACGTATTTATCGGATGAATTTGTCTGGATGAAGAGGAGGATTTG 1980  
 QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
 DDb 1981 TCCGAGAAAGTCAACATCGGAAGCACTACTGATGAACGCAATTTACTTCCAAGATTCA 2040  
 QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700  
 DDb 2041 AATTTCAAGACATTAATAGGCAACGACAGCTGGGTGGGCGGAGGTACAGGGATTACC 2100  
 QY 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720



Db 2101 ATCCAAGAGGGATGACGTATTTAAAGAAAATACGTCACATCATCAGGTACCTTTTCAT 2160  
QY 721 GluCysTyrPrThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
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Db 2161 GAGTCTATCCACATATTGTATCAAAAATCGATGAATCAAAATATAAGCCCTTTACC 2220  
QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
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Db 2221 CGTTATCAATTAAGAGGGATATACGAAGATAGTCAAGACTTAGAAATCTATTATTCGC 2280  
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780  
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Db 2281 TACAATCAAAAACATGAACAGTAAATGTGCCAGTAGGGTTCCTTTATGGCCGCTTCA 2340  
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyrP 800  
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Db 2341 GCCCAAGTCCAAATCGGAAAGTGTGGAGAGCCGAATCGATCGCGCCACACCTTGAATGG 2400  
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820  
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Db 2401 AATCCTGACITAGATTGTTCGTGTAGGATGGAGAAAAGTGTGCCCATCATTCGCATCAT 2460  
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrPVal 840  
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Db 2461 TTCCTCTAGACATGTAGGTAGGATGTACAGACTTAATAGGACCTAGGTGTATGGGGT 2520  
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
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Db 2521 ATCTTTAAGATTAAAGCAAGATGGCCACCAAGACTAGGATCTAGAGTTCTCGAA 2580  
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880  
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Db 2581 GAGAAACCATTAGTAGGAGAGCGCTAGCTGCTGTAAGAGCGGAGAAAAATGGAGA 2640  
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900  
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Db 2641 GACAAAGCTGAAAATTTGGAATGGGAACAAATATCGTTTATAAGAGCGCAAAAGATCT 2700  
QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920  
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Db 2701 GTAGATGCTTTATTGTAACTCTCAATATGATCAATACAGCGGATACGAATATTGCC 2760  
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
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Db 2761 ATGATTTCATCGCGCAGATAAAGCGTTCATAGCATTCGAGAAGCTTATCTCCCTGAGCTG 2820  
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
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Db 2821 TCTGTGATTCGGGTGTCAATCGCGCTATTTTTGAAGAATTAGAAAGCGGTATTTTCACT 2880  
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
|||||  
Db 2881 GCATTCCTCCCTATATGATCGCAGAAATGCTAATTAATGTTGATTTAATAATGGCTTA 2940  
QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000  
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Db 2941 TCCGCTGGAACGTGAAGGCGCATGTAGATGTAGAAGAACAAAACACACCGTTCGGTC 3000  
QY 1001 LeuValValProGluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
|||||  
Db 3001 CTTGTGTTCGGGAATGGGAAGCAGAGTGTCAAGAAGTTCGTGCTGTCCGGGTCTGT 3060  
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
|||||  
Db 3061 GGCTATATCCTTCGTGCACAGCTACAGGAGGATATGGAGAGGTTCGTACCACTT 3120  
QY 1041 HisGluIleGluAsnAsnThrAspLeuLysPheSerAsnCysValGluGluGluVal 1060  
|||||  
Db 3121 CATGAGATCGAAGCAATACAGACGAATCTGAAGTTAGCACTGTGTAGAAGAGAGATA 3180  
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080  
|||||  
Db 3181 TATCCAAACACACCGTAACGTGAATGATTATATCTCGACTCAAGAAGAAATATGAGGGT 3240

QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100  
|||||  
Db 3241 ACGTACACTTCTCGTATPCGAGGATATGCGGAGCTATGAAGCAATCTTCTGTACCA 3300  
QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
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Db 3301 GCTGATTATGCTATGAGCTATGAAGAAAAAGCATATACAGATGGAGCAAGACAATCCT 3360  
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
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Db 3361 TGTGAATCTAACAGAGGATATGGGATATACACCACTACCACTGGCTATGTGACAAA 3420  
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160  
|||||  
Db 3421 GAATGAGTACTTCCCAAGAACCGATAGGATGAGATTCGGAGAACGGAAGGA 3480  
QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174  
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Db 3481 ACATTCATCGTGACAGCGTGAATTAATCTTATGGAGAA 3522

## RESULT 15

US-08-598-305A-28  
; Sequence 28, Application US/08598305A  
; Patent No. 5827514  
; GENERAL INFORMATION:  
; APPLICANT: BRADFISCH, Gregory A.  
; APPLICANT: THOMPSON, Mark  
; APPLICANT: SCHWAB, George E.  
; TITLE OF INVENTION: No. 5827514el Pesticidal Compositions  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/598,305A  
; FILING DATE: 08-FEB-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/349,867  
; FILING DATE: 06-DEC-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA86.D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 352-375-8100  
; TELEFAX: 352-372-5800  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3522 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-598-305A-28  
Alignment Scores:  
Pred. No.: 0 Length: 3522  
Score: 6049.00 Matches: 1143  
Percent Similarity: 97.79% Conservativity: 5  
Best Local Similarity: 97.36% Mismatches: 26  
Query Match: 96.68% Indels: 0

DB: 1 1 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-598-305A-28 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20

Db 1 ATGGAATAAATATTCATCAATCAATCGGTACCTTCAATGTTTAAATCAATCCTGAAGTA 60

QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40

Db 61 GAAATACAGCAAGCAAGCAGCAGCCGCGCTCGACATCAGCCCTGAGCCTT 120

QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheClyLeuPheAsp 60

Db 121 ACACGTTTCTTGGAGTGAATTTGTTCAGGTTGGAGTTGCCGTTGGATTATTGAT 180

QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuIleGlnGln 80

Db 181 TTANTAAGGGTTTATACCTCTCTGATTGGAGCTTATTTCTTTACAGATTGAACA 240

QY 81 LeuIleGluArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100

Db 241 TTGATTGACCAAGATAAAGATGGAAGCAACCGGGCAATTTACTACATTACAGGG 300

QY 101 LeuAlaAspSerThrGluIleTrpIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120

Db 301 TTAGCAGATAGCTATGAAATTTATATTGAGCAGCTAAGAGGTGGGAACCAATCCTAAT 360

QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140

Db 361 AATGCCAATTAAGGAGAGATGCGCTATTTCGATTTCGTAATACAGACGACGCTTAATA 420

QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTrpVal 160

Db 421 ACAGCAATAAATATTTACACTTACAGTTTGAATCCCTCTTTTATCGGTCATGTT 480

QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180

Db 481 CAAGCGGGAATTTACATTTATCACTATTAAAGACGCTGTATCGTTTGGCAGGGTTGG 540

QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200

Db 541 GGACTGGATATAGCTACTGTAAATATCATATTAATAGATTAATAATCTTATTCATAGA 600

QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnClyLeuGluAsnLeuArgGlyThrAsn 220

Db 601 TATACGAACATTTTGGACACATACATCAAGATTAAGAACTTAAGAGGTACTAAT 660

QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240

Db 661 ACTCGAATGGCAAGATTCATCAGTTTGGAGAGATTTAACTTACTTATTAGAT 720

QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260

Db 721 ATCGTTGCTCTTTCCGAACACTAGTGTAGAACATATCCCAATTCACAGCTATCCCAA 780

QY 261 LeuThrArgGluIleTyrThrSerValIleGluAspSerProValSerAlaAsnIle 280

Db 781 TTAACAGGGAAATTTATACAGTTCAAGTCAAGTAAATGAGGATTCCTCAGTTTCTGCTAATA 840

QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300

Db 841 CCATAGGTTTAAATAGGGCGGAATTTGGAGTTAGACCGCCCATCTTATGGACTTTATG 900

QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320

Db 901 AATCTTTGTTGTAAGTGCAGAGACTGTTAGAGTCAAACTGTGTTGGGAGGACACTTA 960

QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340

Db 961 GTTAGTTTCAAGAAATACGGCTGTAAACCGTATAAATTTCCCTAGTTACGGGGTCTCAAT 1020

QY 341 ProGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360

Db 1021 CCTGTGGCCCAATTTGGATTGGAGATGAGATCCAGTCTCTTTTATCGGACATATCA 1080

QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380

Db 1081 GATCCTGTTTGTCCGAGGAGATTTGGAAATCCTCATTTATGTACTGGGSCITAGGGGA 1140

QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400

Db 1141 GTAGCATTTCAACAACCTGGTACCAACACACCCGAAATTTAGAAATAGTGGGACCAT 1200

QY 401 AspSerLeuAspGluIleProGlnAsnAsnSerGlyAlaProTrpAsnAspTyrSer 420

Db 1201 GATTCTCTAGATGAATCCCACTCAGAGTAATAGTGGGACCTTGGCAATGATATAGT 1260

QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440

Db 1261 CATGTATTAATCATGTTTACATTTGTACGATGGCAGGTGAGATTTTCAGGAAGTGATTC 1320

QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460

Db 1321 TGGAGAGCTCAATGTTTCTTGGACGACCGTAGTGCACCCCTACAAATACAAATGAT 1380

QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480

Db 1381 CCGGAGAGGATTCTCAATACCATTTGTTAAAGCAGCATACACTTCAGTCAGGTACTACT 1440

QY 481 ValValArgGlyProGlyPheThrGlyAspIleLeuArgArgThrSerGlyGlyPro 500

Db 1441 GTTGTAAAGAGCGCGGGTTTACGGGAGGATATTCTCGACGAAACAAAGTGGAGGACCA 1500

QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520

Db 1501 TTGCTTATACATTTGTTAATAATAAATGGGCAATACCCCAAGGTATCTGTCGAAGATA 1560

QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540

Db 1561 CGCTATGCTCTACTACAAATCTAAGAAATTTACGTAAAGGTTGCGAGGTGAACGAGTTT 1620

QY 541 AlaGlyGlnPheAsnLysThrMetAspThrClyAspProLeuThrPheGlnSerPheSer 560

Db 1621 GCTGTCAATTTACAAACCAATGGATACCGGTGACCCATTAACTTCCCAATCTTTAGT 1680

QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580

Db 1681 TAGSCAATTTAATACAGCTTTTACATTTCCCAATGAGCCAGCTAGTTTTCACAGTAGT 1740

QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600

Db 1741 GCTGATCTTTTAGTTTTCAGGAATGAAGTTTATATGACAGATTTGAATTTGATTTCCAGTT 1800

QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620

Db 1801 ACTGCAACATTTGAAGCAGATATGATTTGAAAGAGCACAAGGCGGTGAATGCGCTG 1860

QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640

Db 1861 TTTACTTCTATAAACCAATAGGATGAACAGATGTGACGGATTTATCATATCGATCGA 1920

QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660

Db 1921 GTGTCCCAATTTAGTTTACGTATTTTTCGGATGAATTTTGTCTGGATGAAGGAGCAATTG 1980

QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680

Db 1981 TCCGAGAAAGTCAACATCGCAAGCGCTCAGTGCATGAACGCAATTTTACTCCAAGATTCA 2040

QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700

Db 2041 AATTTCAAGACATTAATAGGCAACCGACGCTGGTGGGCGGAGTACAGGATTACC 2100

QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720

Db 2101 ATCCAGAGGGGATGACGTATTATAAGAAAAATACGTACACACTATCAGTACCTTTGAT 2160  
 Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
 Db 2161 GAGTGTATCCCAACATATTGTATCAAAATCGATGAATCAAAATTAAGCCCTTACC 2220  
 Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
 Db 2221 CGTTATCAATTAGAGGGTATATCGAAGATAGTCAAGACTTAGAATCTATTTAATCGC 2280  
 Qy 761 TyrAsnAlaLysHisGluThrValasnValLeuGlyThrGlySerLeuThrProLeuSer 780  
 Db 2281 TACAATGCAAAACATGAACAGTAATGTGCCAGGTACGGGTTCCTTATGCGCGCTTCA 2340  
 Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800  
 Db 2341 GCCCAAGTCCATCGGAAGTGTGGAGAGCCGAATCGATGCGGCCACACCTTGAATGG 2400  
 Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820  
 Db 2401 AATCCTGACTTAGATTGTCGTAGGATGGAGAAAGTGTGCCCATCATTCGCATCAT 2460  
 Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
 Db 2461 TTCTCCTTAGACATTGATGTAGGATGTACAGACTTAATGAGGACCTAGGTGTATGGGTG 2520  
 Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
 Db 2521 ATCTTTAAGATTAAAGCGCAAGATGGCGACGCAAGACTAGGGAACTAGAGTTTCTCGAA 2580  
 Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880  
 Db 2581 GAGAAACCATTAGTAGGAGAGCGGTAGCTCGTGTGAAAGAGCGGAGAAAAATGGAGA 2640  
 Qy 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900  
 Db 2641 GACAAACGTGAATAATGGAATGGGAACCAATAATATCGTTATAAGAGGCAAAAGAACTCT 2700  
 Qy 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGluLeuGluAlaAspThrAsnIleAla 920  
 Db 2701 GTAGATGCTTTATTGTAACTCTCAATATGATCAATTAAGCGGATACGAATATTGCC 2760  
 Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
 Db 2761 ATGATTCAATCGGCGAGATAACGTGTTATAGCATTCGAGAACCTTATCTGCTGAGCTG 2820  
 Qy 941 SerValIleProGlyValAsnValaspIlePheGluGluLeuLysGlyArgIlePheThr 960  
 Db 2821 TCTGTGATTCCGGGTGTCATCGGGTATTTTGTGAAGAATTAGAAGGGCGTATTTTCACT 2880  
 Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
 Db 2881 GCATTCCTCCTATATGATCGGGAATGTCATTAAATGAGTGTATTAATATGGCTTA 2940  
 Qy 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000  
 Db 2941 TCCTGCTGGAACGTGAAGGCGATGTAGATGTAGAAGACAAACCAACCCGCTTCGGTC 3000  
 Qy 1001 LeuValValProGluTrpGluAlaGluValSerGluGluValArgValCysProGlyArg 1020  
 Db 3001 CTGTGTTGTTCCGGATGGGAAGCAGAGTGTACAAAGAAATTCGTCTGTCTCGGGTCTG 3060  
 Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
 Db 3061 GGGTATATCTTCGTGTACAGCGTACAGGAGGATATGGAGAAAGTTGCGTAAACCAT 3120  
 Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluGluVal 1060  
 Db 3121 CATGAGATCGAGAACATAACAGCAGACTGAGCTTTAGCAACTGTGTAGAAGAGGAGTA 3180  
 Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080  
 Db 3181 TATCCAAACAAACGCGTAACGTGTATGATTATTAATCTGCGACTCAAGAGAAATATGAGG 3240

Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100  
 Db 3241 AGTACACTTCTCGTAATCGAGGATATGACGGAGCCTATGAAAGCAATTTCTCTGTACCA 3300  
 Qy 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
 Db 3301 GCTGATTATGCATCAGCCTATGAAGAAAAAGCATATACAGATGAGACGAGACAACTCCT 3360  
 Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProIleGlyTyrValThrLys 1140  
 Db 3361 TGTGAATCTAAACAGAGGATATGGGATTACACACCACCTACCACTGGCTATGTGACAAA 3420  
 Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160  
 Db 3421 GAATTAGATGACTTCCAGAACCCGATAGGTATGGATTGAGATCGGAGAAACGGAAGGA 3480  
 Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
 Db 3481 ACATTTCATCGTGACAGCGTGGAAATTACTTCTTATGGAGAA 3522

Search completed: November 28, 2002, 02:20:26  
 Job time : 306 secs

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 27, 2002, 20:22:40 ; Search time 485 seconds  
(without alignments)  
5451.229 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MNNIQNVCPYCNLNPV.....IGETGTFIVDSVELLMEE 1174

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_p2n.model -DEV=xlp  
-O=/cgn2.1/USPTC.spool/US09837961/runat\_25112002.142415.5911/app\_query.fasta\_1.1351  
-DB=N\_Geneseq\_101002 -QPMF=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -SPART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -LOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09837961 -@CGN\_1.1.380 -@runat\_25112002.142415.5911 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N\_Geneseq\_101002:\*  
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*  
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9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*  
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6244	100.0	3522	12	AAQ10182
2	6244	100.0	3522	14	AAQ47291
3	6244	100.0	3522	19	AAV62081
4	6244	100.0	3522	20	AAV60606
5	6244	100.0	3522	22	AA500565
6	6244	100.0	4020	12	AAQ14648
7	6238	99.9	3522	16	AAQ05270
8	6237	99.9	3522	17	AAT18722
9	6049	96.9	3522	16	AAT05250
10	6049	96.9	3522	17	AAT18702
11	6049	96.9	3522	19	AAV62083
12	5902	94.5	3444	16	AAQ05249
13	5902	94.5	3444	16	AAQ05251
14	5902	94.5	3444	17	AAT18701
15	5902	94.5	3444	17	AAT18723
16	5902	94.5	3444	19	AAV62080
17	5902	94.5	3444	19	AAV62082
18	5879	94.2	3444	20	AAV60604
19	5879	94.2	3444	22	AA500563
20	5674	90.9	3450	16	AAQ05269
21	5674	90.9	3450	17	AAT18721
22	5674	90.9	3450	19	AAV62079
23	5595	89.6	3558	22	AA500420
24	5409	86.6	3504	17	AAT16553
25	4815.5	77.1	3531	19	AAV31161
26	4815.5	77.1	3531	24	ABK11822
27	4812.5	77.1	3534	19	AAV31162
28	4812.5	77.1	3534	24	ABK11833
29	4804.5	76.9	3531	19	AAV31159
30	4804.5	76.9	3531	24	ABK11820
31	4745.5	76.0	3534	19	AAV31163
32	4745.5	76.0	3534	24	ABK11834
33	4706.5	75.4	3531	19	AAV31160
34	4706.5	75.4	3531	24	ABK11821
35	4647.5	74.4	3534	24	ABK11838
36	4636.5	74.3	3534	19	AAV31165
37	4391.5	70.3	3629	10	AAQ12443
38	4385.5	70.2	4438	12	AAQ13073
39	4373	70.0	4999	7	AAQ60239
40	4346.5	69.6	3582	24	AAQ36959
41	4346.5	69.6	14946	24	AAQ36965
42	4346.5	69.6	15503	24	AAQ36964
43	4344.5	69.6	3531	8	AAQ70366
44	4342	69.5	3623	9	AAQ81335
45	4342	69.5	3623	9	AAQ81647

## ALIGNMENTS

RESULT 1  
AAQ10182  
ID AAQ10182 standard; DNA; 3522 BP.  
XX  
AC AAQ10182;  
XX  
20-MAR-1991 (first entry)  
XX  
DT  
XX  
DE Lepidopteran-active toxin D gene.  
XX  
KW Lepidopteran-active toxin D; pest control; ss.  
OS Bacillus thuringiensis PS81L (NRRL B-18484).  
XX  
FN EP405810-A.  
XX  
PD 02-JAN-1991.  
XX

Db	541	GGACTGGATATAGCTACTGTTTAAATAATCATTTATAATAGATTAAATAAATCTTATTCATAGA	600
Qy	201	TyrThrLysHIScysLeuAspThrTyrAsnGlnGlyLeuGluasnLeuArgGlyThrAsn	220
Db	601	TATACGAAACATTTGTCGACATACAAATCAAGAGATTAGAAACCTTAGAGAGGTACTAAT	660
Qy	221	ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp	240
Db	661	ACTCGACAAATGGGCAAGATTCATCAGTTTGGAGAGATTATAACCTTACTGATTATAGAT	720
Qy	241	IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln	260
Db	721	ATCGTTGCTCTTTTCCGAACACTACGATGTTAGAACATATCCAATTCAAACGTCAATCCCAA	780
Qy	261	LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle	280
Db	781	TTAACAAAGGGAATTTATACAACTTCAGTAATTCAGGATTCTCCAGTTTCTGCTAATATA	840
Qy	281	ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet	300
Db	841	CCPAAATGGTTTTAATAGGCGGAAATTGGATGGTTAGACCGCCCATCTTATAGGACTTTATG	900

QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320

Db	901	AAITCTTTGTTGTTAACTCGACGAGACTGTTAGAAAGTCAAACTGTGCGGGAGGACACACTTA	966
Qy	321	VaiSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn	340
Db	961	GTTAGTTTCACGAAATACGGCTGCTGCTACCGGTATAAAATTCCTTAGTTACGGGGTCTTCAT	102
Qy	341	ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer	360

Db 1021 CCTGGTGGCGCCATTTCGATTGCAGATGAGGATCCACGTCCTTTTATCGGACATTATCA 108

		114	GATCCTGTTTTCGCAGGAGGATTGGGAATCCCTCATTTACTGTACTGGGCTTAGGGGA	114
Qy	VaiAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle	400		
Db	1141	GTAGCATTTCAACAAACTGGTACGAACCACACCGCAACATTTAGAATAATGTGGGACCAT	1200	
Qy	AspSerLeuAspGluIleProGlnAspAsnSerGlyAlaProThrPasnAspTyrSer	420		
Db	1201	GATTCTCTAGATGAAPCCCACTCAGGATAATAGTGGGCACTTTGGSAATGATTATAT	1260	
Qy	HisValLeuAsnHisValThrPheValArgTyrProGlyGluIleSerGlySerAspSer	440		
Db	1261	CATGTATTAATCATGTTACATTTTGTCAGTGGCCAGGTGAGATTTTCAGSAGATGATTCA	1320	
Qy	TyrArgAlaProMetPheSerTyrThrHisArgSerAlaThrProThrAsnThrIleAsp	460		
Db	1321	TGGAGAGCTCCAATGTTTTCTTGGACGCACCGTAGTGC AACCCCTACA AATTGAT	1380	
Qy	ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr	480		
Db	1381	CCGGAGAGGATTACTCAAATACCATTGGTAAAAAGCACATACACTTCAGTCAGGTACTACT	1440	
Qy	ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro	500		
Db	1441	GTGTAGAGGGCCCCGGTTTCGGGAGAGAGATTTCTTCGACGAACAAGTGGGAGACCA	1500	
Qy	PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle	520		
Db	1501	TTTGCTTATFACTATTGTTAATATAATGGCCAAATATCCC CAAGGTATCGTGC AAGAATA	1560	
Qy	ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe	540		
Db	1561	CGCTATGCCTCTACTACAANTCTAGAAYTTACGTACACGGTTCGAGGTGAACCGGATTTT	1620	
Qy	AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer	560		
Db	1621	GCMTGGTCAATTTAACAAAACATATGATACCGGTGACCAATTAACTCCATCTCTTTACT	1680	

Qy	561	TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly	580
Db	1681	TACGCAACTATTAAATACAGCTTTTACATTTCCCAATGAGCAGAGTAGTTTCACAGTAGGT	1740
Qy	581	AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal	600
Db	1741	GCTGATACTTTTAGTTCAGGGAATGAAGTTTATATAGACAGATTTCGAATGATTCAGTT	1800
Qy	601	ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu	620
Db	1801	ACTGCAACATTTGAAGCAACAATATGATTTAGAAAGAGCACAAAAGCGGTGATCGCTG	1860
Qy	621	PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln	640
Db	1861	TTTACTTCTTATAACCAATAGGATAAACAGATGTGACGGATTTATCATATTGATCAA	1920
Qy	641	ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu	660
Db	1921	GTATCCAATTTAGTGATTGTTTATCAGATGAATTTTGCTGGATGAAGCGAGAAATTG	1980
Qy	661	SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro	680
Db	1981	TCGGAGAAAGTCAACATCGCAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCA	2040
Qy	681	AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrPArgGlySerThrAspIleThr	700
Db	2041	AACITTCAAAGGCATCAATAGGCAACTAGACCGTGGTGGAGAGGAAGTACGGATATTACC	2100
Qy	701	IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp	720
Db	2101	ATCCAAAGAGGATGACGTATTCAAAGAAATATATSTCACACTACCAGTACCTTTGAT	2160
Qy	721	GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr	740
Db	2161	GAGTGCTATCCAACTATTATATCAAAAATAGATGAGTGTGAAAATTAACACCTATACT	2220
Qy	741	ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuCluIleLysIleArg	760
Db	2221	CGTTATCAATTAAGAGGGTATTTCGAGGATAGTCAGACTTGAATACTATTTTGATCCGC	2280
Qy	761	TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer	780
Db	2281	TATAATGCAAAACACGAAACAGTAATATGTGCTAGGTACGGTCTTTATGCGCGCTTCA	2340
Qy	781	ValGlnSerProIleargLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr	800
Db	2341	GTCCAAAGTCCCAATCAGAAAGTGTGGAGAACCCGAATCGATGCGCGCCACACCTTGAATGG	2400
Qy	801	AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis	820
Db	2401	AATCCTGATCAGATTGTCTTCAGAGACGGGGAAAAATGTGCACATCATTCGCACTAT	2460
Qy	821	PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrPVal	840
Db	2461	TTCTCCTTGGACATTGATGTTGATGTACAGACTTAATAGGAGACTTAGATGTATGGGTG	2520
Qy	841	IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGluLysLeuGluPheLeuGlu	860
Db	2521	ATATTCAGATTTAAGCCCAAGATGGCAATGCAAGACTAGGAAATCTCAGAGTTTCTCGAA	2580
Qy	861	GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg	880
Db	2581	GAGAAACCATTAGTCGGGGAACACTAGTCTGCTGTGCAAAAGACGACAGAAAAATGCGAG	2640
Qy	881	AspLysArgGluLysLeuGluLeuThrAsnIleValTyrLysGluAlaLysGluSer	900
Db	2641	GATAAACGTGAAAAATTGGAATTGGAACAAATATTGTTTATAAGAGGCAAAAGAACTCT	2700
Qy	901	ValAspAlaLeuPheValAsnSerGlnTyrAspGluLeuGluAlaAspThrAsnIleAla	920
Db	2701	GTAGATGCTTTATTTGTAACCTCAATATGATCAATTAACAGCGGATACGTAATTGGC	2760

QY	921	MetIleHisAlaAlaAspLysArgValHisArgIleAargGluAlaTyrLeuProGluLeu	940
DB	2761	ATGATTTCATCGGCAGATAAACCGTGTTCATAGAATTCGGSAACGATATCTTCACAGAGTTA	2820
QY	941	SerValIleProGlyValAsnValaspIlePheGluGluLeuLysGlyArgIlePheThr	960
DB	2821	TCGTGGATTCCGGGGTAAATATAGACATTTTCGAAGAATTAAAGGGCGTATTTTCACT	2880
QY	961	AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu	980
DB	2881	GCATTCCTCTATATGATCCGAGAAATGTCATATAAACGGTGATTTCAATAATAGCTTA	2940
QY	981	SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal	1000
DB	2941	TCATGCTGGAACGTCGAAGGGCATGTAGATGTAGAAGACAAAACAACACCGTTCGGTC	3000
QY	1001	LeuValValProGluTrpGluAlaGluValSerGlnGluValargValCysProGlyArg	1020
DB	3001	CTTGTTGTTCGGGAATGGGAACGAAGTGTCAACAAGAAGTTCTGCTCTCCGGGTCGT	3060
QY	1021	GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle	1040
DB	3061	GGCTATATCTTCGGTGCACGGTACAGAGGAGGATATGGAGAAGGTTGCGTAACCAT	3120
QY	1041	HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal	1060
DB	3121	CATGAGATCGAGAACAATACAGACGAACCTGAAGTTTAGCAACTCGCTAGNAGAGGAATC	3180
QY	1061	TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly	1080
DB	3181	TATCCAAACAACACCGTAACGTTGATGATATATCTGCAAAATCAAGAAGAATACGGGGT	3240
QY	1081	AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro	1100
DB	3241	GGGTACACTCCCGTAATCGTGGATATGACGAACAAATATGGAAAGCAATCTTCTGTACCA	3300
QY	1101	AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro	1120
DB	3301	GCTGATTATGCGTCAGTCTATGAAGAAAATCGATACAGATGGACGAGAGACAATCCT	3360
QY	1121	CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys	1140
DB	3361	TCTGAATCTAACAGAGGATATGGGATTACACACCCTACCAGCTGGCTATGTGCAAAA	3420
QY	1141	GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly	1160
DB	3421	GAATTAGAGTACTTCCGAAACCCGTAAGATGATGATTGAGATCGGAACCGAGGA	3480
QY	1161	ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu	1174
DB	3481	ACATTCATCGTGACAGCGTGAATTAATCTTCTATCGAGGAA	3522
RESULT	2		
AAQ47291			
ID	AAQ47291	standard; DNA; 3522 BP.	
XX	XX		
AC	AAQ47291;		
XX	XX		
DT	28-JAN-1994	(first entry)	
XX	XX		
DE	DE	Delta endotoxin gene.	
XX	XX		
KW	KW	Endotoxin; Bacillus; lice; insecticide; sheep; ss.	
XX	XX		
OS	Bacillus thuringiensis PS81I (Clone A).		
XX	XX		
FH	FH	Location/Qualifiers	
FT	mat_peptide	1..3522	
FT		/*tag= a	
FT		/product= delta endotoxin.	
XX	XX		
PN	PN		
XX	W09314641-A.		
XX	XX		

PD 05-AUG-1993.  
 XX PF 31-DEC-1992; 92W0-US11337.  
 XX PR 29-JAN-1992; 92US-0828788.  
 XX (MYCO ) MYCOGEN CORP.  
 XX Hickie LA, Payne J;  
 PI WPI: 1993-258266/32.  
 DR P-PSDB; AAR39754.  
 XX Controlling biting lice on sheep - comprises administering  
 PT Bacillus thuringiensis toxins to host  
 XX Disclosure; Page 42-43; 64pp; English.  
 CC Many strains of Bacillus thuringiensis (B.t) produce insecticidal  
 CC delta endotoxins. A number of these endotoxins have been found to  
 CC be toxic to Damlinia ovis, the biting louse of sheep. The B.t.  
 CC isolates which produce these toxins can be grown and the delta  
 CC endotoxin which is produced can be recovered by standard procedures.  
 CC The genes encoding these endotoxins can also be transferred to a  
 CC suitable host via a recombinant vector and the resulting  
 CC transformants used in methods to control lice.  
 XX SQ Sequence 3522 BP; 1156 A; 589 C; 782 G; 995 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 3522  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0  
 US-09-837-961-8 (1-1174) x AAQ47291 (1-3522)  
 QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnProGluVal 20  
 DB 1 ATGGAGAATAATATTCACAAATCAATCGGTACCTTCAATATGTTAAATATCCTGAAGTA 60  
 QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 DB 61 GAATATTAAATGAAGAAGAGTACTGCGAGATTACCGTTAGATATATCCCTTATCGCTT 120  
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 DB 121 ACACGTTTCCTTTTGAGTGAATTTATATTCAGGTGTGGAGTTGCGTTTGGATTATTGAT 180  
 QY 61 LeuIleTyrGlyPheIleThrProSerAspTyrPheLeuPheLeuGlnIleGluGln 80  
 DB 181 TTAATATGGGGTTTATATCTCTCTGATGTGAGCTTATTTCTTTACAGATTGAACAA 240  
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 DB 241 TTCAATTGACCAAGATAGAAATGGAATGGAAGAACCGGGCAATTACTACATTACGAGG 300  
 QY 101 LeuAlaAspSerTyrGluIleThrIleGluAlaLeuArgGluThrGluAlaAsnProAsn 120  
 DB 301 TTAGCAGATAGTATGAATTTATATTTGAAGCACTAAGAGAGTGGGAAGCAATCCTAAT 360  
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
 DB 361 ATGCACAAATTAGGGAAGATGTGCGTATTCGATTTCGTAATACAGACCGCTTTAATA 420  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 DB 421 ACAGCAATAAATAATTTTACACTTACAGTTTGAATCCCTTTTATCGGTCATGTT 480  
 QY 161 GlnAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr 180

DB 481 CAAGCGCGGAATTTACATTTATCATTATTAAGAGACGCTGTATCGTTTGGCAGGGTTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuLeuAsnLeuIleHisArg 200  
 DB 541 GGACTGSATAGTACTCTGTAAATATCATTAATAGATTAATAATCTTATTCATAGA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 DB 601 TATACGAACATTTGTTGGACACATACAACTAAGGATTAGAAAACCTTAAGAGTACTAAT 660  
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240  
 DB 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTAAACACTTACTGTATAGAT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 DB 721 ATCGTTGCTCTTTTCCGAACACTAGATGTAGAACATATCCAATTCAACGTCATCCCAA 780  
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 DB 781 TTAACAGGGAATTTATACAGTTTCAGTAATTCAGAGATCTCCAGTTTCTGCTAATA 840  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
 DB 841 CCTAATGGTTTAAATAGGCGGAATTTGGAGTTAGACCGCCCATCTTATGGACTTATG 900  
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
 DB 901 AATTCTTTTGTGTAACCTGAGAGACTGTAGAAAGTCAAACTGTGTGGGAGACACTTA 960  
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 DB 961 GTTAGTTCAGAAATACGCTGTGTAACCGTATAAAATTTCCCTAGTTACGGGGTCTTCAAT 1020  
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
 DB 1021 CCTGTGGCGCCATTTGGATTGCGAGTAGAGATCCACGCTCTTTTATCGGACATTATCA 1080  
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 DB 1081 GATCCTGTTTGTGTCGAGGAGGATTTGGGAATTCCTCATTTACTTGGGGCTTAGGGGA 1140  
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
 DB 1141 GTAGCAATTCACAAACTGTGAGACCAACCCGGAACATTTAGAAATAGTGGGACCA 1200  
 QY 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
 DB 1201 GATTCTCTAGATGAATCCACCTCAGGATAATAGTGGGACCTTGGGAATGATTAGT 1260  
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
 DB 1261 CATGTATTAAATCATGTTTACATTTGTACGATGCCAGGTGAGATTTTCAGAAAGTATCA 1320  
 QY 441 TrpArgAlaProMetPheSerTyrThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 DB 1321 TGGAGAGCTCCAAATGTTTTCCTGGAGCACCGCTAGTGCACCCCTACAAATACATGAT 1380  
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
 DB 1381 CCGGAGAGGATTACTCAAAATACCATTTGGTAAAGACACATACACTTCAGTCAGTACTACT 1440  
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgThrSerGlyGlyPro 500  
 DB 1441 GTTGTAAAGAGGCCCGGGTTTACGGGAGGAGATATCTTCGACGAACAAAGTGGAGACCA 1500  
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
 DB 1501 TTTGCTTATACATTGTTGTTAATAATGGCAATTACCCCAAGGTATTCGTCAAGAAATA 1560  
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
 DB 1561 CGCTATGCTCTACTACAAATCTAGAATTTACGTACCGTTGACGGTTCAGGTGAACGGATTTT 1620

QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
DB 1621 GCTGGTCAATTTAAACAAACATGGATACCGGTGACCCATTAACATCCCAATCTTTTAGT 1680  
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
DB 1681 TAGCGCAACTATTAAATACAGCTTTACATCCCAATGAGCCAGAGTAGTTTCACAGTAGGT 1740  
QY 581 AlaAspThrPheSerSerGlyAsnGlnValTyrIleAspArgPheGluLeuIleProVal 600  
DB 1741 GCTGATACCTTTTAGTTTCAGGGAATGAAGTTTATATAGACAGATTTTGAATGATTCCAGIT 1800  
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
DB 1801 ACTGCAACATTTGAGCAGCAATATGATTTAGAAAGACCAAAAGCGGTGAATGCGCTG 1860  
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
DB 1861 TTTACTTCTATAAACCAATAGGGATAAAACAGATGTGACGGATTATCATATTGATCAA 1920  
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
DB 1921 GATCCAAATTTAGTGGATTGTTTATCAGATGAATTTGTCTGGATGAAAGCGAGAAATTG 1980  
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLysGlnAspPro 680  
DB 1981 TCCGAGAAAGTCAACATCGGAAGCGACTCAGTGATGACGGAAATTTACTTCAAGATCCA 2040  
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700  
DB 2041 AACTTCAAGGCATCAATAGGCACTAGACCGTGGTGGAGAGGAAGTACGGATATTACC 2100  
QY 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
DB 2101 ATCCAAAGAGGAGTACCTATTCAAGAAATATGTCCACTACCGGTACCTTTGAT 2160  
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
DB 2161 GAGTCTATCCCAACGATTTATATCAAAATAATAGATGATCGCAATTAACACCTATACT 2220  
QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
DB 2221 CGTTTATCAATTAAGAGGTPATATCGAGGATAGTCAAGACTTAGAAATCTATTGTATCCGC 2280  
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780  
DB 2281 TATATGCAAAACGAAACAGATAATGTCTAGGTACGGGTCTTTATGGCCGCTTTCA 2340  
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800  
DB 2341 GTCCAAAGTCCCAATCAGAAAGTGTGAGAAACGATCGATGCGCCACACCTTGNATGG 2400  
QY 801 AsnProAspLeuAspCysSerCysArgaspGlyGluLysCysAlaHisSerHisHis 820  
DB 2401 AATCTGTATCTAGATGTTCCTGCGAGACGGGGGAAAAATGTGCATCATTCGCAATCAT 2460  
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
DB 2461 TTCTCTCTGGACATTGATGTTGGATGTACAGACTTAAATGAGGACTTAGATGATGGGTG 2520  
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
DB 2521 ATATTCAAGATTAAAGCGCAAGATGCCCATCAAGACTAGGAAATCTAGAGTTTCTCGAA 2580  
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880  
DB 2581 GAGAAACCAATTTAGTCGGGGAACCACTAGTCTGTTGAAAGAGCAGAGAAAAATGGAGA 2640  
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900  
DB 2641 GATAAACGTGAATAATTTGAATTTGAAACAAATATGTTTATATAAGAGCGCAAAAGATCT 2700

QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920  
DB 2701 GTAGATGCTTTATTTTAAACTCTCAATATGATCAATATACAAGCGGATAGCAATATTGCC 2760  
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
DB 2761 ATGATTCATCGGCAGATAAACGTGTTCATAGAAATTCGGAAGCGATCTCTCCAGAGTTA 2820  
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
DB 2821 TCTGTGATTCGGGTCTAAATGTAGACATTTTCGAAGAATTAAGAGGCGGTATTTTCACT 2880  
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
DB 2881 GCATTTCTTCTATATGATCGAGAAATGCAATTAAGAACGGTGATTTCAATAATGCTTA 2940  
QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000  
DB 2941 TCATGCTGGACGTGAAGGGCATGTAGATGTAGAGAGACAAACACACCGTTCGGTC 3000  
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
DB 3001 CTGTGTTGTTCCGGAATGGGAAGCAGAGTGTCAAGAAAGTTCGTCTCTCCGGTCTGT 3060  
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
DB 3061 GGTATATCTTCGTCTCAGCGTACAAGGAGGATATGGAGAAAGTTGCGTAACCAT 3120  
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
DB 3121 CATGAGATCGAGAACAAATACAGACGAACCTGAAGTTTAGCAACTGCGTAGAGAGGAAGTC 3180  
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080  
DB 3181 TATCCAAACACACACGCTAACGCTGATGATATGATCTACTGCAATCAAGAAATTCCTTCTGTACCA 3240  
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100  
DB 3241 GGTACACHTCCCGTANTCGTGATGATGACGAACACTATGGAAGCAATTCCTTCTGTACCA 3300  
QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
DB 3301 GCTGATATGCGTCAGTCTATGAAGAAANTCSTATACAGATGGAGAGAGACATCCT 3360  
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
DB 3361 TGTGAATCTAAACAGAGGATATGGGATTACACACCCTACCAGCTGGCTATGTGACAAA 3420  
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160  
DB 3421 GAATTAGACTACTTCCAGAAACCGGATAAGGTATGAGATTGAGATCGGAGAAACGGAAGGA 3480  
QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
DB 3481 ACATTCATCGTGACACGCTGGAAATTTACTCTTATGAGGAA 3522  
RESULT 3  
AAV62081  
ID AAV62081 standard; DNA; 3522 BP.  
XX AC  
XX AAV62081;  
XX  
XX 13-JAN-1999 (first entry)  
XX  
DE Plasmid pMYC2243 Bt endotoxin DNA fragment.  
XX  
XX Bt toxin; lepidoptera; pest; cryIIF; chimeric; core toxin; cryIA(c);  
KW synergism; plant; primer; endotoxin; ss.  
XX  
XX Synthetic.  
XX  
XX US5827514-A.  
XX



PD 27-OCT-1998.  
 XX  
 XX 08-FEB-1996; 96US-0598305.  
 PF  
 XX 06-DEC-1994; 94US-0349867.  
 PR  
 XX 08-FEB-1996; 96US-0598305.  
 PR  
 XX (MYCO ) MYCOGEN CORP.  
 PA  
 XX Bradfisch GA, Schwab GE, Thompson M;  
 PI  
 XX WPI: 1998-593944/50.  
 DR  
 DR P-PSDB; AAW6708.  
 XX  
 XX Composition for biological control of lepidopteran pests -  
 PT comprising cells expressing two chimeric Bacillus thuringiensis  
 PT crystal proteins  
 XX  
 XX Example 5; Column 53-58; 75pp; English.  
 PS  
 XX This sequence encodes a Bt endotoxin which is used in a method for  
 CC controlling lepidopteran pests. The method involves the use of cells  
 CC that express the Bacillus thuringiensis delta-endotoxins cryII chimeric  
 CC core toxin-containing protein and CryIA(c) chimeric core toxin-containing  
 CC protein in a combination that have synergistically enhanced activity,  
 CC against e.g. corn earworm (Heliothis zea).  
 XX  
 XX Sequence 3522 BP; 1150 A; 601 C; 786 G; 985 T; 0 other;  
 SQ

Alignment Scores:  
 Pred. No.: 0 Length: 3522  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0

US-09-837-961-8 (1-1174) x AAV62081 (1-3522)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
 Db 1 ARGAAAAATAATATCAAAATCAATGGCTACCTTACAAATTTGTTAAATAATCTTGAAGTA 60  
 Qy 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 Db 61 GAAATACCTGAACGAAGACGACGACCGCCGCTGCGCTGGACATCAGCCTGAGCCTT 120  
 Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 Db 121 ACAGCTTCTCTTTGAGTGAATTTGTTCCAGGTGGGAGTGGGTTGGATTATTGAT 180  
 Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIleGluGln 80  
 Db 181 TTATATGGGGTTTATTAACCTCTTCGATTGGAGCTATTCTTTTACAGATTGACAA 240  
 Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 Db 241 TTGATTGACCAAGAAATAGAAACATTTGAAAGGAAACCGGGCAATTACTACATTACGAGG 300  
 Qy 101 LeuAlaAspSerTrpGluIleTrpIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 Db 301 TTACGAGATAGCTATGAATTTTATTTGAGACCTTAGAGAGTGGGAGCAATTCCTAAT 360  
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140  
 Db 361 AATGCACAATTAAGGGAAGATGCGGTATTTCGATTATGCTATATACAGACGAGCTTAATA 420  
 Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTrpVal 160  
 Db 421 ACAGCAATAAATAATTTTACACTTACAAAGTTTGAAGTCCCTCTTTATCGGCTATGTT 480  
 Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 Db 1561 CGCTATGCCTCTACTACAATTTACGTAACGGTTGACAGGTGACCGGATTTT 1620

Db 481 CAAGCGGCGAATTTACATTTATCACTATTAGAGACGCTGTATCGTTTGGGACGGTGG 540  
 Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 Db 541 GGACTGGATATAGCTACTGTTTAAATCAATTAATAGATTAAATAAATCTTTATTATCAGA 600  
 Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 Db 601 TATACGAAACATTTGTTGGACATACATCAAGGATTAGAAACCTTAAGAGGTACTAAT 660  
 Qy 221 ThrArgGluTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 Db 661 ACTCGACATGGGCAAGATTCAATCAGTTTAGCAGAGATTAACTACTTACTGTATTAGAT 720  
 Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 Db 721 ATCGTTGCTCTTTTCCGAACTACGATGTAGAACATATCAATTCAAACGTCATCCCAA 780  
 Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 Db 781 TTAACAAGGGAATTTATACAAGTTCAAGTAATTGAGGATTCCTCAGTTTCTGCTAATATA 840  
 Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
 Db 841 CCTAATGTTTAAATAGGCGGAATTTGGAGTTAGACGCCCATCTTATGGACTTTATG 900  
 Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyClyHisLeu 320  
 Db 901 AATCTCTTTGTTGTAAGTGCAGAGACTGTAGAACTCAAACTGTGTGGGAGGACACTTA 960  
 Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 Db 961 GTTAGTTTACGAAATACGCGCTGTAACCGTATATAATTTCCCTAGTTAGGGGCTCTCAAT 1020  
 Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
 Db 1021 CCTGGTGGCGCATTTGGATTGCGAGATGAGATCCACGCTCTTTTATTCGGACATTATCA 1080  
 Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 Db 1081 GATCCCTGTTTGTCCGAGGAGATTGGGAATPCCTCATTTATGTACTGGGGCTTAGGGGA 1140  
 Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
 Db 1141 GTAGCATTTCAACAACTGCTACGAACACACCCGCAACATTTAGAAATAGTGGGACCATA 1200  
 Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
 Db 1201 GATTCCTAGATGAAATCCCACTCAGGATAATAGTGGGGCACCTTGGAAATGATTATAGT 1260  
 Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
 Db 1261 CATGTTATTAATCATGTTTACATTTGTACGATGCGCAGGTGAGATTTACGAGGTGATCA 1320  
 Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 Db 1321 TGGAGAGCTCCATGTTTCTTGGACGCGCTAGTGAACCCCTACAAATACAAATGAT 1380  
 Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
 Db 1381 CCGGAGAGATTACTCAATACCATTTGGTAAGGACACATACACTTCAGTCAGGTACTACT 1440  
 Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
 Db 1441 GTTGTAAAGGGGCGCGGGTTTACGGGAGGAGATATTCTTCGACGAACAAGTGGAGGACCA 1500  
 Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
 Db 1501 TTTGCTTATACTATTGTTAATAATGGGCAATTAACCCCAAGGATTCGTCGAAGAATA 1560  
 Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
 Db 1561 CGCTATGCCTCTACTACAATTTACGTAACGGTTGACAGGTGACCGGATTTT 1620

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QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
DB 1621 GCTGGTCAATTTAAACAAACATGGATACCGGTGACCCATTAACATTCCTCAATTTTTAGT 1680
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
DB 1681 TAGCGCAACTATTAAATACAGCTTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGGT 1740
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
DB 1741 GCTGATACCTTTAGTTTCAGCGAATGAAGTTTATATAGACAGATTTGAATGATTCCAGTT 1800
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
DB 1801 ACTGCAACATTTGACGACAGAAATGATTTAGAAAGAGACAAAGCGGTGAATGCGCTG 1860
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
DB 1861 TTTACTTCTATAAACCAAAATAGGATAAAACACAGATGTGACGGATTATCATATTGATCAA 1920
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
DB 1921 GTATCCAAATTTAGTGGATTGTATCAGATGAATTTGTCTGGATGAAAGCGAGAATTG 1980
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
DB 1981 TCCGAAAGTCAAAACATCGGAAGCGACCTCAGTCATGACGCGAATTTACTCAAGATCCA 2040
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700
DB 2041 AACTTCAAAAGGCATCAATAGGCAACTAGACCTGGTGGAGAGGAAGTACGGATATATACC 2100
QY 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
DB 2101 ATCCAAAGGAGATGACGTATTTCAAGAAATTTATGTCACTACCAAGTACCTTTGAT 2160
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
DB 2161 GAGTGTATCCAAACGATTTATATCAAAATAATAGATGAGTCGAAATTAACACCTATACT 2220
QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
DB 2221 CGTTTATCAATTAAGAGGTATATCGAGGATAGTCAAGACTTAGAAATCTATTGATCCGC 2280
QY 761 TyrAsnAlaLysHisGlnThrValAsnValLeuGlyThrClySerLeuTyrProLeuSer 780
DB 2281 TATATGCAAAACACGAAACAGTAAATGTGCTAGGTACGGGTCTTTATGGCGGCTTTCA 2340
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr 800
DB 2341 GTCCAAAGTCCAAATCAGAAAGTGTGGAAACCGAATCGATGCGCGCACACCTTGAATGG 2400
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820
DB 2401 AATCCTGATCTAGATTGTTCCCTGCAGACGCGGGAATAATGTGCATCAITCGCATCAT 2460
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840
DB 2461 TTCTCCTTGGACATTTGATTTGGATGTACAGACTTAAATGAGSACTTAGATGTATGGGTG 2520
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
DB 2521 ATATTCAAGATTAAAGCGCAAGATGCCATGTCAAGACTAGGAATCTAGATTTCTCGAA 2580
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880
DB 2581 GAGAAACCATTTAGTCGGGAAGCACTAGCTCGTGTGAAAGAGCAGAGAAATAATGGAGA 2640
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
DB 2641 GATAACCGTGAATAATTTGGAATTTGGAACAAATAATTTGTTTATAAAGAGCGCAAAAGATCT 2700
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QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuAlaAspThrAsnIleAla 920
DB 2701 GTAGATGCTTTATTTGTAAACTCTCAATATGATCAATTAACAGCGGATACGAAATTTGCC 2760
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
DB 2761 ATGATTCAATGCGGCAGATRAACGTGTCATAGAATTCGGGAAGCGTATCTTCCAGAGTTA 2820
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
DB 2821 TCTGTGATTCGGGTGTAAATGTAGACATTTTCGAAGAATTAAGAGGCGGTATTTTCACT 2880
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
DB 2881 GCATCTTCTATATATGTCGAGAATGTCATTAAACCGTGATTTCAATAATGGCTTA 2940
QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
DB 2941 TCATGCTGGAACGTGAAGGCGCATGTAGATGTAGAAGACAAACACACCGCTTCGGTC 3000
QY 1001 LeuValValProGluTyrPheGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
DB 3001 CTGTGTTGTTCCGGAATCGGAAGCAGAAAGTGTCAACAAGATTCGTCTGTCTCGGGTCGT 3060
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
DB 3061 GGCATATCTCTCGTCTCAGCGTACAGGAGGGATATGGAGAAGTTCGCTGAACCAT 3120
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
DB 3121 CATGAGATCGAGAACAATACAGACGAACCTGAAGTTTAGCAACTGCGTAGAAGAGAAGTC 3180
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
DB 3181 TATCCAAACACACCGTAACGTGTAATGATTATCTACTGCAATCAAGAAGAATAACGGGGT 3240
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
DB 3241 GCGTACACTTCCGTAATCGTGGATATGCGAAACCTTATGGAAGCAATCTTCTGTACCA 3300
QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
DB 3301 GCTGATTATGCTGCTAGCTCTATGAAGAAAATCGTATACAGATGGAAGAGACAATCCT 3360
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
DB 3361 TGTGAATCTAACAGAGGATATGGGATTTACACACCACTACCAGCTGGCTATGTGACAAA 3420
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160
DB 3421 GAATTAGAGTACTTCCAGAACCGATAGGTATGGATTGAGATCGAGATCGAAGAACCGAAGGA 3480
QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
DB 3481 ACATTCATCGTGACACGCGTGAATTTACTCTTATGGAGAA 3522
RESULT 4
AA60606
ID AAX60606 standard; DNA; 3522 BP.
XX
AC AAX60606;
XX
DT 27-JUL-1999 (first entry)
XX
DE Wild-type B.t cryIF toxin gene 811A.
XX
KW Plant-optimised gene; pesticidal toxin; CryIF; CryIaC; CryIc; 158C2c;
XX 31G1a; CryIaB protoxin; insect control; chimeric; ss.
XX
OS Bacillus thuringiensis.
XX
PN W09924581-A2.
XX
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PD 20-MAY-1999.  
 XX 04-NOV-1998; 98WO-US23457.  
 XX 23-OCT-1998; 98US-0178252.  
 PR 12-NOV-1997; 97US-0065215.  
 PR 02-MAR-1998; 98US-0076445.  
 XX (MYCO ) MYCOGEN CORP.  
 PA Cardineau GA, Narva KE, Stelman SJ;  
 PI WPI: 1999-327409/27.  
 XX P-PSDB: AAY16792.  
 DR Nucleic acids encoding pesticidal proteins, optimized for plant  
 XX expression  
 PT Disclosure; Page 29-30; 67pp; English.  
 PS The invention relates to nucleic acid sequences, optimised for  
 XX expression in plants, that encode: (i) one of the pesticidal toxins  
 CC CryIa, CryIb, CryIc, 15822c or 31Gla, or (ii) a portion of the CryIa  
 CC protoxin. The pesticidal toxins (AAV16790, AAV16792-Y16798) are used for  
 CC pest, especially insect control, particularly on plants. The nucleic acid  
 CC sequences are used to produce (truncated or chimeric) toxins, and related  
 CC fusion genes or proteins, particularly they are used to generate  
 CC transgenic plants that show increased resistance to pests. Compared with  
 CC wild-type Bacillus thuringiensis sequences, the optimised sequences are  
 CC better suited to expression in plants. The present sequence represents a  
 CC polynucleotide sequence for a wild-type, full-length B.t toxin gene  
 CC designated 81IA.  
 XX Sequence 3522 BP; 1156 A; 589 C; 782 G; 995 T; 0 other;  
 SQ

Alignment Scores:  
 Pred. No.: 0 Length: 3522  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0

US-09-837-961-8 (1-1174) x AAX60606 (1-3522)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnProGluVal 20  
 Db 1 ATGGAGATATATTCAAATCAATGCGTACCTTACATTTGTTAAATATCCTGAGTA 60  
 Qy 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 Db 61 GAATATATAATGAAGAAGAGTACTGGCAGATTACCGTTAGATATATCTTATCGCTT 120  
 Qy 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 Db 121 ACAGCTTCCTTTTGTAGTGAATTTGTCCAGGTGTGGAGTGTGGATTTATTCAT 180  
 Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80  
 Db 181 TTAATATGGGTTTATTAACCTCTCTGATTTGGAGCTATTTCTTTTACAGATTGAACAA 240  
 Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 Db 241 TTGATTTGACCAAGAAATAGAACAATTTGAAGAAGAACCGGCAATTAATACATACGAGG 300  
 Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 Db 301 TTAGCAGATAGCTATGAAATTTATATTGAACACTAAGAGAGTGGAGCAATCCTTAT 360  
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
 Db 361 AATGACAAATTAAGGGAAGATGTGCTATTGCTATTGCTAATACAGACGAGCTTTAATA 420

QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTrpVal 160  
 DB 421 ACAGCAATAATAATTTTACACTTACAAGTTTGAATCCCTCTTTTATCGTCTATGTT 480  
 QY 161 GlnAlaIleAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 DB 481 CAAGCGCGAATTTTACATTTATCCTATTAAAGAGACGCTGTATCGTTTGGGCGAGGTTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 DB 541 GGACTGGATATAGCTACTGTTAATTAATCATATATAGATTAAATAATCTTATTCAATAGA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 DB 601 TATACGAACATTTGTTGGACACATACAACTCAAGGATTAGAAACTTAAGAGGACTAAT 660  
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 DB 661 ACTCCACATGGGCAAGATTCAATCAGTTAGGAGAGATTAAACACTTACTGTATTAGAT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 DB 721 ATCGTTGCTCTTTTCCGAACCTACGATGTAGACATATCCAATTCAAACGCTCATCCAA 780  
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 DB 781 TTAACAAGGGAATTTATACAAGTTCAAGTAUTGAGGATCTCCAGTTCTCGCTAATAATA 840  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProHisLeuMetAspPheMet 300  
 DB 841 CCTAATGGTTTAAATAGGCGGAATTTGGAGTTAGACCGCCCATCTTTATGGACTTAIG 900  
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
 DB 901 AATTTCTTTTGTAACTGCAGAGACTGTTAGAATCAAACTGTGTGGGAGGACACTTA 960  
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 DB 961 GTTACTTCACGAATACGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGCTCTCAAT 1020  
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
 DB 1021 CCTGTTGGCGCATTTGGATTGCAGATGAGGATCCACGCTCTTTTATTCGGACATTATCA 1080  
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 DB 1081 GATCCTGTTTGTCCGAGGAGGATTTGGGATCTCTCATTTATGTACTGGGCTTAGGGA 1140  
 QY 381 ValAlaPheGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
 DB 1141 GTAGCATTTTCAACAACTGGTACGAACACACACCGCAACATTTAGAAATAGTGGGACCAT 1200  
 QY 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
 DB 1201 GATTTCTAGATCAAAATCCCACTCAGGATATATAGTGGGACCTTGGATGATTATAT 1260  
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
 DB 1261 CATGTATTAAATCATGTTTACATTTTACGATGGCCAGGTGAGATTTCAGGAAGTGATTCA 1320  
 QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 DB 1321 TGGAGCTCCCAATGTTTCTTGGGACGACCGGTAGTGCACCCCTTACAAATACAAATGAT 1380  
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
 DB 1381 CCGGAGAGGATTTACTCAATACCATTTGTTAAAGACACATACACTTCAGTCAGGTACTACT 1440  
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
 DB 1441 GTTGTAAAGGCGCGGGTTTACGGGAGGAGATATTCTTCGACGAACAAGTGGAGGACCA 1500  
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520

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Db 1501 TTTGGCTTATACCTTAAATAAATGGCAATACCCAAAGGTATCGTGCAAGAATA 1560
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
Db 1561 CGCTATGCCCTCTACTACAACTCTAGAAATTCAGTAAACGGTTGCAGGTGAACCGGATTTT 1620
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGGTCAATTTAAACAAACAATAGGATACCGGTGACCCCAATTAACATTCCTTCTTAGT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TAGCGAACCTATTAAACACGCTTTTACATTCCTCAATGAGCAGAGTAGTTTTCACAGTAGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATCTTTAGTTTCAGGGAATGAAGTTTATATAGACAGATTTGAATTGATTCAGTT 1800
Qy 601 ThrAlaThrPheGluAlaGlnTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAGCAGAAATATGATTTAGAAAGACACAAAGCGGTGAATCGCGTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTACTTCTATRAACCAATAGGATAAACAACAGATGTCAAGGATTTATCATATTGATCAA 1920
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGlnLysArgGluLeu 660
Db 1921 GTATCCAATTTAGTGATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAATG 1980
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680
Db 1981 TCCGAGAAAGTCAACATCGGAAGCACTCAGTGATCAGCGGAATTTACTTCAAGATCCA 2040
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700
Db 2041 AACTTCAAGGCATCAATAGGCAACTAGACCGTGGTGGAGAGGAAGTACGGATATTACC 2100
Qy 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAGAGGAGATCAGCTATTCAAGAAATTTATGTACACTACCAAGTACCTTTGAT 2160
Qy 721 GluCystyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
Db 2161 GAGTGCTATCCAAGTATTATATCAAAATAAATAGATGAGTCGGAATTAACACCTATACT 2220
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTTATCAATTAAGAGGGTATATCGAGGATAGTCAAGACTTTAGAAATCTATTGTATCCG 2280
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780
Db 2281 TATATGCAAAACACGNAACAGTAATGTGCTAGGTACGGGTCTTATGCGCGCTTCA 2340
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr 800
Db 2341 GTCCAAAGTCCAATCAAGAAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTGAATG 2400
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
Db 2401 AATCCTGATCTAGATTCTTCTCGAGAGCGGGAAATGTGCACATCAITTCGCATCAT 2460
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840
Db 2461 TTTCTCTTGGACATGATGTGGTGTACAGACTTAATAGGACTTAGATGTATGGGTG 2520
Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2521 ATATTCAAGATTAAAGCGCAAGATGGCCATGCAAGACTAGGAATCTAGAGTTTCTCGAA 2580
Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysTyrArg 880

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Db 2581 GAGAAACCATTAGTGGGGAAGCACCTAGCTCGTGTGAAAAGACGAGAGAAAATGAGA 2640
Qy 881 AspLysArgGluLysLeuGluLeuThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 2641 GATAAACGTCGAAATTTGGAATTTGGAACAAATATTTCTTTATAAAGAGGCAAAAGATCT 2700
Qy 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
Db 2701 GTAGATGCTTTATTGTAAACTCTCAATATGATCAATTAACAGCGGATACGAATATGCC 2760
Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 2761 ATGATTTCATCGCGCAGATAAACGTTTCATAGATTCGCGAGCGTATCTCCAGAGTTA 2820
Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
Db 2821 TCTGTGATTCGGGTGTAATGTAGACATTTTCGAAGAATTAAGGCGCTATTTCACT 2880
Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 2881 GCATTCCTCTATATGATGCGAGAAATGTCTATPAAAAACGGTGATTTCAATATGGCTTA 2940
Qy 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000
Db 2941 TCATGCTGGAACGTGAAAGGCGATGTAGATGTAGAGAACAAAAACAACCCCTCGGTC 3000
Qy 1001 LeuValValProGluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 3001 CTTGTGTTCGGGAATGGGAAGAGAGTGTCACAGAAGTTCTGTCTGCCGGTCTG 3060
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
Db 3061 GGCATATATCTTCTGTCACAGCGTACAAAGGAGGATATGGAGAAGTTGCGTAACCAAT 3120
Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3121 CATGAGATTCGAGAACATACACAGCAACTGAACTTACCAACTCGGTAGAGAGAGATC 3180
Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080
Db 3181 TATCCAAACACACGGTAACTGTAATGATTTACTGCAATCAAGAGAAATACGGGGT 3240
Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluTyrThrTyrGlySerAsnSerSerValPro 1100
Db 3241 CGGTACACTTCCCGTAATCGTGGATATCAGCAAACTTATGGAACCAATCTCTGTACCA 3300
Qy 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
Db 3301 GCTGATTATGGTCACTCTATGAAGAAAAATCGTATACAGATGGACGAAGAGACATCCT 3360
Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
Db 3361 TGTGAATTAACAGAGGATATGGGATTTACACACACTACACAGCTGGCTATGTGACAAA 3420
Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160
Db 3421 GAATTAGAGTACTTCCAGAACCGATAAGGTATGGATGAGATCGGAGAAACGGAAGGA 3480
Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCTGGACAGCGTGAATTTACTCTTATGGAGGA 3522

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RESULT 5  
AAS00565  
ID AAS00565 standard; DNA; 3522 BP.

XX AAS00565;

XX 14-MAY-2001 (first entry)

XX B. thuringiensis toxin gene 81IA (cryIa).

XX Toxin gene 81IA; cryIa; cutworm; pesticide; corn; soybean; canola;

KW Agrotis ipsilon; Agrotis malefida; Porasagrotis gypaetiana; sunflower;  
 KW Xylomyges curialis; Tribe Agrotini; Feltia jaculifera; Euxoa sp.; ds;  
 KW cotton.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..3522  
 FT CDS /\*tag= a  
 FT /product= "B. thuringiensis toxin 81A (CryIa)"  
 XX  
 PN WO200113731-A1.  
 XX  
 XX 01-MAR-2001.  
 XX  
 XX 23-AUG-2000; 2000WO-US23156.  
 XX  
 XX 23-AUG-1999; 99US-0150319.  
 XX  
 XX (MYCO ) MYCOGEN CORP.  
 XX  
 XX Stockhoff BA, Conlan C;  
 XX  
 XX WPI: 2001-211270/21.  
 XX P-PSDB; AAU00533.  
 XX  
 XX Controlling outworm pests especially black outworm comprises contacting  
 PT the pest with crystal protein CryIF toxin -  
 XX  
 XX Example 5; Page 42-43; 52pp; English.  
 XX  
 XX The sequence represents the native polynucleotide of the wild-type, full  
 CC length bacillus thuringiensis toxin gene 81A (cryIa). Full-length,  
 CC truncated and chimeric CryIF genes and proteins can be used for  
 CC controlling outworm pests, by contacting the pest with a Bacillus  
 CC thuringiensis toxin comprising a pesticidal portion of a CryIF toxin.  
 CC These genes and proteins are useful for controlling outworm pests such as  
 CC Agrotis ipsilon, Agrotis malefida, Porasagrotis gypaetiana, Xylomyges  
 CC curialis, members of the Tribe Agrotini, Feltia jaculifera, Euxoa  
 CC messeria, Euxoa scandens, Euxoa auxiliaris, Euxoa detersa, Euxoa  
 CC tessellata, Euxoa ochragaster and Peridroma saucia in plants such as  
 CC corn, sunflower, soybean, canola and cotton. The plants are transformed  
 CC with a polynucleotide encoding a Cry IF protein such that the transformed  
 CC plant cells express pesticidal proteins in tissues consumed by the target  
 CC pests.  
 XX  
 XX Sequence 3522 BP; 1156 A; 589 C; 782 G; 995 T; 0 other;

## Alignment Scores:

Prod. No.: 0 Length: 3522  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00 Conservative: 0  
 Best Local Similarity: 100.00 Mismatches: 0  
 Query Match: 100.00 Indels: 0  
 DB: 22 Gaps: 0

US-09-837-961-8 (1-1174) x AAS00565 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
 DB 1 ATGGAGAAATATATCAAAATCAATGCGTACCTTACAAATGTTTAAATATCTGGAAGA 60  
 QY 21 GluIleLeuAsnGluAluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 DB 61 GAAATATTAATGAAGAAGAAGTACTGGCAGATTACCGTTAGATATATCTTATCGCTT 120  
 QY 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 DB 121 ACACGTTTCCTTTGAGTGAATTTGTCCAGGTGTCGGAGTTGCGTTTGGATTATTGAT 180  
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIleGluGln 80  
 DB 181 TTAATATGGGGTTTATTAACCTCTCTGATGGAGCTTATCTTTTACAGATTGACAA 240

QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 DB 241 TTGATTGAGCAACAATAGAAACATTGGAAGGAAACCGGCAATTACTACTACGAGGG 300  
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 DB 301 TTACAGATAGCTATGAAATTTATATTGAAGCAGCTAAGAGAGTGGGAGCAAAATCCCTAAT 360  
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140  
 DB 361 AATGCACAATTAAGGAGAGATGCGTATTTCGATTTCCTAATACAGACGACGCTTAAATA 420  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTrpVal 160  
 DB 421 ACAGCAATAAATAATTTTACACTTACAAAGTTTGAATCCCTCTTTTATCGGCTATGTT 480  
 QY 161 GlnAlaIleAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 DB 481 CAAGCGGCAATTTACATTTATCACTATTAGAGACCTGTATCGTTTGGGAGGGTTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 DB 541 GGAATGATATAGCTACTGTTAATCAATATATAATAGATTATAAATCTTATTATCATA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 DB 601 TATACGAACATTTGTTGGACACATCAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660  
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 DB 661 ACTCGACATGGGCAAGATCAATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 DB 721 ATCGTTGCTCTTTTCCGAATAGAGATGTTAGAACAATATCAAAATTCGAAGCTATCCCAA 780  
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 DB 781 TTACAGAGGAATTTATACAGTTTCAAGTTTCAAGATTTCCAGTTTCTGCTAATAATA 840  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
 DB 841 CCTAATGTTTAAATAGSGCGAATTTGGAGTTAGACCGCCCATCTTATGGAGCTTTATG 900  
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
 DB 901 AATCTTTTGTGTAACGTCGACAGACCTGTAGAAGTCAAACTGTGCGGAGGACACTTA 960  
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 DB 961 GTTAGTTCACGAAATACGCTGTTAAACCGTATAAATTTCCCTAGTTACGGGGCTCTCAAT 1020  
 QY 341 ProGlyGlyAlaIleThrPheAlaAspClnAspProArgProPheTyrArgThrLeuSer 360  
 DB 1021 CCTGTGGCGCCATTGGAATTCAGATGAGGATCCAGCTCTTTTATCGGACATTATCA 1080  
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 DB 1081 GATCCTGTTTGTCCGAGGAGGATTTGGGAATCCTCATTTATGTTAGTGGGCTTAGGGGA 1140  
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgSerGlyThrIle 400  
 DB 1141 GTAGCATTTCAACAACTGGTACGAACACACACCCGAACTTTAGAAATAGTGGACCATTA 1200  
 QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTrpSer 420  
 DB 1201 GATTCCTAGATGAATCCCACTCAGATAAATAGTGGGCAACCTTGGATGATTATAGT 1260  
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
 DB 1261 CATGTATTAAATCATGTTACATTTGTACGATGGCCAGGTGAGATTTTCAGGAAGTGATTCA 1320

QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
|||||  
Db 1321 TGGAGAGCTCCAATGTTTCTTGAGCGCACCGTAGTGCAACCCCTACAAATACAATTGAT 1380  
  
QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
|||||  
Db 1381 CCGGAGAGGATTACTCAATACCATGTGTAAAGACACATACACTTCAGTCAGGTACTACT 1440  
  
QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
|||||  
Db 1441 GTGTAAAGAGGCCCGGTTTACGGGAGGAGATATCTTCGACGACACAGTGGAGGACCA 1500  
  
QY 501 PheAlaTyThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyArgAlaArgIle 520  
|||||  
Db 1501 TTTGCTTACTATTGTTAAATAAATGGCAATTACCCCAAGGTATCGTGCAGAAATA 1560  
  
QY 521 ArgTyAlaSerThrThrAsnLeuArgIleTyValThrValAlaGlyGluArgIlePhe 540  
|||||  
Db 1561 CGCTATGCTCTACTACAAATCTAAGAAATTTACGTAAACGGTTTCAGGTTCAACGGATTTT 1620  
  
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
|||||  
Db 1621 GCTGTCAATTTACAAACAAATGATACCGGTGACCCATTAACATTCOAATCTTTTAT 1680  
  
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
|||||  
Db 1681 TACGCAACATTAATPACAGCTTTTACATTCCTCCAAATGAGCAGAGTAGTTTCACAGTAGT 1740  
  
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyIleAspArgPheGluLeuIleProVal 500  
|||||  
Db 1741 GCTGATCTTTTAGTTACAGGAATGAGTTTATATAGACAGATTTGAAATGATTCACGTT 1800  
  
QY 601 ThrAlaThrPheGluAlaGluTyArgLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
|||||  
Db 1801 ACTGCAACATTTGAGCAGATATCATTTAGAAAGGACACANAAGCGGTGATCGCGTG 1860  
  
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyHisIleAspGln 640  
|||||  
Db 1861 TTTACTTCTATAAACCAATAGGGATAAAACAGATGTGACGGATATCATATTGATCAA 1920  
  
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGlnLeu 560  
|||||  
Db 1921 GTATCCAAITTAGTGGAATGTTTATCAGATGAATTTGTCTGGATGAAAGCGAAATG 1980  
  
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
|||||  
Db 1981 TCCGAGAAAGTCAACATCGCAAGCGCTCAGTGATGAGCGGAATTTACTTCAAGATCCA 2040  
  
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyTrpArgLysSerThrAspIleThr 700  
|||||  
Db 2041 AACTTCAAGGCATCAATAGGCAACTAGACCGTGTGTTGGAGAGGAAGTACGGATATTACC 2100  
  
QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyValThrLeuProGlyThrPheAsp 720  
|||||  
Db 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAATTAATGTCACACTACCGAGTACCTTTGAT 2160  
  
QY 721 GluCysTyProThrTyLeuTyGlnLysIleAspGluSerLysLeuLysProTyThr 740  
|||||  
Db 2161 GAGTGTCTATCCAACTATTATATCAAAAAATAGATGATGATGAGTAAATTAACCCCTACT 2220  
  
QY 741 ArgTyGlnLeuArgGlyTyIleGluAspSerGlnAspLeuGluIleTyLeuIleArg 760  
|||||  
Db 2221 CGTTATCAATTAAGAGGTATATCGAGATATGCAAGACTTAGAAATCTATTGATCCGC 2280  
  
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyProLeuSer 780  
|||||  
Db 2281 TATATGCAAAACAGCAACAGTAGTAATGTGTAGTACCGGTTCTTTATGCGCGCTTCA 2340  
  
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800  
|||||  
Db 2341 GTCCAAAGTCCAAATCAGAAAGTGGAGAACCGAATCATCGCGCCACACCTTGAATGG 2400  
  
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820  
|||||

Db 2401 AATCTGATCTAGATTGTTCTCGACAGACGGGAAAAATGTGCATCATCTTCGCATCAT 2460  
  
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
|||||  
Db 2461 TTTCTCTTGACATTCATGTTGATGTACAGACTTAAATGAGACTTAGATGTATGGGTG 2520  
  
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
|||||  
Db 2521 ATATTCAAGATTAAACGCAAGATGCCATGCAAGACTTAGGAAATCTAGAGTTTCTCGAA 2580  
  
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880  
|||||  
Db 2581 GAGAAACCATTTAGTCGGGAGACACTAGTCTCGTGTGAAAGAGCAGAAAAATGGACA 2640  
  
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyLysGluAlaLysGluSer 900  
|||||  
Db 2641 GATAAACCTGAAAAATTTGGAATTTGGAACAAATATTGTTTATAAAGAGCAAAAGAACT 2700  
  
QY 901 ValAspAlaLeuPheValAsnSerGlnTyArgPheGlnLeuGlnAlaAspThrAsnIleAla 920  
|||||  
Db 2701 GTAGATGCTTTTATTGTAACCTCTCAATATGATCAATTAACAAGCGGATACGAAATATTGCC 2760  
  
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyLeuProGluLeu 940  
|||||  
Db 2761 ATGATTCAATGCGCAGATAAACGTGTTTCATACAAITCGGSAAGCGTATCTTCCAGATTA 2820  
  
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
|||||  
Db 2821 TCTGTGATTCGGGTGTAATGTAGACATTTTCGAAGAATTTAAAGGGCGTATTTCAC 2880  
  
QY 961 AlaPhePheLeuTyAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
|||||  
Db 2881 GCAATCTTCCATATATGATCGGAGAAATGTCATTAACACGGTGATTTCAATATGGCTTA 2940  
  
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000  
|||||  
Db 2941 TCATCTGCAAGCTGCAAGGGCATGTAGATGTAGAAGAACAAACACCCGTCGGTTC 3000  
  
QY 1001 LeuValValProGluTyTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
|||||  
Db 3001 CTTGTGTGTCGGAATGGGAAGCAGAAAGTGTACAGAAGTTCGTCGTCTCGGGTCTG 3060  
  
QY 1021 GlyTyIleLeuArgValThrAlaTyLysGluGlyTyArgGluGlyCysValThrIle 1040  
|||||  
Db 3061 GGTATATCTTCTGTCACCGGTACAGAGGAGGATATGAGAGAGTTTGGTAACCAT 3120  
  
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
|||||  
Db 3121 CATGAGATCGAGAACATACAGACGAAGTGAAGTTTACCACTGCGTAGAGAGGAAGTC 3180  
  
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyThrAlaAsnGlnGluGluTyArgGly 1080  
|||||  
Db 3181 TATCCAAACACACGTAACGTGTAATGATATATCTGCAAAATCAAGAAGAAATACGGGGT 3240  
  
QY 1081 AlaTyThrSerArgAsnArgGlyTyArgPheGluTyArgGlySerAsnSerSerValPro 1100  
|||||  
Db 3241 CGGTACACTTCCGTAAATCGTGATATGACGAAACTTTATGGAAGCAATTCITCTGTACCA 3300  
  
QY 1101 AlaAspTyAlaSerValTyGluLysSerTyThrAspGlyArgArgAspAsnPro 1120  
|||||  
Db 3301 GCTGATTATGCTCAGTCTATGAGAAAAATCGTATACAGATGGACGAGAGACAACTCT 3360  
  
QY 1121 CysGluSerAsnArgGlyTyArgAspTyThrProLeuProAlaGlyTyValThrLys 1140  
|||||  
Db 3361 TGTGAATCTAACAGAGGATATGGGATTTACACACACTACCGACTGGCTGTATGTGACAAA 3420  
  
QY 1141 GluLeuGluTyThrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGly 1160  
|||||  
Db 3421 GAATTAGAGTACTTCCCAAGAACCGATAAGGTATGGATTGATTCGGAGAAACCGAAGGA 3480  
  
QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174  
|||||

Db 3481 ACATTCATCGTGACACGCTGGGAATTAACCTTATGGAGGAA 3522

# RESULT 6

AAQ14648  
ID AAQ14648 standard; DNA; 4020 BP.

XX AC AAQ14648;

XX DT 31-JAN-1992 (first entry)  
XX DE cryIF gene.

XX KW Insecticide; Lepidoptera control; ss.  
XX OS Bacillus thuringiensis.

XX FH Key Location/Qualifiers  
XX FT CDS 478..4002  
XX FT RBS /\*tag= a  
XX FT RBS 467..471  
XX FT RBS /\*tag= b  
XX PN WO9116434-A.  
XX PD 31-OCT-1991.  
XX PF 15-APR-1991; 91WO-US02560.  
XX PR 16-APR-1990; 90US-0510327.  
XX PA (ECOG-) ECOGEN INC.  
XX PI Gawron-Burke CM, Chambers JA, Gonzalez JM;  
XX DR WPI; 1991-339822/46.  
XX DR P-PSDB; AAR14856.  
XX PT Purifying and isolating CRY-I type genes - from novel *Bacillus*  
XX PT thuringiensis strain as insecticides  
XX PS Claim 1; Fig 1A-E; 100pp; English.  
XX SS The sequence is that of the cryIF gene which was isolated from  
XX CC *Bacillus thuringiensis* strains ES6345 and ES6346 obtd. from a maize  
XX CC grain dust sample. The toxin produced by the cryIF gene can be used  
XX CC in insecticide compsns. to control lepidoptera, esp. *Ostrinia*  
XX CC *nubilalis*, *Spodoptera exigua*, and *Plutella xylostella*. See also  
XX CC AAQ14649.  
XX SQ Sequence 4020 BP; 1349 A; 636 C; 870 G; 1165 T; 0 other;

## Alignment Scores:

Pred. No.: 0 Length: 4020  
Score: 6244.00 Matches: 1174  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-837-961-8 (1-1174) x AAQ14648 (1-4020)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
Db 478 ATGGAGAATAATATCAAAATCAATCGGTACCTTACAAATGTTTAAATAATCCTGAAGTA 537  
Qy 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
Db 538 GAAATATTAATGAAGAAGAAGTACTGGCAGATTACCGTTAGATATATCCTTATCGCTT 597  
Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaLapheGlyLeuPheAsp 60  
Db 598 ACACGTTCCCTTTGAGTGAATTTGTTCCAGAGTGGAGGTTGGCTTGGATTATTGAT 657

Qy 61 LeuIleTyrGlyPheIleThrProSerAspTyrPheLeuPheLeuLeuGlnIleGln 80  
Db 658 TTAATATGGGTTTATAACCTCTCTGATGGAGCTTATTTCTTTACAGATTGAACA 717  
Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100  
Db 718 TTGATTTGACRAAGAATAGAAACATTTGAAAGGACCGGCAATTACTACATTACGAGG 777  
Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrGluAlaAsnProAsn 120  
Db 778 TTAGCAGATAGCTATGCAATTTATATTGAACACTAAGAGAGTGGAAAGCAATCCTAAT 837  
Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140  
Db 838 AATGCACAATTAAGGGAAGATGTGCGTATTCGATTGTGTAATACAGACGACGCTTTAATA 897  
Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
Db 898 ACAGCAATAAATAATTTTACACTTACAAGTTTTGAAATCCCTCTTTATCGGTCTATGTT 957  
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr 180  
Db 958 CAAGCGGGAATTTACATTTATCACTATTAGAGAGCGCTGTATCGTTTGGCAGGTTGG 1017  
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuLeuLeuLeuHisArg 200  
Db 1018 GGACTGGATATAGCTACTGTTAATAATCATTAATAGATTAAATAAATCTTTATTCTAGA 1077  
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
Db 1078 TATACGAACATTTGTCACACATACAAATCAAGGATTAGAAACTTAAAGAGGTACTAAT 1137  
Qy 221 ThrArgGlnTyrPheAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240  
Db 1138 ACTCGACAATGGCAAGATTCAATCAGTTTAGAGAGAGATTTAAACACTTACTGTATTAGAT 1197  
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
Db 1198 ATCGTGTCTTTTCCGAACCTACCATGTTAGAACATATCCAAATTCAAACGTCATCCCAA 1257  
Qy 261 LeuThrArgGluIleTyrThrSerValIleGluAspSerProValSerAlaAsnIle 280  
Db 1258 TTAACAAGGGAATTTATACAGTTTCAGTAATTTAGAGATTTCCAGTTTCTGCTAATA 1317  
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
Db 1318 CCTAATGTGTTTAAATAGGCGGAATTTGGAGTAGACCGCCCATCTTATGGACTTTATG 1377  
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTyrGlyGlyHisLeu 320  
Db 1378 AATCTTGTGTTGTAACCTGCAGAGACTGTTAGAACTCAAACTGTGTGGGAGGACACTTA 1437  
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
Db 1438 GTTAGTTTACGAATAACCGCTGTACCGTATAAAATTTCCCTAGTAGCGGCTTCTCAAT 1497  
Qy 341 ProGlyGlyValIleTyrIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
Db 1498 CTGTGTGGCGCCATTGGATTGCAGATGAGGATCCACGCTCTTTTATCGGACATTATCA 1557  
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
Db 1558 GATCTGTTTTTGTCCGAGGAGGATTTGGGAATCTCATATTATGTACTGGGCTTAGGSGA 1617  
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
Db 1618 GTAGCATTTCAACAACCTGGTACGAACCCACACCCCAACATTTAGAAATAGTGGGACATA 1677  
Qy 401 AspSerLeuAspGluIleProProGlnAsnSerGlyValAlaProTyrAsnAspTyrSer 420  
Db 1678 GATTCTCTAGATGAATCCCACTCAGGATAATAGTGGGACCTTGGGAATATTAGT 1737  
Qy 421 HisValLeuAsnHisValThrPheValArgTyrProGlyGluIleSerGlySerAspSer 440



Db 1738 CATGATTAATCATGTTACATTTGTACGATGCCAGGTGAGATTTTCAGAGATGATCA 1797  
 QY 441 TTPArgAlaProMetPheSerThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 Db 1798 TGGAGAGCTCCAATGTTTCTTGGACGACCGTAGTGCACACCCCTACAANTGAT 1857  
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
 Db 1858 CCGAGAGAGATTACTCAAAATACCAATCGTAAAGACACATACACTTCAGTCAGGTACT 1917  
 QY 481 ValValArgGlyProGlyPheThrGlyAspIleLeuArgThrSerGlyGlyPro 500  
 Db 1918 GTTGTAGAGGCCCGGTTTCGGGAGAGATATCTTCGACGACACAGTGGAGACCA 1977  
 QY 501 PheAlaThrIleValAsnIleAsnGlyGlnLeuProGlnArgThrArgAlaArgIle 520  
 Db 1978 TTTGCTTATACTATGTTATATATAATGAGCAATTCACCCAAAGGTATCGTGCAGAATA 2037  
 QY 521 ArgTyraLaserThrAsnLeuArgIleThrValThrValAlaGlyGluArgIlePhe 540  
 Db 2038 CGCTATGCCCTACTACAAATCTAAGAAATTTACGTACGGTTGCAGGTGAACGGATTTT 2097  
 QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
 Db 2098 GCTGGTCAATTTAAACAAACAAATGATACCGGTGACCCATTAACTTCCAAATCTTTAGT 2157  
 QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
 Db 2158 TACCGCACTATTAAACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTTCACAGTAGT 2217  
 QY 581 AlaAspThrPheSerSerGlyAsnGluValTyraIleAspArgPheGluLeuIleProVal 600  
 Db 2218 GCTGATACTTTTACTTCAGGGAATGAAGTTTATATACACAGATTTTGAATTTGATTCAGTT 2277  
 QY 601 ThrAlaThrPheGluAlaGluTyraPheLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
 Db 2278 ACTGCAACATTTGAGGAGAAATAGTTTAAAGAGACAAAGGCGGTGAATGCGCGTG 2337  
 QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyraIleAspGln 640  
 Db 2338 TTTACTTCTATAACCAATAGGATGAACACAGATGTGACGGATTATCATATGTATCAA 2397  
 QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
 Db 2398 GTATCCCAATTTAGTGGATTGTTTATCATGAAATTTGCTGGATGAACGCGAGAATTG 2457  
 QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680  
 Db 2458 TCCGAGAACTCAACATGCGACGGACTCACTGATGAGCGGAATTTACTTCAAGATCCA 2517  
 QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700  
 Db 2518 AACTTCAAGGCAATCAATAGCAACTAGACCGTGGTAGGAGGAAGTACGGATATATACC 2577  
 QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyraValThrLeuProGlyThrPheAsp 720  
 Db 2578 ATCCAAAGAGAGATGAGTATTCAAGAAATTTATGTACACTACCCAGGTACCTTTGAT 2637  
 QY 721 GluCysTyraProThrTyraLysGlnLysIleAspGluSerLysLeuLysProTyraThr 740  
 Db 2638 GAGTGTATCCCAACGATTTTATATCAAAAAATAGATGAGTCGAAATTTAAACCCATACT 2697  
 QY 741 ArgTyraGlnLeuArgGlyTyraIleGluAspSerGlnAspLeuGluIleTyraLeuIleArg 760  
 Db 2698 CGTTATCAATTAAGAGGTATATCGAGGATAGTCAAGACTTAGAAATCTATTTGATCCGC 2757  
 QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlnGlyThrGlySerLeuTrpProLeuSer 780  
 Db 2758 TATATGCAAAACACGAAACAGTAAATGCTAGGTACGGTTCTTTATGCGCCCTTCA 2817  
 QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800

Db 2818 GTCCAAAGTCCCAATCAGAAAGTGTGGAGAACCGAATCGATGCGCCGCCACACCTTGAATGG 2877  
 QY 801 AsnProAspLeuAspCysSerCysArgaspGlyGluLysCysAlaHisHisSerHisHis 820  
 Db 2878 AATCTGATCTAGATTGTCTTCGACAGACGGGAAAAAATGTGCACATCATTCGCATCAT 2937  
 QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
 Db 2938 TTTCTCTTGGACATTTGATGTTGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG 2997  
 QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
 Db 2998 ATATTCAAGATTAAAGACGCAAGATGCCATGCAACACTAGGAAATCTAGAGTTTCTCGAA 3057  
 QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysTrpArg 880  
 Db 3058 GAGAAACCAATTTAGTTCGGGAGACACTAGCTGTGTGAAGAGACGAGAAAAAATGGAGA 3117  
 QY 881 AspLysArgGluLysLeuGluLeuThrAsnIleValTyraLysGluAlaLysGluSer 900  
 Db 3118 GATAACCTGAAAATTCGAATTTGGAACAAATATTGTTATAAGAGACCAAAATCT 3177  
 QY 901 ValAspAlaLeuPheValAsnSerGlnTyraPheGlnLeuGlnAlaAspThrAsnIleAla 920  
 Db 3178 GTAGATGCTTTTATTTGTAACCTCTCAATGATCAATTACAGCGGATACGAATATTGCC 3237  
 QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyraLeuProGluLeu 940  
 Db 3238 ATGATTTCATCGCGCAGATAAACCTGTTTCATAGAATTCGGAAGCGTATCTTCCAGAGTTA 3297  
 QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
 Db 3298 TCTGTGATTCCGGGTGTAATGTAGACATTTTCGAAGAATTTAAAGGCGGTATTTTCTACT 3357  
 QY 961 AlaPheLeuTyraPheAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
 Db 3358 GCATCTTCTATATGATCGGAGAAATGTCATTAACACGGTGATTTCAATATGGCTTA 3417  
 QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluAsnAsnHisArgSerVal 1000  
 Db 3418 TCATGCTGGAACGTGAAGGCGATGTAGATGTAGAAGAACAAACACACCGTTCCGTC 3477  
 QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
 Db 3478 CTGTGTTTCCGGAATGGGAGACAGAGTGTACAGAAAGTTTCGTGTCTGTCGGGTGCT 3537  
 QY 1021 GlyTyraIleLeuArgValThrAlaTyraLysGluGlyTyraGlyGlyCysValThrIle 1040  
 Db 3538 GGCATATCTTCTGTCACACGTCACAGGAGGAGGATATGAGAGAGTTGCGTAACCAT 3597  
 QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
 Db 3598 CATGAGATCGAGAACATACAGCAACTGAAGTTTAGCACTGCGTAGAGAGAAAGTC 3657  
 QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyraThrAlaAsnGlnGluGluTyraGly 1080  
 Db 3658 TATCCAAACACACCGTAAACGTTAATGATATATCTGCAAAATCAGAGAAATPACGGGT 3717  
 QY 1081 AlaTyraThrSerArgAsnArgGlyTyraPheAspGluThrTyraGlySerAsnSerValPro 1100  
 Db 3718 GCGTACACTTCCGTAATCGTGGATATGCAAACTATGGAAGCAATTTCTTCTGTACCA 3777  
 QY 1101 AlaAspTyraLaserValTyraGluLysSerTyraThrAspGlyArgAspAsnPro 1120  
 Db 3778 GCTGATTTATCGCTCAGTCTATGAAGAAAAATCGTATACAGATGGCAGAGACAAATCCT 3837  
 QY 1121 CysGluSerAsnArgGlyTyraGlyAspTyraThrProLeuProAlaGlyTyraThrLys 1140  
 Db 3838 TGTGAATCTACAGAGGATATGGGATPACACACCACTACCACTGGCTATGTGTGACAAA 3897  
 QY 1141 GluLeuGluTyraPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160  
 Db 3898 GAATTAGAGTACTTCCAGAAACCGATAGGTATGGATTGAGATCGGAGAAACGGAAGA 3957



QY 1161 ThrPheLeValAspSerValGluLeuLeuLeuMetGluGlu 1174  
 Db 3958 ACATTTCATGCTGGACAGCTGGAATTACTCTTATGGAGGAA 3999

## RESULT 7

AA05270  
 ID AAT05270 standard; DNA; 3522 BP.

AC AAT05270;

XX 23-JUN-1996 (first entry)

XX CryIF toxin with limited codon rework coding sequence.

XX Delta endotoxin; crystal protein; chimeric toxin; codon rework;  
 KW insecticide; pesticide; Pseudomonas fluorescens;  
 KW biological control agent; transgenic plant; insect resistance;  
 KW disease resistance; crop improvement; protein engineering; ss.  
 OS Bacillus thuringiensis.

XX Key Location/Qualifiers

XX mat\_peptide 1..3522

XX /product= cryIF\_sequence\_with\_codon\_rework

XX /note= "plasmid pMYC243 sequence"

XX W09530753-A1.

XX 16-NOV-1995.

XX 05-MAY-1995; 95WO-US05431.

XX 06-MAY-1994; 94US-0239476.

XX (MYCO ) MYCOGEN CORP.

XX Schwab GE, Thompson M;

XX WPI; 1995-404120/51.

XX P-ESDB; AAR84735.

XX Nucleic acid encoding chimeric Bacillus thuringiensis

XX delta-endotoxin - providing increased expression in Pseudomonas,

XX esp. for control of lepidoptera pests.

XX Example 5: Page 45-47; 91pp; English.

XX The sequence represents the cryIF toxin sequence with codon rework,

XX engineered using oligonucleotide primers H, I, J and K (see

XX AAT05262-T05265), and present in plasmid pMYC2523. This codon

XX reworked sequence can be used in the construction of chimeric

XX toxins, which are expressed in Pseudomonas fluorescens better than

XX native delta endotoxins. Host cells expressing the chimeric gene

XX and producing chimeric toxin may be used in insecticide

XX compositions. Where the host cells are plant cells, the gene confers

XX insect resistance to the transformed plant.

XX Sequence 3522 BP; 1149 A; 600 C; 788 G; 985 T; 0 other;

## Alignment Scores:

Pred. No.: 0 Length: 3522

Score: 6238.00 Matches: 1173

Percent Similarity: 99.91% Conservative: 0

Best Local Similarity: 99.91% Mismatches: 1

Query Match: 99.90% Indels: 0

DB: 16 Gaps: 0

US-09-837-961-8 (1-1174) x AAT05270 (1-3522)

QY 1 MetGluAsnAsnIleGluAsnGluCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
 Db 1174

Db 1 ATGGAATAAATATTCAAATCAATGCGTACCTTCAATTTGTTAAATAATCTCCTGAAGTA 60  
 QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 Db 61 GAAATACTGACGAAGACGACGACGCGCTGCGCTGGACATCAGCCTTGAGCCTT 120  
 QY 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheasp 60  
 Db 121 ACACGTTTCCCTTTTGGTGAATTTGTTCCAGGTGTGGAGTTGCGTTTGGATTATTGAT 180  
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIleGluGln 80  
 Db 181 TTAATATGGGGTTTATTAACCTCTTCGATGGAGCTTATTTCITTTACAGATTGAACRA 240  
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100  
 Db 241 TTGATTGACAAAGAATAAGAAATTTGGAAGGAACCGGGCAATTAATACATTACGAGGG 300  
 QY 101 LeuAlaAspSerTyrGluIleThrLeuGluAlaLeuArgGluTrpGluAlaAsnProasn 120  
 Db 301 TTAGCAGATAGCTATGAAATTTATATTGAAGCACTAAGAGAGTGGGAAGCAAAATCCTAAT 360  
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
 Db 361 AATGCACAATTAAGGGAAGATGTCGTATTCGATTTGCTAATACAGACGACGCTTAAATA 420  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 Db 421 ACAGCAATAAATAATTTTACACTTACAGTTTGAATTTCCCTCTTTATCGTCTATGTT 480  
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 Db 481 CAAGCGCGAATTTACATTTATCACTATTAAAGACGCTGTATCGTTGGGCGAGGTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 Db 541 GGACTGGATATAGTACTCTCTTAATAATCATTAATAGATTAAATAATCTTATTATACA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 Db 601 TATACGAAACATTTGTTGGACATACATAATCAAGGATTAGAAAATTAAGAGGTACTAAT 660  
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 Db 661 ACTCGACAATGGCAAGATTCATCAGTTTAGAGAGATTAACTTACTTACTTATAGAT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 Db 721 ATCGTTGCTCTTTTCCGAACACGATGTAGAACAATATCCAAATCAACACGTCATCCCAA 780  
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 Db 781 TPACAGGGGAATTTATACAGTTTCAAGTANTGAGGATTCCTCCAGTTCTCTCTAATA 840  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetaspPheMet 300  
 Db 841 CCTAATGGTTTAAATAGGCGGAATTTGGAGTTAGACCCGCCCTCTTATGAGCAATTATG 900  
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
 Db 901 AATTCITTTGTTGTAACCTCAGAGACTGTTAGAAGTCAACGTCGTGGGAGGACACTTA 960  
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 Db 961 GTTAGTTTACGAAATACGCGTGGTAACCGTATAAAATTTCCCTAGTTACGGGGTCTTCAAT 1020  
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
 Db 1021 CCTGGTGGCGCCATTTGGATTGCAGATGAGGATCCACGCTCTTTTATTCGGGACATATCA 1080  
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValIleGlyLeuArgGly 380  
 Db 1081 GATCCTGTTTTGTCCGAGGAGATTGGGAATCTCATTAATGTTACTGGGGCTTTAGGGGA 1140

QY 381 ValAlaPheClnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
DB 1141 GTAGCATTTTCAACAACTGTCAGAACACACCCGAACTTTAGAAATAGTGGACCAT 1200  
QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
DB 1201 GATTCCTCTAGATGAATCCACCTCAGGATAATAGTGGGCACCTTGGAAATGATTAGT 1260  
QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
DB 1261 CATGTATTAAATCATGTTACATTTGACGATGGCCAGGTGAGATTTCCAGGAAGTGATTC 1320  
QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
DB 1321 TGGAGAGCTCCCAATGTTTCTTGGAGCACCGTAGTGCAACCCCTACAAATACAAATGAT 1380  
QY 461 ProGluArgIlePheGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
DB 1381 CCGGAGAGATTACTCAATACCATTTGGTAAAGACATACATTCAGTCAGGTACTACT 1440  
QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
DB 1441 GTTGTAAAGAGGCCCGGTTTACGGGAGGAGATATCTTCGACGACACAGTGGAGGACCA 1500  
QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
DB 1501 TTTGGCTTATACATTTGTTAATAATAATGGCAATTTACCCCAAAAGGTATCGTCAAGAATA 1560  
QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
DB 1561 CGCTATGCTCTACFACAAATCTAAGAATTTAGCTAACGGTTCGACGGTGAACGGATTTT 1620  
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
DB 1621 GCTGTGCAATTTAAACAAACAATGGATACCGGTGACCCATTCACATTCCAATCTTTAGT 1680  
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
DB 1681 TACGCAACTATTAAATACAGCTTTTACATTTCCCAATGACGACAGTAGTATTTCACAGTAGT 1740  
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
DB 1741 GCTGATACATTTTAGTTCAGGAGATGAGTTTATATAGACAGATTTGAATGATTCAGTT 1800  
QY 601 ThrAlaThrPheClnAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
DB 1801 ACTGCAACATTTGACGACAGATATGATTTAGAAAGACACAAAGCGGTGAATGCGCTG 1860  
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
DB 1861 TTTACTTCTTATAAACCAATAGGGATAAAAGGGATGTGACGAGTATCATATTGATCAA 1920  
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
DB 1921 GRATCCAATTTAGTGATTTGTTATCAGATGAAATTTGTCTGTGATAAAGCGAGAAATG 1980  
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680  
DB 1981 TCCGAGAAAGTCAACATCGGAGGACATCAGTGATGACCGGAATTTACTTCAAGATCCA 2040  
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700  
DB 2041 AACTTCAAGAGGATCAATAGGCAACTAGACCGTGGTGGAGAGGAAGTACGGATATTACC 2100  
QY 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
DB 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAAAATATGTACACACTACCGAGGTACCTTTGAT 2160  
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
DB 2161 GAGTGCTATCCAACTGATTTATATCAAAAAATAGATGAGTCGAAATTTAAACCCCTATACT 2220

QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
DB 2221 CGTTATCAANTTAGAGGTTATATCGAGGATAGTCAAGACTTAGAAATCTATTGATCCGC 2280  
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780  
DB 2281 TATAATGCAAAACACGAAACAGTAATGTCTAGGTACGGTCTTTTATGCCGCTTCA 2340  
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800  
DB 2341 GTCCAAAGTCCAATCGAAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTGAATGG 2400  
QY 801 AspProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820  
DB 2401 AATCCYGAICTAGATTGTTCTCTCAGAGACGGGAAAAATGTGCACATCATTCGCATCAT 2460  
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
DB 2461 TTTCTCCTTGGACATTTGATTTGGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG 2520  
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
DB 2521 ATATTCAAGATTAAAGACGCAAGATGCCATGCAAGACTTAGGAAATCTAGAGTTTCTCGAA 2580  
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880  
DB 2581 GAGAAACCATTTAGTCGGGAGGACACTAGCTCGTGTGAAGACGACAGAAAAATGGAGA 2640  
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900  
DB 2641 GATAAACGTTGAAAAATTTGGAATTTGAAACAAATATTGTTTATAAGAGGCAAAAGATCT 2700  
QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920  
DB 2701 GTAGATGCTTTATTGTTAACTCTCAATATGATCAATTAACAGCGGATAGAAATTTGCC 2760  
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
DB 2761 ATGATTTCATCGCGCAGATTAACGTTTCATAGATTTCCGGAACGCTATCTTCCAGAGTTA 2820  
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
DB 2821 TCTGTGATTTCCGGGTATAATGTAGACATTTTCGAAAGATTAAGAGGCGCTATTTTCACT 2880  
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
DB 2881 GCATCTTCTTATGATGCGAGAAATGTCATTAACACGGTGATTTCAATAATGCTTA 2940  
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000  
DB 2941 TCATGCTGCAACGTTGAAAGGCGCATGTAGATGTAGAAGACAAACAAACCCGTTCCGGTC 3000  
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
DB 3001 CTGTGTTGTTCCGGAAATGGGAAGCAGAGTGTCAAGAAAGTTCGTCTGTCTCGGTCGT 3060  
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGlyGlyTyrGlyGluGlyCysValThrIle 1040  
DB 3061 GCGTATATCTTCCGTGTCACGCTACAAGGAGGATATGGAGAGGTTTCGCTACACCAT 3120  
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
DB 3121 CATGAGATCGAACAATACACACGACTGAACTTAGCACTGCGTAGAAGAGGAAGTC 3180  
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyGly 1080  
DB 3181 TATCCAAACAAACACGTAACGTTAATGATTATCTGCAAACTCAAGAAATACGGGGT 3240  
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100  
DB 3241 GCGTACACTTCCGTAATCGTGATATGCAAACTTATGGAAGCAATTTCTTCTGTACCA 3300  
QY 1101 AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120

||||| 3301 GCTGATTATCGTCAGTCTATGAAGAAATCGTATACAGATGAGCAAGACATCCCT 3360  
 QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
 Db 3361 TGTGAATCTAACAGAGATATGGGATTACACACCCTACACAGCTGGCTATGTGACAAAA 3420  
 QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrPheGlyGluThrGluGly 1160  
 Db 3421 GAATTAGATACITCCAGAACCGATAGGTATGATGAGATCGGAGAAACGGAGGA 3480  
 QY 1161 ThrPheLeuValAspSerValGluLeuLeuLeuMetGluGlu 1174  
 Db 3481 ACATTTCGTCGACAGCGTGGAAATTAATCTCCTTATGGAGAA 3522  
 RESULT 8  
 ID AAT18722 standard; DNA; 3522 BP.  
 AC AAT18722;  
 DT 18-AUG-1996 (first entry)  
 DE Codon-reworked CryIF toxin gene from pMYC2243.  
 KW CryIF; crystal protein; chimeric toxin; protoxin; pMYC2243;  
 KW delta-endotoxin; codon usage; splice overlap extension;  
 KW mutagenesis; chimeric gene; fusion protein; Pseudomonas fluorescens;  
 KW CryIA(b); CryIA(c); synergy; Lepidoptera; insect;  
 KW biological control agent; transgenic plant; insect resistance;  
 KW crop improvement; ss.  
 OS Bacillus thuringiensis.  
 PN US5508264-A.  
 PD 16-APR-1996.  
 PF 06-DEC-1994; 94US-0349867.  
 PR 06-DEC-1994; 94US-0349867.  
 PA (MYCO ) MYCOGEN CORP.  
 PI Bradfisch GA, Schwab GE, Thompson M;  
 DR WPI; 1996-208745/21.  
 XX P-PSDB; AAR94914.  
 PT Compsn. for controlling lepidopteran pests - comprises CryIF and  
 XX CryIA(c) chimeric core toxin-contg. proteins.  
 PS Example 5; Column 53-56; 59pp; English.  
 CC This sequence encodes a Bacillus thuringiensis CryIF delta-  
 CC endotoxin. A gene from pMYC2047 has been subjected to splice  
 CC overlap extension to alter codons in a limited region in the cryIF  
 CC fragment to favor G or C in the wobble position, to improve  
 CC expression in Pseudomonas spp. Correct clones are identified by  
 CC PCR using primers P and Q (AAT18717-18), and the resulting clone is  
 CC pMYC2243. The cryIF fragment may be fused with cryIA(b) and/or  
 CC cryIA(c) fragments to give fusion proteins by recombinant DNA  
 CC methods. The resulting chimeric genes may be cloned in a  
 CC Pseudomonas fluorescens lactose-inducible strain to produce  
 CC chimeric toxins. The toxins, when combined in synergy, have  
 CC unexpected enhanced toxicity to lepidopteran pests.  
 CC fluorescens or B. thuringiensis cells expressing the genes may be  
 CC used as insect biological control agents, or transgenic plants  
 CC expressing the genes may become resistant to insect attack.  
 XX Sequence 3522 BP; 1150 A; 602 C; 785 G; 985 T; 0 other;  
 Alignment Scores:

Prod. No.: 0 Length: 3522  
 Score: 6237.00 Matches: 1173  
 Percent Similarity: 99.91% Conservative: 0  
 Best Local Similarity: 99.91% Mismatches: 1  
 Query Match: 99.89% Indels: 0  
 DB: 17 Gaps: 0  
 US-09-837-961-8 (1-1174) x AAT18722 (1-3522)  
 QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnProGluVal 20  
 Db 1 ATGGAAATAATATTCAAATCAATCGTACCTTACAATGTTTAATAATCTCTGAGTA 60  
 QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 Db 61 GAAATACCTGAACGAAGACGACGACCGCGCGCTCGCGTGGACATCAGCCCTGAGCCT 120  
 QY 41 ThrArgPheLeuSerGluPheValProGlyValIcIyValAlaPheGlyLeuPheAsp 60  
 Db 121 ACACGTTTCTTTTGAGTGAATTTGTCAGGTGTGGAGTTCGGTTTGGATTATTGAT 180  
 QY 61 LeuIleTyrPheIleThrProSerAspTyrSerLeuPheLeuGluIleGluGln 80  
 Db 181 TTAATATGGGTTTTTATACTCTCTCTGATGGAGCTTATCTTTTACAGATTGACAA 240  
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 Db 241 TTGATTGAGCAAGAATAAGAACATTGGAAAGAACCGGCAATTACTACATTACGAGG 300  
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrPheLeuAsnProAsn 120  
 Db 301 TTAGCAGATAGCTATGAAATTTATATTGAAGCCTTAAGAGAGTGGGAACAAATCTAAT 360  
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
 Db 361 AATGCACAATTAAGGGAAGATGTGGTATTCGATTGCTTAATACAGACCGCTTTAATA 420  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 Db 421 ACAGCAATAAATAATTTTACACTTACAGTTTGAATCCCTCTTTATCGGCTATGTT 480  
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr 180  
 Db 481 CARGCGCGAATTTACATTTATCATTATAGAGACGCTGTATCGTTGGCAGGCTTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 Db 541 GGACTGGATATAGCTACTGTTAATAATCATTTATAATAGATTAAATAATCTTATTCATA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 Db 601 TATACGAACATGTTTGGACACATACATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660  
 QY 221 ThrArgGlnTyrPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 Db 661 ACTCGACAATGGCAGATTCATCAATCAGTTTAGSAGANGATTACACTTACTCTATTAGT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 Db 721 ATCGTTGTCTCTTTTCCGAACATACATGTAGAATATCCAAATCAACACGTCATCCCAA 780  
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 Db 781 TTACAAGGGAAATTTATACAGTTCACTAATGAGGATTCCTCCAGTTCTTCGCTAATATA 840  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
 Db 841 CCTAATGTTTAAATAGGCGGAATTTGGAGTTAGACCGCCCATCTTATGGACTTTATG 900  
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTyrPheGlyHisLeu 320  
 Db 901 AATTCTTTTGTAACTGCAGAGACTGTTAGAACTCAAACTGCTGTGGGAGGACACTTA 960

QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
DB 961 GTTAGTTCAGAAATACGGCTGTAACCGTATAAATTCCTAGTTACGGGTCITCAAT 1020  
QY 341 ProGlyGlyAlaIleThrPheAlaAspGluAspProArgProPheThrArgThrLeuSer 360  
DB 1021 CCTGGTGGCGCCATTGGGATTCAGATGAGGATCCAGCTCTTTTATCGGACATTATCA 1080  
QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
DB 1081 GATCCTGTTTTCTCGAGAGGAGATTGGGAATCCATATGCTAGCTGGGCTTAGGGGA 1140  
QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
DB 1141 GTAGCATTTCAACAACTGGTACGACACACACCCGAACATTTAGAAATAGTGGACCAATA 1200  
QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
DB 1201 GATTCCTAGATGAATCCCACTCAGGATAATAGTGGGGCACCTTGGGAATGATTATAGT 1260  
QY 421 HisValLeuAsnHisValThrPheValArgTyrProGlyGluIleSerGlySerAspSer 440  
DB 1261 CATGTATTAAATCATCTTACATTGTACGATGCCAGGTGAGATTTACAGAGTGNATCA 1320  
QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
DB 1321 TGGAGAGCTCCAATGTTTTCTTGGACGCCCTAGTGCACCCCTACAAATACAATTGAT 1380  
QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
DB 1381 CCGGAGAGATTACCAATACCATTTGGTAAAGACACATACACTTCAGTCAGGTACTACT 1440  
QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
DB 1441 GTTGAAGAGGCCCGGGTTTACGGGAGGAGATATTCCTCGACGACACAGTGGAGGACCA 1500  
QY 501 PheAlaIleThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
DB 1501 TTTGGTTTACTATTGTTAAATAAATGGGCAATTTACCCCAAGGTATCGTGCAAGAATA 1560  
QY 521 ArgTyrAlaSerThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
DB 1561 CGCTATGCTCTACCAATCTAGAAATTTACGTTAAGCGTTGACGGTGAACGGATTTT 1620  
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
DB 1621 GCTGTGCAATTTAACAACAATATGATACCGGTGACCCATTAACATTCCTCAATTTTAGT 1680  
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
DB 1681 TACGCAACTATTAAATACAGCTTTTACATTCCTCAATGAGCCAGATAGTTTCACAGTAGT 1740  
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
DB 1741 GCTGATATTTTAGTTCAGGAATGAGTTTATATAGACAGATTGGAATTGATTCAGTT 1800  
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
DB 1801 ACTGCAACATTTGAAGCAGATATGATTTAGAAAGAGCACAAAAGCGGTGNAATCGCGTG 1860  
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
DB 1861 TTTACTTCTATAAACCAATAGGATAAAACAGATGTGACGGATATCAVATTGATCAAA 1920  
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
DB 1921 GTATCCAATTTAGTGGATGTTTATCAGATGAATTTTCTCGGATGAAAGCGAGAAATG 1980  
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
DB 1981 TCCGAGAAAGTCAACATGCGAGGACTCAGTGNATGAGCGGAATTTACTTCAAGATCCA 2040  
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700

DB 2041 AACTTCAAGGCATCATATAGGCACCTAGACCGTGGTGGAGAGAGTAGCAGGAATATACC 2100  
QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
DB 2101 ATCCAAGAGGAGATGACGTATTCAAGAAAAATTATGTACACACTACCAAGTACTTTGAT 2160  
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLysLeuLysProTyrThr 740  
DB 2161 GAGTGTATCCCAACGATTATATCAAAAAATAGATGAGTCGAAATATAAACCCCTACT 2220  
QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
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QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780  
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QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800  
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QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820  
DB 2401 AATCCTGATCTAGATGTTCTCGAGAGCGGGAAAAATGTGCACATCATTTCCGATCAT 2460  
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
DB 2461 TTCTCCTTGGACATGATGTTGGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG 2520  
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
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QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880  
DB 2581 GAGAAACCATTAGTCGGGGAACCACTAGCTCGTGTGAAAGAGCAGAGAAAAATGAGCA 2640  
QY 881 AspLysArgGluLysLeuGluLeuThrAsnIleValTyrLysGluAlaLysGluSer 900  
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DB 2701 GTAGATGCTTTATTGTTAAACTCTCAATGATCATTAATACAAAGCGGATACGAAATATGCC 2760  
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
DB 2761 ATGATTCATCGGCACATAAAGCTGTTTCATAGAATTCGGGAAGCGTATCTTCCAGATTA 2820  
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
DB 2821 TCTGTGATTCGGGTGTAATGTAGACATTTTCGAAGAAATTAAGAGGCGTATTTTCACT 2880  
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
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QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000  
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QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
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QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
DB 3061 GGCATATCTCTGTCGTCACAGCGTACAGGAGGATATGAGAGAGGTTCGCTAACCAT 3120  
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060

Db 3121 CATGAGATCGAGAACAAATACAGACGAAGTGAAGTTTACCAACTCGCTAGAGAGGAGTC 3180  
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 Db 3181 TATCCAAACACACCGGTAACTGTATGATATATCTGCAATCAAGAGATACGGGGT 3240  
 QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100  
 Db 3241 GCGTACACTTCCCGTAATCGTGGATATGACGAACCTTATGGAACCAATCTTCTGTACCA 3300  
 QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
 Db 3301 GCTGATTATCGGTCAGCTCTATGAGAAATCGTATACAGATGAGAGAGCAATCC 3360  
 QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
 Db 3361 TGTGAATCAACAGAGGATATGGGATATACACCACTACAGCTGGCTATGTGCAAAA 3420  
 QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160  
 Db 3421 GAATTAGAGTACTTCCAGAAACCGATAGGATATGATGATGATGATGATGATGATGAT 3480  
 QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174  
 Db 3481 ACATTATCGTGGACAGCGTGAATTAATCTCTTATCGAGGAA 3522  
 RESULT 9  
 AAT05250  
 ID AAT05250 standard; DNA; 3522 BP.  
 XX AC AAT05250;  
 XX DT 27-MAY-1996 (first entry)  
 DE CryIF/436 chimeric toxin coding sequence.  
 KW Delta endotoxin; crystal protein; chimeric toxin; insecticide;  
 KW pesticide; pseudomonas fluorescens; biological control agent;  
 KW transgenic plant; insect resistance; disease resistance;  
 KW crop improvement; protein engineering; ss.  
 XX OS Bacillus thuringiensis.  
 XX FH Key Location/Qualifiers  
 FT mat\_peptide 1..3522  
 FT /tag= a  
 FT /product= cryIF/436\_chimeric\_toxin  
 FT /note= "plasmid pMYC2254 sequence"  
 XX W09530753-A1.  
 XX PN 16-NOV-1995.  
 XX PD 05-MAY-1995; 95WO-US05431.  
 XX PF 06-MAY-1994; 94US-0239476.  
 XX PR (MYCO ) MYCOGEN CORP.  
 XX PA Schwab GE, Thompson M;  
 XX PI WPI; 1995-404120/51.  
 XX DR P-PSDB; AAR84732.  
 XX DT Nucleic acid encoding chimeric Bacillus thuringiensis  
 PT delta-endotoxin - providing increased expression in Pseudomonas,  
 PT esp. for control of lepidoptera pests.  
 XX Claim 10; Page 56-57; 91pp: English.  
 PS The sequence represents the cryIF/436 chimeric toxin  
 CC coding sequence of plasmid pMYC2254. The chimeric toxin is  
 CC expressed in Pseudomonas fluorescens better than native

CC delta endotoxins. Host cells expressing the chimeric gene and  
 CC producing chimeric toxin may be used in insecticide compositions.  
 CC Where the host cells are plant cells, the gene confers insect  
 CC resistance to the transformed plant.  
 XX Sequence 3522 BP; 1140 A; 606 C; 795 G; 981 T; 0 other;  
 SQ Alignment Scores:  
 Pred. NO.: 0 Length: 3522  
 Score: 6049.00 Matches: 1143  
 Percent Similarity: 97.79% Conservative: 5  
 Best Local Similarity: 97.36% Mismatches: 26  
 Query Match: 96.88% Indels: 0  
 DB: 16 Gaps: 0  
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 Db 1 ATGGAAATATATTCARAAATCAATCGTACCTTACAATTTGTTAAATATCTCGAGTA 60  
 QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 Db 61 GAAATACTGACGAAAGAACGACGACCGCGCGCTGGACATCAGCCTGAGCCT 120  
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 Db 121 ACACCTTTCCTTTTGGTGAATTTGTCAGGTGGGAGTGGCTTTGGATATTTGAT 180  
 QY 61 LeuIleTyrGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIleGluGln 80  
 Db 181 TTAATATGGGGTTTATAACTCTTCTGATGGAGCTATTTCTTTACAGATTGAACA 240  
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100  
 Db 241 TTGATTGACAAAGAAATAGAAACATTGGAAGAAACCGGCAATTAATACAGAGCGCTTAA 300  
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 Db 301 TTACAGATAGCTATGAATTTATTTAGAGACCTTAAGAGAGTGGAGAGCAATCTAAT 360  
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
 Db 361 AATGACAATTAAGGAGAGATGTGGTATTCGATTGCTAATACAGAGAGCGCTTAA 420  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 Db 421 ACAGCAATTAATAATTTTACACTTACAAGTTTGAATCCCTTTTATCGGCTATGTT 480  
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 Db 481 CAAGCGCGCAATTTACATTTATCACTATTAGAGAGCGCTGTATCGTTTGGCAGGTTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuLeuAsnLeuHisArg 200  
 Db 541 GGACTGGATATAGTACTCTTTAATATCAATTAATAGATTAATAAATCTTATTCATAGA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 Db 601 TATACGAACATTTGTTGGACACATACATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660  
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 Db 661 ACTCGACAATGGCAAGATTCAATCAGTTTAGAGAGATTTAAACACTTACTGTATTAGAT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 Db 721 ATCGTTGCTCTTTTCCGAACTACCATGTTAGAACAATATCCCAATTCACACGTCATCCAA 780  
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 Db 781 TTAACAAGGGAATTTATACAAGTTCAGTAAATGAGGATCTCCAGTTCTCCGATATATA 840

Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
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Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu 320  
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Qy 321 ValSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
Db 961 GTTAGCTTCAGCAAAATACCGCTGTGTACCGTATAAATTTCCCTAGTTACGGGCTTCAAT 1020  
Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
Db 1021 CCTGTGCGCCCATTTGGATTGCAGATGAGGATCCACGTCCTTTTATCGGACATTAICA 1080  
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
Db 1081 GATCCTGTTTTGTCGAGGAGGATTTGGGAATCCTCATATTATGTACTGGGGCTTAGGGGA 1140  
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
Db 1141 GTAGCATTTTCACAACATGTTGACAGACACACACCCGAAACATTTAGAAATAGTGGGACCATTA 1200  
Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
Db 1201 GATTCCTCAGATGAAATCCCACTCAGGATAATAGTGGGCACCTTGGAAATGATTATAGT 1260  
Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
Db 1261 CATGTATTAAATCATGTTTACATTTGTACGATGGCCAGGTGAGATTCAGGAAGTGATTAICA 1320  
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
Db 1321 TGGAGAGCTCCAAATGTTTCTTGACCGCACCGTAGTCAACCCCTACAAATACAAATGAT 1380  
Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
Db 1381 CCGGAGAGGATTACTCAAAATACCAATGTTGTAAGACACATACATTCAGTCAGGTACTACT 1440  
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
Db 1441 GTTGTAAAGGCGCGGTTTACGGGGAGAGATATCTTCGACGAAACAAGTGGAGGACCA 1500  
Qy 501 PheAlaTyrThrIleValAlaIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
Db 1501 TTGCTTATATTGTTAATAATAATGGCAATTTACCCCAAGGTATCGTCCAGATA 1560  
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyLeuArgIlePhe 540  
Db 1561 CGCTATGCTCTACTACAAATCTAAGAAATTTACGTAAACGGTTGACGGTGAACGGGATTTT 1620  
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
Db 1621 GCTGTCATTTTACAAACAATGAGTACCGGTACCGCATTAACATTCATCTTTTATG 1680  
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
Db 1681 TACGCAACTATTATACAGCTTTTACATTCCTCAATGACCCAGAGTAGTTTCACAGTAGT 1740  
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
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Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
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Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
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Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660

Db 1921 GFGTCCCAATTTAGTTACGTATTTATTCGGATGATTTTGTCTCGATCAAAAGCGAGATTG 1980  
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Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700  
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Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
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Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
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Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
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Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780  
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QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
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Db 3481 ACATTCATCGTGACAGCGTGAATTAATCTCTCTATGGAGAA 3522
RESULT 10
AAT18702
ID AAT18702 standard; DNA; 3522 BP.
XX AC AAT18702;
XX DT 18-AUG-1996 (first entry)
XX DE CryIF/436 chimeric toxin gene from pMYC2254.
XX KW CryIF; CryIA(c); CryIA(b); crystal protein; chimeric toxin;
XX KW protoxin; pMYC2254; delta-endotoxin; chimeric gene; fusion protein;
XX KW Pseudomonas fluorescens; synergy; Lepidoptera; insect;
XX KW biological control agent; transgenic plant; insect resistance;
XX KW crop improvement; ss.
XX OS Bacillus thuringiensis.
XX FH key Location/Qualifiers
XX FT mat_peptide 1..1803
XX FT /**tag= a
XX FT /note= "CryIF toxin gene fragment"
XX FT 1804..3444
XX FT /**tag= b
XX FT /note= "CryIA(c)/CryIA(b) 436 protoxin gene fragment"
XX US508264-A.
XX PN
XX XX 1..1803
XX PD 16-APR-1996.
XX PF 06-DEC-1994; 94US-0349867.
XX XX 06-DEC-1994; 94US-0349867.
XX XX (MYCO ) MYCOGEN CORP.
XX XX Bradfisch GA, Schwab GE, Thompson M;
XX XX WPI; 1996-208745/21.

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DR P-PSDB; AAR94908.
XX
PT Compsn. for controlling lepidopteran pests - comprises CryIF and
XX CryIA(c) chimeric core toxin-contg. proteins.
PS Claim 7; Column 71-74; 59pp; English.
XX
CC This sequence encodes a Bacillus thuringiensis chimeric CryIF/436
CC delta-endotoxin. The toxin contains a full toxin portion of cryIF
CC and a heterologous protoxin segment derived from cryIA(c)-cryIA(b)
CC toxin 436. The sequence is constructed by substitution of 436
CC protoxin module for the cryIA(b) protoxin fragment in pMYC2523
CC (AAT18723). The 436 protoxin sequence (AAR94911) consists of cryIA(c)
CC sequence except at the very C-terminus. Protoxin DNA is amplified
CC by PCR with primers F (AAT18708) and M (AAT18719), using plasmid
CC pMYC467 as a template. A 3-piece ligation is set up with SpeI-PvuII
CC toxin DNA and SpeI-BstEII vector DNA from pMYC2523 and PvuII-BstEII
CC PCR protoxin module DNA. Correct plasmids are identified by PCR
CC using primers F and G (AAT18709). The resulting chimeric gene may be
CC cloned in a Pseudomonas fluorescens lactose-inducible strain to
CC produce a chimeric toxin. The toxin, when combined with another
CC chimeric toxin in synergy, has unexpectedly enhanced toxicity to
CC lepidopteran pests. P. fluorescens or B. thuringiensis cells
CC expressing the gene may be used as an insect biological control
CC agent, or a transgenic plant expressing the gene may become resistant
CC to insect attack.
SQ Sequence 3522 BP; 1140 A; 606 C; 795 G; 981 T; 0 other;

Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6049.00 Matches: 1143
Percent Similarity: 97.79% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 26
Query Match: 96.88% Indels: 0
DB: 17 Gaps: 0

US-09-837-961-8 (1-1174) x AAT18702 (1-3522)
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Db 1 ATGGAAAATAATATTCAAAATCAATCGCTACCTTACAATGTTTAAATAATCCTGAAGTA 60
QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
Db 61 GAAATACTGACGAAGAAGACGACGACCGCCGCTGCGCTGACATCAGCCTGAGCCTT 120
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
Db 121 ACACGTTTCCITTTGAGTGAATTTCTCCAGGTGTGGAGTTGCGTTGGATTATTGAT 180
QY 61 LeuIleTyrGlyPheIleThrProSerAspTyrSerLeuPheLeuGluIleGluGln 80
Db 181 TTAATATGGGGTTTTATACTCCTTCTGATTGGAGCTTATTTCTTTACAGATTGAACA 240
QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100
Db 241 TTGATTGACCAAGAAATAGAAACATTGGAAAGGAAACCGGCAATTACTACATTAGAGGG 300
QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrGluAlaAsnProAsn 120
Db 301 TTAGCAGATAGCTATGAAATTTATATTGAAGCACTAAGAGAGTGGGAAGCAATCCTAAT 360
QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
Db 361 AATGCACAAATTAAGGGAAGATGTCGTATTTCGATTTCGTAATACAGACGACGCTTATA 420
QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
Db 421 ACAGCAATAATAATTTTACACTTACAAAGTTTGAATCCCTCTTTATCCGCTATGTT 480
QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr 180

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Db 481 CRAAGCGGGAATTTACATTTATACATATTAAAGACAGCGCTGTATCGTTGGCGAGGTTGG 540  
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
Db 541 GCAGTGGATATAGCTACTGTTAATAATCATATTAATAGATTAATAATCTTATTCATAGA 600  
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
Db 601 TATACGAACAATGTTTGGACATACATCAATCAAGGATTAGAAAACCTTAGAGGCTACTAAT 660  
Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
Db 661 ACTCGAATATGGCAAGATTCATACAGTTTGGAGAGATTTACACACTTACTGTATTAGAT 720  
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
Db 721 ATCGTTGCTCTTTTCCGAACTACGATGTTAGAACATATCCAAATTCACAGCTATCCCAA 780  
Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
Db 781 TTAACAAGGGAATTTATACAAAGTTCAGTAATAGGATTCTCCAGTTTCTGCTAATATA 840  
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
Db 841 CTTAATGGTTTTAATAGGCGGAATTTGGAGTAGACCGCCCACTTTATGGACTTTATG 900  
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
Db 901 AANTCTTTGTTGTAACTCAGAGACTGTTAGAGTCAAACTGTGTTGGGAGGACACTTA 960  
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
Db 961 GTTAGTTACGAATAACGGCTGGTACCGTATACCGTATAAAATTTCCCTAGTTACGGGCTCTCAAT 1020  
Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
Db 1021 CTTGTTGGCGCCCACTTGGATTCCAGATGAGGATCCACGTCCTTTTATCGGACATTATCA 1080  
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
Db 1081 GATCTGTTTTTGTCCGAGGAGATTGGGAATCCTCATTTATGTACTGGGCTTAGGGGA 1140  
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
Db 1141 GTAGCATTTCAACAACCTGGTACGACCAACACCCGCAACATTTAGAAATAGTGGACATA 1200  
Qy 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyValaProtrpAsnAspTyrSer 420  
Db 1201 GATTCCTAGATGAATCCCACTCAGGATATATAGTGGGCACCTTGGATGATTATAGT 1260  
Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
Db 1261 CATGTATTAAATCATGTTACATTTGTACCATGGCCAGGTGAGATTTTCAGGAAGTGATTCA 1320  
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
Db 1321 TGGAGAGTCCAAATGTTTCTTGGACGCCCTAGTGTAGCAACCCCTACAAATACAAATGAT 1380  
Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
Db 1381 CCGGAGAGATTACTCAATATACATCTGGTAAAGACATACACTTCAGTCAGGTACTACT 1440  
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
Db 1441 GTTGTAAAGAGGCCCGGGTTTACGGGAGGAGATATTTCTTCGACGAACAGTGGAGACCA 1500  
Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGluArgTyrArgAlaArgIle 520  
Db 1501 TTTGCTTATACATTATGTTTAAATAATAGGCAATTTACCCCAAGGTATCTGTCAGAATA 1560  
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
Db 1561 CCCTATGCCCTCTACTACAATCTAAGAAATTTACGTAACGGTTGCAGGTGAACGGATTTT 1620

Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
Db 1621 GCTGGTCAATTTTAAACAAAACATGGATACCGGTGACCATTAACATTCCTCAATCTTTAGT 1680  
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
Db 1681 TAGGCAACTATTAAATACAGCTTTTACATTTCCCAATGAGCCAGAGTAGTTTCACAGTAGGT 1740  
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Db 1741 GCTGATACCTTTAGTTTCAAGGAATGAAGTTTATATAGACAGATTGAAATTCATCCAGTT 1800  
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Db 1801 ACTGCAACATTTGAACAGAAATATGATTTAGAAAGAGACAAAAGCGGTGAATGGCGTG 1860  
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
Db 1861 TTTACTTCTATAAACCAATAGGGATAAANAACAGATGTGACGGATTATCATATCGATCGA 1920  
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Db 1921 GTGTCCAATTTAGTTTACGTATTATCGGATGAATTTTGTCTGGATGAAAAGCGAGAATTG 1980  
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
Db 1981 TCCGAAAGAGTCANACATCGAAGCGACTCAGTGATGAACGCAATTTACTCCAGGATTCA 2040  
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700  
Db 2041 AATTTCAAAGACATTAATAGGCAACCAACGCTGGTGGGCGGGAAGTACAGGATTAAC 2100  
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
Db 2101 ATCCAAGGAGGGGATGACGTATTTAAAGAAATTTAGTCACACTACAGTACCTTTGAT 2160  
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
Db 2161 GAGTGTCTTCCACATATTTGTTATCAAAAATTCGATGAATCAAAATTAAGAGCTTTACC 2220  
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
Db 2221 CGTTATCAATTAAGAGGTATATCGAAGATAGTCAAGACTTAGAAGATCTATTTAATTCGC 2280  
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780  
Db 2281 TACAATGCAAAACATGAAACAGTAAATGTGCCAGGTACGGGTTCCCTTATGGCGCTTTCA 2340  
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr 800  
Db 2341 GCCCAAGTCCATCGGAAGTGTGGAGAGCCGAATCGATGCGGCCACACCTTGATGG 2400  
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820  
Db 2401 AATCTGTACTTAGATTGTTCTGTAGGATGGAGAAAAGTGTGCCCATCATTCGCATCAT 2460  
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
Db 2461 TTCTCCTTAGACATTGATGTAGATGTACAGACTTAAATGAGGACCTAGGTGTATGGTG 2520  
Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
Db 2521 ATCTTTAAGATTAAAGCCAGATGGGCACGCAAGACTAGGGAATCTAGAGTTTCTCGAA 2580  
Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880  
Db 2581 GAGAAACCATTTAGTAGGAGAGCGGTAGCTCGTGTGAAAAGAGCGGAGAAAAATGAGCA 2640  
Qy 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900  
Db 2641 GACAAACGCTGAAAAATTTGGAATGGGAACCAATATCGTTTATAAAGAGGCAAAAGAACTCT 2700



QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGluLeuGlnAlaAspThrAsnIleAla 920  
 Db 2701 GTAGATGCTTTATTGTAACCTCAATATGATCAATACAGCGGATAGATATGCC 2760  
 QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
 Db 2761 ATGATTATGCGGCGATGAACGTGTTCATAGCATTCGAGAACTTATCTGCTGAGCTG 2820  
 QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
 Db 2821 TCTGTGATTCGGGTCTCAATGCGGCTATTTTTCAGAAATTAAGAGGCGTATTTTCACT 2880  
 QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
 Db 2881 GCATTCCTCCCTATATGATCGAGAAATGTCATTAATAATGGTGATTTTAATAATGCTTA 2940  
 QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000  
 Db 2941 TCTGTCTGGAAGGTGAAGGGCATGTAGATGTAGAAGAACAAACACACCCTTCGGTC 3000  
 QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
 Db 3001 CRTGTTGTCGGAATGGAAGCAGAGAGTCTCAAGAAGTTCGTGTCTGTCGGGTCTGT 3060  
 QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluCysValThrIle 1040  
 Db 3061 GGTATATCTCTCGTCTACAGCGTACAGAGGAGGATATGGAGAGGTTCCGTAAACAT 3120  
 QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
 Db 3121 CATGAGATCGAAGCAATACAGCAAGTCAAGTTTAGCAACTGTGTAGAAGAGGA 3180  
 QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyGly 1080  
 Db 3181 TATCCAAACACACCGTACGTTAGTATGATTTACTGCCACTCAAGAAGAATATGAGGT 3240  
 QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100  
 Db 3241 ACGTACACTCTCGTAATCGAGGATATGACGGAGCTATGAAGCAATTTCTGTACCA 3300  
 QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgAspAsnPro 1120  
 Db 3301 GCTGATTATGCTATGACCTTATGAAGAAAGCATATACAGATGGACGAGACAATCCT 3360  
 QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
 Db 3361 TGTGAATCTACAGAGGATATGGGATACACACCCTACCCAGCTGGCTATGTGACAAA 3420  
 QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGly 1160  
 Db 3421 GAATTAGAGTACTTCCAGAAACCCGATAAGGTATGGATTGAGATCGGAGAAACGGA 3480  
 QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174  
 Db 3481 ACATTCATCGTGAGCGGTGGAATTAATCTTCTATGAGGAA 3522

RESULT 11

AAV62083

ID AAV62083 standard; DNA; 3522 BP.

XX AAV62083;

AC AAV62083;

XX 13-JAN-1999 (first entry)

DT 13-JAN-1999 (first entry)

DE Plasmid pMYC2254 cryIF/436 chimeric toxin DNA fragment.

XX Bt toxin; lepidoptera; pest; cryIF; chimeric; core toxin; cryIA(c);

KW synergism; plant; primer; endotoxin; ss.

XX Synthetic.

OS Synthetic.

XX US5827514-A.

PN

XX,

PD 27-OCT-1998.

XX 08-FEB-1996; 96US-0598305.

XX 06-DEC-1994; 94US-0349867.

PR 08-FEB-1996; 96US-0598305.

XX (MYCO ) MYCOGEN CORP.

XX Bradfisch GA, Schwab GE, Thompson M;

XX WPI; 1998-593944/50.

XX P-PSDB; AAW76710.

XX Composition for biological control of lepidopteran pests -

XX comprising cells expressing two chimeric Bacillus thuringiensis

XX crystal proteins

XX Example 8; Column 73-76; 75pp; English.

XX This sequence encodes a Bt endotoxin which is used in a method for

XX controlling lepidopteran pests. The method involves the use of cells

XX that express the Bacillus thuringiensis delta-endotoxins cryIF chimeric

XX core toxin-containing protein and CryIA(c) chimeric core toxin-containing

XX protein in a combination that have synergistically enhanced activity,

XX against e.g. corn earworm (Heliothis zea).

XX SQ Sequence 3522 BP; 1140 A; 606 C; 795 G; 981 T; 0 other;

XX Alignment Scores:

XX Pred. No.: 0 Length: 3522

XX Score: 6049.00 Matches: 1143

XX Percent Similarity: 97.79% Conservative: 5

XX Best Local Similarity: 97.36% Mismatches: 26

XX Query Match: 96.88% Indels: 0

XX DB: 19 Gaps: 0

XX US-09-837-961-8 (1-1174) x AAV62083 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20

Tb 1 ATGGAATAATATTAATCAATCAATGCGTACCTTACAATGTTTAATAATCTGAGTA 60

QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40

Tb 61 GAATACTGAACGAGAACGACGACCGCGCTGCGCTGACATCATGAGCCCTGAGCCCT 120

QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60

Tb 121 ACACGCTTCCCTTTGAGTGAATTTGTTCCAGGTGGGAGTTGGGTTTGGATTATTGAT 180

QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80

Tb 181 TTAATATGGGTTTATAAATCTCTGATGAGCTTATTTCTTTTACAGATTGACAA 240

QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100

Tb 241 TTGATTGAGCAAGAAATGAACATTTGGAAGAACCGGCAATTAATACATTACGAGGG 300

QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120

Tb 301 TTACAGATAGCTATGAATTTATATTGAACACTTAAGAGAGTGGGAGCAATCTTAA 360

QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140

Tb 361 AATGCACAAATTAAGGAGAGATGCGTATTCGATTTCGTAATACAGACGACGCTTATA 420

QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160

Tb 421 ACAGCAATATAAATTTTACACTTACAAGTTTGAATCCCTCTTTATCGCTCTATCT 480

QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180

Tb 181 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 180

Db 481 CAAAGCGCGAAATTACATTATACATTATTAAGAGACGCTGTATCGTTTGGGCGAGGTTCG 540  
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
Db 541 GGACTGGATATAGCTACTGTTAATAAICATTAATAAGATTAAATAATCTTATTCATAGA 600  
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
Db 601 TATACGAAACATGTTTGGACACATACATCAAGGATTAGAAACCTTAGAGGTACTAAT 660  
Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrValLeuAsp 240  
Db 661 ACTCGACATGGCGAAGATTCAATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT 720  
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
Db 721 ATCGTGTCTCTTTTCCGAACTACGATGTTAGAACATATCCAAATCCAAACGTCATCCCAA 780  
Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
Db 781 TTAACAAGGGAATTTATACAGTTCAGTAATGAGGATCTCCAGTTCCTGCTAATATA 840  
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
Db 841 CCTAATGTTTAAATAGGCGGAAITGGAGTTAGACCGCCCATCTTATGACCTTTATG 900  
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu 320  
Db 901 AATCTCTTGTAACTCGAGACTGTTAGAAGTCAAACTGTGGGGAGGACACTTA 960  
Qy 321 ValSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
Db 961 GTTAGTTCAGAAATACGCGTGTACCCCTGATAAATTTCCCTAGTTACGGGCTTCCTCAAT 1020  
Qy 341 ProGlyGlyAlaIleThrPheAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
Db 1021 CTGTGGCGCCCATTTGGATTGCAGATGAGGATCCACGTCCTTTTATCGGACATTATCA 1080  
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
Db 1081 GATCTGTTTGTCCGAGAGGATTTGGGAATCCTCATTTAGTACTGGGCTTAGGGGA 1140  
Qy 381 ValAlaPheGlnIleThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
Db 1141 GTAGCATTTCAAACTGGTACGACACACACCCGGAACATTTAGAAATAGTGGGACCAATA 1200  
Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
Db 1201 GATTCCTAGATGAATCCACCTCAGGATAATAGTGGGACCTTGGAAATGATTATAGT 1260  
Qy 421 HisValLeuAsnHisValThrPheValArgTTPProGlyGluIleSerGlySerAspSer 440  
Db 1261 CATGTATTAATCAATGTTACATTTGTACNATGGCCAGGTGAGATTTACAGAAAGTATCA 1320  
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
Db 1321 TGGAGAGCTCCAATGTTTCTTGGACGACCGTAGTGGCAACCCCTACAAATACAAATGAT 1380  
Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
Db 1381 CCGGAGAGATTACTCAAAATACCATTTGGTAAAGACATACATCTTCAGTCAGGTACTACT 1440  
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
Db 1441 GTTGTAAAGAGGCGCGGTTTACGGAGAGAGATATTCTTCGAGGAACAAGTGGAGGACCA 1500  
Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
Db 1501 TTTGCTTATCTATTCTTAATAAATGGCAATTTACCCCAAGGTATCGTGCAGAAATA 1560  
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
Db 1561 CGCTATGCTCTACTACAAATCTAAGAATTTACGTAAAGGTTTCAGGTGAACGGATTTT 1620

Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
Db 1621 GGTGGTCAATTTAAACAAAACATGGATACCGGTGACCCCAATTAACATTCCAATCTTTTAGT 1680  
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
Db 1681 TAGCGAACTATTAAATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGGT 1740  
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Db 1741 GCTGATACTTTTAGTTTCAGGGAATGAAGTTTATATAGACAGATTTTGAATGATTCCAGTT 1800  
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Db 1801 ACTGCAACATTTGAACAGAAATGATTTAGAAAGACACAAAGGGGTGAATGGCGTG 1860  
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
Db 1861 TTTACTTCTATAAACCAANTAGGATAAAACAGATGTGACGGATTATCATATCGATCGA 1920  
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Db 1921 GTCTCCATTTAGTTACGTATTATTCGGATGAATTTTGTCTGGATGAAAGCGAGAATTG 1980  
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680  
Db 1981 TCGAGAAAGTCAACATCGAAGCCACTCAGTGTAGAACGCAATTTACTCCAGGATCA 2040  
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700  
Db 2041 AATTTCAAAGACATTAATAGGCAACAGACGTTGGTGGGCGGAAGTACAGGATTAAC 2100  
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
Db 2101 ATCCAAGGAGGGGATCACGTATTTAAGAAATATAGTCCACTATCAGGTACTCTTGAT 2160  
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
Db 2161 GAGTGTATCCCAACATATTGTATCAAAAATATCGATGAATCAAAATTAAGAGCCTTACC 2220  
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
Db 2221 CGTTATCAATTAAGAGGTATATCGAAGATAGTCAAGACTTAGAATCTATTTAATTCGC 2280  
Qy 761 TyrAsnAlaLysHisGlnThrValAsnValLeuGlyThrClySerLeuTrpProLeuSer 780  
Db 2281 TACAATGCAAAACATGAACACGTAAATGTGCCAGGTACGGGTTCCCTATGCGCGCTTCA 2340  
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAspArgCysAlaProHisLeuGluTrp 800  
Db 2341 GCCCAAGTCCCAATCGAAGAGTGGAGAGCCGAATCGATGCCGCCACACCTTGAATGG 2400  
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGlyLysCysAlaHisSerHisHis 820  
Db 2401 AATCCTGACTTAGATTGTCGTAGGGATGGAGAAAGTGTGCCCATCATTCGCATCAT 2460  
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
Db 2461 TTTCTCTTAGACATTCATGTAGGATGTACAGCTTAAATGAGGACCTAGGTGTATGGGTG 2520  
Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
Db 2521 ATCTTTAAGATTAAAGCAGCAAGATGGCAGCAGCAAGACTAGGAATCTAGAGTTTCTCGAA 2580  
Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880  
Db 2581 GAGAAACCATTAGTAGGAGAGCGCTAGCTCGTGTCAAAAGAGCGGAGAAAATGGAGA 2640  
Qy 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900  
Db 2641 GACAAACGTGAAAAATTTGGAATGGGAAACAAATATCTGTTTATAAAGAGCGCAAAAGATCT 2700

Qy	901	ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla	920
Db	2701	GTAGATCGCTTATTGTGAAACTCTCAATATGATCAATTACAAGCGGATACGAATATTGCC	2760
Qy	921	MetIleHisAlaAlaAspIysArgValHisArgIleArgGluAlaTyrLeuProGluLeu	940
Db	2761	ATGATTCAATCGGCAGATAAAGCTGTTACATCAATCTCAGAAGCTTATCTCCCTGAGCTG	2820
Qy	941	SerValIleProGlyValAsnValAspIlePheGluGluLeuLeuLysGlyArgIlePheThr	960
Db	2821	TCGTGTATTCCGGGTGTCATCGCGCTATTTTGAAGAAATAGAAGCGGTATTTTTCCT	2880
Qy	961	AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu	980
Db	2881	GCATCTCCCTATATGATCGGAAATGTCATAAATAATGGTGATTTTAATAATGGCTTA	2940
Qy	981	SerCysTrpAsnValLysGlyHisValAspValGluGluAsnAsnHisArgSerVal	1000
Db	2941	TCCTGCTGGAACGTGAAGGGCATGTAGATGTAGAAGAACAAACAACACCGTTCGGTC	3000
Qy	1001	LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg	1020
Db	3001	CTTGTTGTTCCGGAATGGGAACGACAAGTGTCCACAAGAAGTTCGTGTCGCGGGCTGT	3060
Qy	1021	GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle	1040
Db	3061	GGCTATATCCTTCGTGTCACGCGTACAGGAGGGATATGAGAAGGTTTCGTAACCAATT	3120
Qy	1041	HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal	1060
Db	3121	CATGAGATCGAGAACAAATACAGCAACTGAAGTTTACCACTGTGTAGAAGAGAGTA	3180
Qy	1061	TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly	1080
Db	3181	TATCCCAACAAACAGGTAAACGTGTAATGATTATATCTCGCACTCAAGAAGAATATGAGGT	3240
Qy	1081	AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro	1100
Db	3241	ACGTACACTCTCGTAATCGAGGATATACGGAGCGCTATGAAGCAATTTCTTCTGTACCA	3300
Qy	1101	AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro	1120
Db	3301	GCGTGATTATGCATCAGCCTATGACAAAAAGCATATACAGATGCACGACGACCAATCCT	3360
Qy	1121	CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProIleGlyTyrValThrLys	1140
Db	3361	TGTGAATCTAACAGAGGATATGGGATTACACACACTTACCAGCTGCGCTATGTGCAAAA	3420
Qy	1141	GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGlyGly	1160
Db	3421	GAATTAGAGTACTTCCACAAAACCGATAAGGTATGGATTGACATCGGAGAAACGGAGGA	3480
Qy	1161	ThrPheIleValAspSerValGluLeuLeuMetGluGlu	1174
Db	3481	ACATTCTGCTGGACCGTGGAAATTACTTCTTATGGAGGAA	3522

Key	Location/Qualifiers
mat_peptide	1..3444
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	/product= cryIF/cryIA(b)_chimeric_toxin
	/note= "plasmid pMC2244 sequence"
WO9530753-A1.	
16-NOV-1995.	
05-MAY-1995;	95WO-US05431.
06-MAY-1994;	94US-0239476.
(MYCO ) MYCOGEN CORP.	
Schwab GE, Thompson M;	
WPT; 1995-404120/51.	
P-PSDB; AAR84731.	
Nucleic acid encoding chimeric <i>Bacillus thuringiensis</i> delta-endotoxin - providing increased expression in <i>Pseudomonas</i> , esp. for control of lepidoptera pests.	
Claim 7; Page 40-42; 91pp; English.	
The sequence represents the cryIF/cryIA(b) chimeric toxin coding sequence of plasmid pMC2244. The chimeric toxin is expressed in <i>Pseudomonas fluorescens</i> better than native delta endotoxins. Host cells expressing the chimeric gene and producing chimeric toxin may be used in insecticide compositions. Where the host cells are plant cells, the gene confers insect resistance to the transformed plant.	
Sequence 3444 BP; 1125 A; 580 C; 765 G; 974 T; 0 other;	
Alignment Scores:	
Pred. No.:	0
Score:	5902.00
Percent Similarity:	96.08%
Best Local Similarity:	95.49%
Query Match:	94.52%
DB:	16
	Gaps: 1
	Length: 3444
	Matches: 1121
	Conservative: 7
	Mismatches: 20
	Indels: 26
	Gaps: 1
US-09-837-961-8 (1-1174) x AAT05249 (1-3444)	
QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20	
Db 1 ATGAGAAATAATATCAAAATCAATGCGTACCTTACAAATGTTTAAATAATCTCGAAGTA 60	
QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40	
Db 61 GAAATATTAATGAAGAAAGAGTACTGGCAGATTACCGTTAGATATATCTTATCGCTT 120	
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60	
Db 121 ACAGITTCCTTTTGTAGTGAAITTTGTCAGGTGTGGAGTTGGGTTTGGATTATTGTAT 180	
QY 61 LeuIleTrpGlyPheIleThrProSerAsnTrpSerLeuPheLeuGlnIleGluGln 80	
Db 181 TTATATGGGGTTTATAACTCCTTCGTATGGAGCTATTCTTTACAGATTGAACAA 240	
QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100	
Db 241 TTGATTGAGCAAGATAGAAACATTTGAAGAGAACCGGCAATTACTACATTACGAGGG 300	
QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120	
Db 301 TTAGCAGATAGCTATGAAATTTTATATTGAAGCACTAAGAGAGTGGGAAGCAAAATCTAAT 360	
QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140	

Db 361 AATGCACAAATTAAGGAGATGTCGCTATTCGATTGGCTAATACAGACGACGCTTTAATA 420  
Qy 141 ThrAlaIleAsnAsnPhetThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
Db 421 ACAGCAATAAATAATTTACACTTACAGTTTGAAGTTTGAATCCCTCTTTTTCGCTCATGTT 480  
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
Db 481 CAAGCGCGCAATTTACATTTATCATTATAGAGACGCTGTATCGCTTTGGCGAGGTTGG 540  
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
Db 541 GGACTGGATATAGCTACTGTTAATAATCATTAATAATAGATTAATAAATCTTATTCATAGA 600  
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
Db 601 TATACGAACAATGTTTGGACACATACAAATCAAGGATTAGAAACTTAAAGAGGTACTAAT 660  
Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
Db 661 ACTCGACATGGCAGGATTCATCAGTTTAGGAGAGATTTAACACTTACTGTATTAGAT 720  
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
Db 721 ATCGTGTGCTCTTTTCCGAACATPACGATGTTAGACATATCCCAATTCAAACGTCATCCCAA 780  
Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
Db 781 TTAACAAGGGAATTTATACAAGTTTCAAGTAATGAGGATCTCCAGTTTCTGCTAATATA 840  
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
Db 841 CCTAATGTTTAAATAGGCGGAATTTGGAGTAGAGCCGCCCATCTTAAGACATTATG 900  
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
Db 901 AATCTCTTGTGTTAACTGCAGAGACTGTAGAACTCAAACTGTGTGGGAGGACACTTA 960  
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
Db 961 GTTAGTTTCAGGAATACGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGTCTTCAAT 1020  
Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
Db 1021 CCTGTTGGCGCCATTTGGATTCAGATGAGATCCACGTCCTTTTATCGACATTATCA 1080  
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
Db 1081 GATCCTGTTTTTTCGAGAGGAGATTGGGAATCCCTCATATGTACTGGGGCTTAGGGGA 1140  
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
Db 1141 GTAGCATTTCAACAACCTGGTAGCAACACCCGGAACATTTAGAATAATAGTGGACCATA 1200  
Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
Db 1201 GATTCTCTAGATGAATCCACCTCAGGATAATAGTGGGACCTTTGGAATGATTATAGT 1260  
Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
Db 1261 CATGTATTAAATCATGTTTACATGTTGACATGGCCAGGTGAGATTTTCAGGAAGTGTATCA 1320  
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
Db 1321 TGGAGAGCTCCCAATGTTTCTTGGAGCGCCGTTAGTGGCAACCCCTACAATACAAATTGAT 1380  
Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
Db 1381 CCGGAGAGGATTTACTCAATATACATTTGGTAAGACACATACACTTCAGTCAGGTACTACT 1440  
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
Db 1441 GTTGTAAAGAGGGCCGGTTTACGGGAGGAGATATTCTTCGAGGAACAAGTGGAGGACCA 1500

Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgile 520  
Db 1501 TTTGCTTATACTATTGTTAATAATAATGGCAATTTACCCCAAGGTATCGTCCAGAATA 1560  
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
Db 1561 CGCTATGCTCTACTACAAATCTAAGAATTTACGTAACGGTTGCAAGGTGAACGGATTTT 1620  
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
Db 1621 GCTGTGTCATTTAACAACCAATGGATACCGGTGACCAATTAACATTCCAATCTTTTAGT 1680  
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
Db 1681 TACGCACTATTAAATACAGCTTTTACATTTCCCAATGAGCCAGAGTAGTTTCACAGTAGT 1740  
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Db 1741 GCTGATACTTTTAGTTTCAGGGAATGAAGTTTATATAGACAGATTTGAATTGATTCCAGTT 1800  
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Db 1801 ACTGCAACATTTGAAGCAGAAATATGATTTAGAAAGAGCACAAAGCGGTGAATGCGCTG 1860  
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
Db 1861 TTTACTTCTATAACCAATAGGGATAAAACAGATGTCACGGATTATCATATCGATCGA 1920  
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Db 1921 GTATCCAAATTTAGTTGAGTGTATTCTGATGAATTTGTCTGATGAAAAAAGAAATG 1980  
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680  
Db 1981 TCCGAGAAAGTCAACATCGAAGCGACTTAGTAGAGCGGAATTTACTTCAAGATCCA 2040  
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700  
Db 2041 AACTTTAGAGGATCAATAGACAACTAGACCGTGGCTGGAGAGAGTAGGATATACC 2100  
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
Db 2101 ATCCAAGGAGCGGATGACGTATTCAAAAGAGAAATACGTTACGCTATTTGGGTACCTTTGAT 2160  
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740  
Db 2161 GAGTGTATCCCAACGTTATTATATCAAAATAATAGATGAGTCGAAATTAAGAGCCTATACC 2220  
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
Db 2221 CGTTACCAATTAAGAGGTATATCGAAGATAGTCAAGACTTAGAATCTATTAAATCCG 2280  
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780  
Db 2281 TACAATGCCAAACACGAAACAGTAAATGTCCAGGTACGGGTCTCCATTATGCGGCTTTCA 2340  
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800  
Db 2341 GCCCCAAGTCCCAATC----- 2355  
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820  
Db 2356 -----GGAAATGTCCCATCATTTCCCATCAT 2382  
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840  
Db 2383 TTCTCCTTGGACATTGATGTTGGATGTACAGACTTAAATGAGGACTTAGGTGTATGGGTG 2442  
Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
Db 2443 ATATTCAAGATTAAAGCAAGATGCCATGCAAGACTAGAAATCTAGAAATTTCTCGAA 2502

Qy	861	GlulysProLeuValGlyGluLeuAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg	880
Db	2503	GAGAAACCATAGTAGGAGAACCACTAGCTCGTGTGAAAGACGCGAGAAAATGGAGA	2562
Qy	881	AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer	900
Db	2563	GACAAACGTGAANAATTTGGAAATGGGAACAAATATTGTTTATAAGAGCGAAAAGAAATCT	2622
Qy	901	ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla	920
Db	2623	GTAGATGCTTATTGTGAACCTCAATATGATAGATTACAAAGCGATACCAACATCGCG	2682
Qy	921	MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu	940
Db	2683	ATGATTTCATCGCGCAGATAAACCGTTTCATAGCATTCGAGAAGCTTATCTGCCTGAGCTG	2742
Qy	941	SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr	960
Db	2743	TCGTGTGATTCGGGTGTCAATGCGGCTATTTTGAAGAATTAGAAGGCGTATTTTCACT	2802
Qy	961	AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu	980
Db	2803	GCATTCTCCCTATATGATCGGAATGTCATAAATGGTGATTTTAAATATGGCTTA	2862
Qy	981	SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal	1000
Db	2863	TCCTGCTGGAACTGAAAGGCGATGATGATGTAGAGAACAACAAACACCGGTCGGTC	2922
Qy	1001	LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg	1020
Db	2923	CTTGTTGTTCCGGAATGGAGACAGAAGTGTCCACAGAAGTCTCGTGTCTGTCCGGGTCGT	2982
Qy	1021	GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle	1040
Db	2983	GGCTATATCCTTCGTCTCACAGCTACAGAGAGGGATATGGAGAGGTTGCGTAAACCAT	3042
Qy	1041	HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal	1060
Db	3043	CATGAGATCGAGAACCAATACAGACAACTTGAAGTTTAGCAACTGTGTAGAGAGAGAA	3102
Qy	1061	TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyGlyGly	1080
Db	3103	TATCCAAACAACACGGTACGTTACGTGTATGATTATATCTCGACTCAAGAAGAAATATGAGGT	3162
Qy	1081	AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro	1100
Db	3163	ACGTACACTTCTCGTAATCGAGATATACGGAGCGCTATGAAGCAATCTCTCTGTACCA	3222
Qy	1101	AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro	1120
Db	3223	GCTGATTATGTCATCACCCATATGAAGAAAAGCATATACAGATGCGAAGAGACAATCCT	3282
Qy	1121	CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys	1140
Db	3283	TGTGAATCTAACAGAGCATATGGGATTACACACCATACCAGCTGCGCTATGTGACAAA	3342
Qy	1141	GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly	1160
Db	3343	GAATTAGAGTACTTCCAGAAACCGATAAGGTATGATTTGAGATCGAGAAACGGAGGA	3402
Qy	1161	ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu	1174
Db	3403	ACATTCTGTTGGACACGCTGGAATTACTTCTTATGGAGGAA	3444
RESULT 13			
AAAT05251			
ID	AAAT05251 standard; DNA; 3444 BP.		
XX	AAAT05251;		
XX	XX		
DT	27-MAY-1996 (first entry)		
XX	XX		
DE	CryIF/cryIA(b) chimeric toxin coding sequence.		

Db 241 TTGATTGACCAAGAATAAGAACATTTGGAAAGAACCGGGCAATTAATTAATACATTACGAGGG 300  
 Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrGluAlaAsnProAsn 120  
 Db 301 TTAGCAGATAGCTATGAATATTTATTTGAGGACCTAAGAGAGTGGGAACAATCCTAAT 360  
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140  
 Db 361 AATGCACAATTAAGGAAGATGCGTATTCGATTTGCTAATACAGACGACGCTTTAATA 420  
 Qy 141 ThrAlaIleAsnAspPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 Db 421 ACAGCAATAAATAATTTACATTTCAAGTTTGAATCCCTTTTATCGGCTCATGTT 480  
 Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGluGlnGlyTyr 180  
 Db 481 CAAGGGCGGAATTTACATTTTACATTTTAAGAGAGCGCTGTATCGTTTGGGAGGGTTGG 540  
 Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 Db 541 GGACTGGATATAGCTACTGTTAATATCATTTAATATAGATTAATTAATCTTATTCATAGA 600  
 Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 Db 601 TATACCAACATGTTTGGACACATACATCAAGATTAAGAACTTAAGAGGTACTAAT 560  
 Qy 221 ThrArgGlnTyrAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 Db 661 ACTCGACAATGGCAAGATTCATCAGTTTAGGAGAGATTTAACACTTACTGTATTAGAT 720  
 Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 Db 721 ATCGTTGTCTCTTTTCCGAACATPACGATGTTAGAACATATCCCAATTCACACGTCATCCCAA 780  
 Qy 261 LeuThrArgGluIleTyrThrSerValIleGluAspSerProValSerAlaAsnIle 280  
 Db 781 TTAACAGGGAATTTATACAGTTTCAAGTTTCAAGTTTCAAGTTTCCAGTTTCTCTTAATATA 840  
 Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
 Db 841 CCTAATGGTTTAAATAGGCGGAATTTGAGTTAGACCCGCCCATCTTATGACCTTTATG 900  
 Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTyrGlyGlyHisLeu 320  
 Db 901 AATCTCTTTGTTTAACTGCAGAGACTGTAGAACTCAAACTGTGTGGGAGGACACTTA 960  
 Qy 321 ValSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 Db 961 GTTAGCTCACGAAATACGGCTGGTACCGTATTAANTTTCCCTAGTTACGGGCTCTTCAAT 1020  
 Qy 341 ProGlyGlyAlaIleTyrPheAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
 Db 1021 CCTGTGGCGCCATTTGGATTTCAGATGAGGATCCAGTCCTTTTTATCGGACATTATCA 1080  
 Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 Db 1081 GATCTCTTTTGTCCGAGGAGGATTTGGGAATCCTCATATATGCTAGTGGGCTTAGGGGA 1140  
 Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
 Db 1141 GTAGCATTTCAACAACCTGGTACGAACACACCCCGAACATTTAGAAATAGTGGGACCATTA 1200  
 Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTyrAsnAspTyrSer 420  
 Db 1201 GATTCCTAGATGAATCCCACTCAGGATATAGTGGGACCTTGGGAATGATTATAGT 1260  
 Qy 421 HisValLeuAsnHisValThrPheValArgTyrProGlyGluIleSerGlySerAspSer 440  
 Db 1261 CATGTATTAAATCATGTTTACATTTTACCATGGCCAGGAGATTTCCAGGAAGTGATTCA 1320  
 Qy 441 TrpArgAlaProMetPheSerThrPheHisArgSerAlaThrProThrAsnThrIleAsp 460  
 Db 1321 TGGAGAGCTCCCAATGTTTCTTGGAGCGCACCGTAGTGAACCCCTACAAATACAATTGAT 1380

Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
 Db 1381 CCGGAGAGATTACTCAAAATACCATTTGGTAAAGCACAATACACTTCAGTCAGTACTACT 1440  
 Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
 Db 1441 GTTGTAAAGAGGCCCGGGTTTACGGGAGGAGATATTCTTCGACGAACAAGTGGAGGACCA 1500  
 Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
 Db 1501 TTTGCTTTATACATTGTTAATAATGGAATTAACCCCAAGGTATCGTGAAGAATA 1560  
 Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
 Db 1561 CCTATGCTCTACTACAAATCTAAGAAATTTAGTAAACGGTTGACGGTGAACGGATTTT 1620  
 Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
 Db 1621 GCTGTCATTTTAAACAACATGGATACCGGTGACCATTAACATTCCAATCTTTTATG 1680  
 Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
 Db 1681 TAGGCAACTATTAAATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGT 1740  
 Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluIleProVal 600  
 Db 1741 GCTGATCTTTTAGTTCAGGGAATGAAGTTTATATAGACAGATTTTGAATGTATTCAGTT 1800  
 Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
 Db 1801 ACTGCAACATTTGAAGCAGAAATATGATTTAGAAAGACACAAAGCGGTGAATGGCTG 1860  
 Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
 Db 1861 TTTACTTCTATAAACCAATAGGGAATAAAACAGATGTGACGATTTATCATATCGATCGA 1920  
 Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
 Db 1921 GTATCCAAATTTAGTTGAGTGTATCTGATGAATTTTGTCTGGATGAAAAAAGAATTG 1980  
 Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
 Db 1981 TCCGAGAAAGTCAACATCGGAAGCGACTTAGTGATGACGGAATTTACTTCAAGATCCA 2040  
 Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrPargGlySerThrAspIleThr 700  
 Db 2041 AACTTTAGAGGATCAATAGACAACACTAGACCGTGGCTGGAGAGGAAGTACGGATATACC 2100  
 Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
 Db 2101 ATCCAAGGAGGCGATCAGCTATTCAAGAGAAATACGTTACGCTATGCGTATGTTGAT 2160  
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 Db 2161 GAGTGTATCCCAACGATTTATATCAAAAAATAGATGAGTCGAAATTAAGACCTATACC 2220  
 Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760  
 Db 2221 CGTTACCAATTAAGAGGATATATCGAAGATAGTCAAGACTTAGAAATCTATTAAATCCG 2280  
 Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780  
 Db 2281 TACATGCCAACACCAACAGTAATGTGCCAGGTACGGGTTCCTTATGGCCGCTTTCA 2340  
 Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr 800  
 Db 2341 GCCCAAGTCCCAATC----- 2355  
 Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820  
 Db 2356 -----GGAAAAATGTGCCCATCATTCCTCCATCAT 2382

QY 821 pheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTTPVal 840  
 DQ 2383 TTCTCCTTGGACATTGATGTTGGATGTACAGACTTTAAATGAGGACCTTAGGTGTATGGGTG 2442  
 QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860  
 DQ 2443 ATATTCAAGATTAAAGACGCAAGATGCCATGCAAGACTAGGAATCTAGAAATTTCTCGAA 2502  
 QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTTPArg 880  
 DQ 2503 GAGAAACCATTTAGTAGGAGGACACTAGCTCGTGTGAAAGACGCGAGAAAATCGAGA 2562  
 QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900  
 DQ 2563 GACAAACGTGAAATTTGATGCGGAAACAAATATTTGTTTAAAGAGGCAAAAGAAATCT 2622  
 QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920  
 DQ 2623 GTAGATGCTTTATTTGTAACCTCAATATGATAGATTACAAGCGGATACCAACATCGCG 2682  
 QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940  
 DQ 2683 ATGATTCATCGCGCATAAACCGCTCATAGCATTCGAGAACTTATCTGCTGAGCTG 2742  
 QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960  
 DQ 2743 TCTGTGATTCGGGTGCTCAATCGGCTATTTTGAGAAATTAGAAGCGGTATTTTCACT 2802  
 QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980  
 DQ 2803 GCATTCCTCCTATATGATCGGAGAAATGTCATTAATAATGGTGATTTTAATAATGCTTA 2862  
 QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGluAlaAsnHisArgSerVal 1000  
 DQ 2863 TCTGCTGGAAGCTGAAAGGCGATGTAGATGTAGAGAAACAAACACACCCGTTCCGTC 2922  
 QY 1001 LeuValValProGluTyrPheGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020  
 DQ 2923 CTTGTGTTCCGGATGGAGCAAGAGTGTACAGAAAGTTCGTGTCGTCCGGGTCT 2982  
 QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040  
 DQ 2983 GGCATATATCCTTCGTGCACGGTACAGAGGAGGATATGGAGAGTTGCGTAACCAT 3042  
 QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060  
 DQ 3043 CATGATTCGAGAAATACAGACCAACTGAAGTTAGCAACTGTGTAGAGAGGAAGTA 3102  
 QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080  
 DQ 3103 TATCCAAACACACCGTACGTTACGTTATGATGATGATGATGATGATGATGATGATG 3162  
 QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100  
 DQ 3163 ACCTACACTCTCGTAATCGAGGATATGACGGAGCCTATGAAGCAATCTTCTGTACCA 3222  
 QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAsnPro 1120  
 DQ 3223 GCTGATATGATCAGCTCATGAGAAAGCAATATACAGATGGAGGAGCAATCTCT 3282  
 QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140  
 DQ 3283 TGTGAATCTACAGAGGATATGGGATACACACCACTACCACTGCTATGTGACAAA 3342  
 QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160  
 DQ 3343 GAATTAGAGTACTTCCGAAACCGATAGGTATGATGATGATGATGATGATGATGATG 3402  
 QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
 DQ 3403 ACATTCATCGTGAGACGCTGGAATTACTTCTTATGGAGGA 3444

RESULT 14

ART18701  
 ID AAT18701 standard; DNA; 3444 BP.  
 AC AAT18701;  
 DT 18-AUG-1996 (first entry)  
 DE CryIF/cryIA(b) chimeric toxin gene from pMYC2244.  
 KW CryIF; CryIA(b); crystal protein; chimeric toxin; protoxin;  
 KW pMYC2244; delta-endotoxin; chimeric gene; fusion protein;  
 KW Pseudomonas fluorescens; CryIA(c); synergy; Lepidoptera; insect;  
 KW biological control agent; transgenic plant; insect resistance;  
 KW crop improvement; ss.  
 OS Bacillus thuringiensis.  
 FT mat\_peptide 1-1803 Location/Qualifiers  
 FT mat\_peptide /\*tag= a  
 FT mat\_peptide /note= "CryIF toxin gene fragment"  
 FT mat\_peptide 1804..3444  
 FT mat\_peptide /\*tag= b  
 FT mat\_peptide /note= "CryIA(b) protoxin gene fragment"  
 US5508264-A.  
 16-APR-1996.  
 06-DEC-1994; 94US-0349867.  
 06-DEC-1994; 94US-0349867.  
 (MYCO ) MYCOGEN CORP.  
 Bradfisch GA, Schwab GE, Thompson M;  
 WPI: 1996-208745/21.  
 P-PSDB; AAR94907.  
 Compsn. for controlling lepidopteran pests - comprises CryIF and  
 CryIA(c) chimeric core toxin-contg. proteins.  
 Claim 6; Column 45-48; 59pp; English.  
 This sequence encodes a Bacillus thuringiensis chimeric  
 CryIF/CryIA(b) delta-endotoxin. The toxin contains a full toxin  
 portion of CryIF and a heterologous protoxin segment derived from  
 CryIA(b). The sequence is constructed by substitution of an Apal  
 fragment from cryIF clone pMYC2047 with the Apal fragment in  
 pMYC2239 (AAT18721, containing cryIA(c) at the N-terminus, cryIF up  
 to the toxin-protoxin junction, and a cryIA(b) protoxin segment)  
 to give pMYC2244. The product contains cryIF up to the  
 toxin-protoxin junction and cryIA(b) to the end of the coding  
 region. The resulting chimeric gene may be cloned in a Pseudomonas  
 fluorescens lactose-inducible strain to produce a chimeric toxin.  
 The toxin, when combined with a CryIA(c) chimeric toxin in synergy,  
 has unexpectedly enhanced toxicity to lepidopteran pests. P.  
 fluorescens or B. thuringiensis cells expressing the gene may be  
 used as an insect biological control agent, or a transgenic plant  
 expressing the gene may become resistant to insect attack.  
 Sequence 3444 BP; 1125 A; 580 C; 765 G; 974 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 3444  
 Score: 5902.00 Matches: 1121  
 Percent Similarity: 96.08% Conservatives: 7  
 Best Local Similarity: 95.49% Mismatches: 20  
 Query Match: 94.52% Indels: 26  
 DB: 17 Gaps: 1  
 US-09-837-961-8 (1-1174) x AAT18701 (1-3444)



Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
Dbb  
Dbb 1 ATGGAGATATATATCAAAATCAATCGCTACTTACAAATGTTTAAATAAATCCTGAAGTA 60  
Qy 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
Dbb  
Dbb 61 GAAATATTAAATGAAGAAAGAGTACTGGCAGATTACCGTTAGATATATCCTTATCGCTT 120  
Qy 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
Dbb  
Dbb 121 ACACGTTTCCTTTTGAGTGAATTTCTTCAGGTGGAGTTCGCTTTGGATTATTGAT 180  
Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80  
Dbb  
Dbb 181 TTAATATGGGTTTATACCTCTCTGATGGAGCTTATTTCTTTACAGATTGAACAA 240  
Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
Dbb  
Dbb 241 TTGATTGACAAAGAAATAGAAACATTGGAAGAACCGGGCAATTACTACATTACGAGGG 300  
Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
Dbb  
Dbb 301 TTAGCAGATAGCTATGAATTTATATGAAGCACCTAAGAGAGTGGGAACAAATCCTAAT 360  
Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140  
Dbb  
Dbb 361 AATGCACAAATTAAGGAGAGATGGGTATTCATTTGCTAATACAGACGACGCTTAAATA 420  
Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
Dbb  
Dbb 421 ACAGCAATAAATAATTTACACTTACAAGTTTGAAGTCCCTCTTTTATCGGCTATGTT 480  
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
Dbb  
Dbb 481 CAAGCGCGAATTTACATTTATCATATTAAGACGCTGTATCGTTTGGGAGGGTGG 540  
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
Dbb  
Dbb 541 GGACTGGATATAGCTACTTAAATCAATCAATATATAGTAAATAAATCTTATCATAGA 600  
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
Dbb  
Dbb 601 TATACGAACATTTGTTGGACACATACATCAAGGATTAGAAACTTAAGAGGTACTAAT 660  
Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
Dbb  
Dbb 661 ACTCCAAATGGGCANGATTCAATCAGTTTAGAGAGATTTAACACTTACTGTATTAGAT 720  
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
Dbb  
Dbb 721 ATCGTTGCTCTTTTCCGAACCTACGATGTTAGAACATATCCAAATCAACGCTATCCCAA 780  
Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
Dbb  
Dbb 781 TTAACAGGGAATTTATACAAGTTTCAAGTTAGGATTCCTCAAGTTTCTGCTAATATA 840  
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
Dbb  
Dbb 841 CCTATGTTTAAATAGGCGGAATTTGGAGTTAGCCGCCCCCAATCTTATGACITTTATG 900  
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
Dbb  
Dbb 901 AANTCTCTTTGTTAACTGCAGAGACTGTTAGAGTCAAACTGTGTGGGAGGACACTTA 960  
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
Dbb  
Dbb 961 GTTAGTTACGAAATACGGCTGTAACCGTATAAAATTTCCCTAGTTACGGGGTCTTCAAT 1020  
Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
Dbb  
Dbb 1021 CCTGGTGGCGCCATTTGGATTGCAGATAGGATCCACGCTCTTTTATCGGACATTATCA 1080

Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
Dbb  
Dbb 1081 GATCCTGTTTTTGTCCGAGGAGATTGGGATCCTCATTAATGTACTGGGCTTAGGGA 1140  
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
Dbb  
Dbb 1141 GTAGCATTTCAACAACCTGGTACGAACACACCCGGAACATTTAGAAATAGTGGGACCATA 1200  
Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
Dbb  
Dbb 1201 GATTCCTAGATGAATCCCACTCAGGATAATAGTGGGCACCTTTGGAAATGATTATAGT 1260  
Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
Dbb  
Dbb 1261 CATGTATTAAATCATGTTACATTTGTACATGCCAGGTGAGATTTTCAGGAAGTATTC 1320  
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
Dbb  
Dbb 1321 TGGAGAGCTCCAATGTTTCTTGGACGCCCTAGTGAACCCCTACAATAACAATTGAT 1380  
Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
Dbb  
Dbb 1381 CGGGAGAGATTACTCAAAATACCATTTGGTAAAGCACATACACTTCAGTCAGGTACTACT 1440  
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
Dbb  
Dbb 1441 GTTGTAAAGAGGCCCGGGTTTACGGGAGGAGATATCTTCGACGAACAAGTGGAGGACCA 1500  
Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
Dbb  
Dbb 1501 TTTGCTTATACTATTGTTAAATAAATGGCAATTAACCCCAAGGTATCGTCAAGAATA 1560  
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
Dbb  
Dbb 1561 CGCTATGCTCTTACACAAATCTAAGAAATTTACGTAACGGTTGCGAGGTGAACGGATTTT 1620  
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
Dbb  
Dbb 1621 GCTGTCAATTTAACAAACAATGGATACCGGTGACCCCAATTAACATTCCAATCTTTT 1680  
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
Dbb  
Dbb 1681 TACGCAACTATTAAATACAGCTTTTACATTTCCCAATGAGCCAGAGTAGTTTCACAGTAGT 1740  
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
Dbb  
Dbb 1741 GCTGTACTTTTAGTTCAGGGAATGAAGTTTATATAGACAGATTTGAATGATTCAGTT 1800  
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
Dbb  
Dbb 1801 ACTGCAACATTTTGAAGCAGAATATGATTTAGAAAGAGACACAAAGCGGTGAATGCGGTG 1860  
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspThrHisIleAspGln 640  
Dbb  
Dbb 1861 TTTACTTCTATAAACCAATAGGGATAAAACAGATGTACCGGATTATCATATCATGATCA 1920  
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
Dbb  
Dbb 1921 GTATCCAATTTAGTTCAGTGTTTATCTGATGAATTTTGTCTGGATGCAAAAAGAAATG 1980  
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680  
Dbb  
Dbb 1981 TCCGAGAAAGTCAACATCGGAAGCGACTTACTGATGAGCGGAATTTACTTCAAGATCCA 2040  
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700  
Dbb  
Dbb 2041 AACTTTAGAGGGATCAATAGACAACCTAGACCGTGGCTGGAGAGGAAGTACGGATATTAC 2100  
Qy 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720  
Dbb  
Dbb 2101 ATCCAAAGGAGCGGATGACGTATTCAAAAGAGAAATACGTTACGCTATTTGGGTACCTTT 2160  
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740



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Db 2161 GAGTGTATCCACGATATTTATATCAAAATAGATGAGTCGAAATTAAGCCCTATACC 2220
QY 741 ArgTyrGluLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTTACCAATTAAGAGGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTAAATCGC 2280
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGluThrClySerLeuIlePProLeuSer 780
Db 2281 TACAATGCCAAACAGAAACAGTAAGATGTCAGGAGTACGGGTTCCCTATATGGCCGCTTCA 2340
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
Db 2341 GCCCAAGTCCATC----- 2355
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820
Db 2356 -----GGAAATGTGCCATCATCCCATCAT 2382
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
Db 2383 TTCCTCTGGACATTCATGTTGGATGTACAGACTTAATGAGGACCTAGGTGTATGGTG 2442
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaAArgLeuGluAsnLeuGluPheLeuGlu 860
Db 2443 ATATTCAAGATTAAAGACGCAAGATGCCATGCAAGACTAGGAATCTAGAAATTCGGA 2502
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880
Db 2503 GAGAAACCAATTAGTAGAAGACACTAGCTGCTGTGAAAGAGCGGAGAAAAAATGGAGA 2562
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 2563 GACAAACGTGAANAATGGATGGGAACAANAATATTGTTTAAAGAGGCAAAAGAAATCT 2622
QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
Db 2623 GTAGATGCTTTATTGTAACTCTCAATATGATAGATTACAGCGGATACCAACATCGCG 2682
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 2683 ATGATTTCGCGCGACATAAACCGTTCATAGCAATTCGAGAACTTATCTGCGTGAGCTG 2742
QY 941 SerValIleProGlyValAsnValAspIlePheGluLeuLysGlyArgIlePheThr 960
Db 2743 TCTGTGATTCGGGTGCTCAATGCGGTATTTTGAAGAATTAGAAGGCGGTATTTCACT 2802
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 2803 GCATTCCTCCTATATCATCGAGAAATGTCATTAAAAATGGTGATTTTAATAATGCTTA 2862
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluAsnAsnHisArgSerVal 1000
Db 2863 TCTGCTGGAAGCTGAAGCGGATGATGATGTAGAGAACAACAAACACCCGTTCCGTC 2922
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 2923 CTTGTGTTCCGGAATGGAACGACGAACTGTCAACAAGACTTCGTGCTCCGGTCTGT 2982
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluCysValThrIle 1040
Db 2983 GCGTATATCCTTCGTGTACAGCGGTACAAGGAGGATATGGAGAAGTTGCGTAACCAT 3042
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3043 CATGAGATCGAACAATACAGCAACCTGAAGTTTAGCAACTGTGTAGAAGAGGAAGTA 3102
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGluGluTyrGlyGly 1080
Db 3103 TATCCAAACACACGCTACGTTGTAATGATTACTGCGACCTCAAGAAGAAATATGAGGT 3162
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100

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Db 3163 ACGTACACTCTCTGTAATCCAGGATATGACGGAGCCTATGAAAGCAATTTCTTGTACCA 3222
QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
Db 3223 GCTGATTATGATCAGCTATGAAAGAAAGCATATACAGATGACGAGAGACAATCCT 3282
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
Db 3283 TGTGAATCTAACAGAGATATGGGATTACACACCACTACAGCTGGCTATGTGACAAA 3342
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
Db 3343 GAATTAGACTACTTCCAGAAACCGATAGGTATGATGAGATCGAGAAACGGAGGA 3402
QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3403 ACATTCATCGTGACAGCGTGAATTTACTTCTTATGGAGAA 3444

RESULT 15
AAT18723
ID AAT18723 standard; DNA; 3444 BP.
XX
AC AAT18723;
DT 18-AUG-1996 (first entry)
XX
DE CryIF/CryIA(b) codon-reworked chimeric toxin gene from pMYC2523.
XX
KW CryIF; CryIA(b); crystal protein; chimeric toxin; protoxin;
KW pMYC2523; delta-endotoxin; codon usage; splice overlap extension;
KW mutagenesis; chimeric gene; fusion protein; Pseudomonas fluorescens;
KW CryIA(c); synergy; Lepidoptera; insect; biological control agent;
KW transgenic plant; insect resistance; crop improvement; ss.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..1803
FT /tag= a
FT /note= "CryIF toxin gene fragment"
FT mat_peptide 1804..3444
FT /tag= b
FT /note= "CryIA(b) protoxin gene fragment"
XX
US5508264-A.
PN
XX
PD 16-APR-1996.
XX
PF 06-DEC-1994; 94US-0349867.
XX
PR 06-DEC-1994; 94US-0349867.
XX
PA (MYCO ) MYCOGEN CORP.
XX
PI Bradfisch GA, Schwab GE, Thompson M;
XX
DR WPI; 1996-208745/21.
DR P-PSDB; AAR94907.
XX
Compsn. for controlling lepidopteran pests - comprises CryIF and
CryIA(c) chimeric core toxin-contg. proteins.
XX
Example 6; Column 61-66; 59pp; English.
XX
This sequence encodes a Bacillus thuringiensis chimeric
CryIF/CryIA(b) delta-endotoxin. The toxin contains a full toxin
portion of cryIF and a heterologous protoxin segment derived from
cryIA(b). A cryIF gene from pMYC2047 has been subjected to splice
fragment extension to alter codons in a limited region in the cryIF
fragment to favor G or C in the wobble position, to improve
expression in Pseudomonas spp., giving pMYC2243 (AAT18722). An ApaI
fragment from this clone is substituted for an ApaI fragment from
pMYC2244 (AAT18701), to give pMYC2523. The product contains cryIF up

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CC to the toxin-prototoxin junction and cryIA(b) to the end of the coding  
 CC region. The resulting chimeric gene may be cloned in a Pseudomonas  
 CC fluorescens lactose-inducible strain to produce a chimeric toxin.  
 CC The toxin, when combined with a CryIA(c) chimeric toxin in synergy,  
 CC has unexpectedly enhanced toxicity to lepidopteran pests. P.  
 CC fluorescens or B. thuringiensis cells expressing the gene may be  
 CC used as an insect biological control agent, or a transgenic plant  
 CC expressing the gene may become resistant to insect attack.  
 XX  
 SQ Sequence 3444 BP; 1119 A; 592 C; 769 G; 964 T; 0 other;

Alignment Scores:

Pred. No.: 0 Length: 3444  
 Score: 5902.00 Matches: 1121  
 Percent Similarity: 96.08% Conservative: 7  
 Best Local Similarity: 95.49% Mismatches: 20  
 Query Match: 94.52% Indels: 26  
 DB: 17 Gaps: 1

US-09-837-961-8 (1-1174) x AAT18723 (1-3444)

QY 1 MetGluAsnAlaGlnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
 Db 1 ATGGAAATTAATATCAAAATCAATCGTACCTTACAATTTGTTAAATAATCCTGAAGTA 60  
 QY 21 GluileLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 Db 61 GAAATACTGAACGAGAACGCCACCCGCCGCTGCCGCTGGACATCAGCCCTGAGCCTT 120  
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 Db 121 ACACGTTTCCTTTTGAGTGAATTTGTTCCAGGTGTGGAGTTGCGTTTGGATTATTGAT 180  
 QY 61 LeuileTrGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80  
 Db 181 TTAATATGGGTTTATACTCCTCTGATTGGAGCTTATTTCTTTACAGATTGAACAA 240  
 QY 81 LeuileGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100  
 Db 241 TTGATTGACCAAGATAGAAACATTTGGAAGGACCGGCCAATTACTACATTACGAGGG 300  
 QY 101 LeuAlaSerSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 Db 301 TTACGAGATAGCTATGAAATTTATATTAGACACCTAAGACAGTGGGAAGCAATCCTAAT 360  
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuile 140  
 Db 361 AATGCACATTAAGGAAGATGTCGCTATTGCTAATACAGACGACGCTTTAATA 420  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
 Db 421 ACAGCAATAAATAATTTTACACTTACAAAGTTTGAATCCCTCTTTATCGGCTATGTT 480  
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 Db 481 CAAGCGCGCAATTTACATTTATCATTATTAAAGAGCGCTGTATCGTTTGGCGAGGTTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuileAsnLeuileHisArg 200  
 Db 541 GGCTGGATATAGCTATGTTAATAATCATTAATAAGATTAATAATCTTATTCATAGA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
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 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 Db 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAACACTTACTGTATTAGAT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 Db 721 ATCGTGTCTCTTTTCCGAACTACGATGTAGAACATATATCCAAATTCAAACGTCATCCCAA 780

QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 Db 781 TTACACAGGGAATTTATACAGTTTCAAGTTTGAAGATTCTCCAGTTTCTGCTTAATA 840  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProHisLeuMetAspPheMet 300  
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 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
 Db 901 AATTCCTTTGTTTAACTGCGAGAGCTGTTAGAACTGTAAGTCAAACTGTGGGAGGACACTTA 960  
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 Db 961 GTTAGTTCACAAATACGGCTGTACCGTATAAATTTCCCTAGTTACGGGCTTTCAT 1020  
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 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
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 QY 461 ProGluArgIleThrGlnIleProLeuValIleAlaHisThrLeuGlnSerGlyThrThr 480  
 Db 1381 CCGGAGAGGATTACTCAATPACCATTTGGTAAAGACACATACACTTCAGTCAGGTACTACT 1440  
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgThrSerGlyGlyPro 500  
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 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
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 QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640

1861 TTTACTTCTATAAACCAATAGGATATAAACACAGATGACGGATTATCATATCGATCGA 1920  
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1981 TCCGAGAAAGTCAACATCGAACCGACTTAGTGTATGAGCGGAATTTACTTCAAGATCCA 2040  
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2356 -----GGAAATGTGCCCATCTCCCATCAT 2382  
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2683 ATGATTCATGGCGCAGATAAACGGGTTTCATAGCATTCGAGAGGCTTATCTCGCTGAGCTG 2742  
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2863 TCTGCTGGAACTGAAAGGGCATGTAGATGTAGAGAAACAAAAACAACACCGTTCTGGTC 2922  
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3103 TATCCAAACACACGCTAACGCTGTAATGATTATCTGCGACTCAAGAGAAATATGAGGT 3162  
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3163 ACGTACACTTCTCGTAATCGAGGATATGACGGAGCCTATGAAAGCAATTCCTCTGTACCA 3222  
QY AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120  
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3343 GAATTAGAGTACTTCCCAAGAACCCGATAGGTATGATGAGATCGGAGAAACGGAGGA 3402  
QY ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174  
3403 ACATTCATCGTGACAGCGTGGAAATTTACTTCTTATGGAGGAA 3444

Search completed: November 27, 2002, 23:36:56

Job time : 700 secs

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run On: November 27, 2002, 20:24:30 : Search time 6507 Seconds  
(without alignments)  
5250.760 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MNNIQNCVPCYNCLNNEPV.....IGETGTGTFIVDSVELLMEE 1174

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+\_p2n.model -DEV=xlp  
-O=/cgn2.1/USPTO.spool/US09837961/runat\_25112002\_142415\_5921/app\_query.fasta.1.1351  
-DB=GenEmbl -QMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cgi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=plo -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
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-NO\_XLPXY -NO\_MMAL -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*

29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	6244	100.0	3522	6	AR050193 Sequence
2	6244	100.0	3522	6	AR060321 Sequence
3	6244	100.0	3522	6	AR105486 Sequence
4	6244	100.0	3522	6	AX088274 Sequence
5	6244	100.0	3522	6	I19464 Sequence 24
6	6244	100.0	3522	6	I22418 Sequence 24
7	6244	100.0	3522	6	I76417 Sequence 7
8	6244	100.0	3525	1	BACCRXIF
9	6244	100.0	5649	1	BACCRIFA
10	6049	96.9	3522	6	AR050195 Sequence
11	6049	96.9	3522	6	AR060323 Sequence
12	6049	96.9	3522	6	I19466 Sequence 28
13	6049	96.9	3522	6	I22420 Sequence 28
14	5902	94.5	3444	6	AR050192 Sequence
15	5902	94.5	3444	6	AR050194 Sequence
16	5902	94.5	3444	6	AR060320 Sequence
17	5902	94.5	3444	6	AR060322 Sequence
18	5902	94.5	3444	6	I19463 Sequence 22
19	5902	94.5	3444	6	I19465 Sequence 26
20	5902	94.5	3444	6	I22417 Sequence 22
21	5902	94.5	3444	6	I22419 Sequence 26
22	5902	94.5	3444	6	AX088270 Sequence
23	5674	90.9	3450	6	AR050191 Sequence
24	5674	90.9	3450	6	AR060319 Sequence
25	5674	90.9	3450	6	I19462 Sequence 20
26	5674	90.9	3450	6	I22416 Sequence 20
27	5595	89.6	3558	6	AX088008 Sequence
28	5415	86.7	3504	6	AR085763 Sequence
29	5415	86.7	3504	6	I73041 Sequence 3
30	5406	86.6	4120	1	BTCPYPRTD
31	5399.5	86.5	3649	1	AF062350 Bacillus
32	4815.5	77.1	3531	6	AR107431 Sequence
33	4815.5	77.1	3531	6	AR156713 Sequence
34	4815.5	77.1	3531	6	AR166479 Sequence
35	4815.5	77.1	3531	6	AR179209 Sequence
36	4815.5	77.1	3531	6	AX383785 Sequence
37	4815.5	77.1	3531	6	BD007655 Sequence
38	4812.5	77.1	3534	6	AR107442 Sequence
39	4812.5	77.1	3534	6	AR156724 Sequence
40	4812.5	77.1	3534	6	AR166490 Sequence
41	4812.5	77.1	3534	6	AR179220 Sequence
42	4812.5	77.1	3534	6	AX383797 Sequence
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44	4812.5	77.1	3534	6	AR107429 Sequence
45	4804.5	76.9	3531	6	

# ALIGNMENTS

RESULT 1

AR050193  
LOCUS AR050193 3522 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 24 from patent US 5827514.  
ACCESSION AR050193  
VERSION AR050193.1 GI:5972918  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3522)  
AUTHORS Bradfisch, G.A., Thompson, M. and Schwab, G.B.  
TITLE Pesticidal compositions  
JOURNAL Patent: US 5827514-A 24 27-OCT-1998;  
FEATURES Location/Qualifiers  
1..3522  
/organism="unknown"  
BASE COUNT 1150 a 601 c 786 g 985 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 0 Length: 3522  
Score: 6244.00 Matches: 1174  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0  
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QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeu 40  
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QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
Db 121 ACACGTTTCCTTTTGGTGAATTTGTTCCAGGTGTTGGAGTTCGGTGGATTTTAT 180  
QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80  
Db 181 TTAATATGGGGTTTATAACTCTCTGATTGGAGCTTATTTCTTTACAGATTGAACAA 240  
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 ACCESSION AR060321  
 VERSION AR060321.1 GI:5986771  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 3522)  
 AUTHORS Thompson,M. and Schwab,G.E.  
 TITLE .beta.-Endotoxin expression in pseudomonas fluorescens  
 JOURNAL Patent: US 5840554-A 24 24-NOV-1998;  
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US-09-837-961-8 (1-1174) x AR060321 (1-3522)

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VERSION AR105486.1 GI:12819083
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3522)
AUTHORS Payne,J. and Sick,A.J.
TITLE Bacillus thuringiensis isolate active against lepidopteran pests,
and genes encoding novel lepidopteran-active toxins
JOURNAL Patent: US 6096708-A / 01-AUG-2000;
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## RESULT 4

AX088274

LOCUS AX088274 3522 bp DNA linear PAT 17-MAR-2001

DEFINITION Sequence 5 from Patent WO0113731.

ACCESSION AX088274

VERSION AX088274.1 GI:13397177

## KEYWORDS

SOURCE Bacillus thuringiensis.

## ORGANISM

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

## REFERENCE

1 (bases 1 to 3522)  
Stockhoff,B.A. and Conlan,C.  
Methods of controlling cutworm pests  
Patent: WO 0113731-A 5 01-MAR-2001;

## JOURNAL

Mycogen Corporation (US)

## FEATURES

Location/Qualifiers  
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/db\_xref="taxon:1428"

BASE COUNT 1156 a 589 c 782 g 995 t

## ORIGIN

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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DEFINITION Sequence 24 from patent US 5527883.
ACCESSION I22418
VERSION I22418.1 GI:1602772
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1. (bases 1 to 3522)
AUTHORS Thompson,M. and Schwab,G.E.
TITLE Delta-endotoxin expression in pseudomonas fluorescens
JOURNAL Patent: US 5527883-A 24 18-JUN-1996;
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VERSION I76417.1 GI:3012571  
KEYWORDS



SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 3522)  
 AUTHORS Payne,J. and Sick,A.J.  
 TITLE Bacillus thuringiensis isolate active against lepidopteran pests  
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 Db 1441 GTTGTAAAGAGGCGCGGGTTTACGGGAGGAGATATTCTTCGACGAACAAGTGGAGGACCA 1500

Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
 Db 1501 TTTGCTTATACATTGTTTAAATTAATGGGCAATTTACCCCAAGGTATCGTCAAGAATA 1560

Qy 521 ArgTyrAlaSerThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
 Db 1561 CCTATGCTCTACTACAAATCTAGAAATTTACGTACGGTTGCAGGTGAACGGATTTT 1620

Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
 Db 1621 GCTGTCAATTTAACAACAAATGGATACCGGTGACCCCATTAACATTCCAATCTTTTACT 1680

Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
 Db 1681 TAGCAACTATTAAATACAGCTTTTACATTTCCCAATGAGCAGAGTAGTTTTCACAGTAGT 1740

Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600  
 Db 1741 GCTGATCTTTTAGTTTCAGGGAAATGAAGTTTATATAGACAGATTTGAATTTGATCCAGTT 1800

Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620  
 Db 1801 ACTGCAACATTTGAGCAGATATGATTTAGAAAGAGCACAAAGCGGTGATCGCTG 1860



Qy	621	PhetRSerIleasnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln	640
Db	1861	TTTACTTCTATAACCAATAGGGATAAAACAGAGATGTGACGGATATTATCATATTGATCAA	1920
Qy	641	ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu	660
Db	1921	GTATCCAATTAGTGGATTGTTTATCAGATGAATTTTGTCTGGATGAACACGGAATG	1980
Qy	661	SerGluLysValLysHisAlaLysArgLeuSerAspGluuArgAsnLeuLeuGlnAspPro	680
Db	1981	TCCGAGAAAGTCAACATCGAAGCGACTCACTGATGAGCGGAATTTACTTCAAGATCCA	2040
Qy	681	AsnPhelysGlyIleAsnArgGlnIleuAspArgGlyTTPArgGlySerThrAspIleThr	700
Db	2041	AACCTTCAAGCGATCAATAGGCAACTAGACCGTGGTGGAGAGAACTACGGATATTATACC	2100
Qy	701	IleGlnArgGlyAspAspValPheLysGlnAsnTyrValThrLeuProGlyThrPheAsp	720
Db	2101	ATCCNAGAGGAGATCAGCTATTCAAAGAAATTTATGTCACACTACAGGTACCTTTGAT	2160
Qy	721	GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr	740
Db	2161	GAGTGTATCCACGATTATTATCAAAATAATAGATGAGTCGAATTAACAAACCTATACT	2220
Qy	741	ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg	760
Db	2221	CGTTATCAATTAGACGGTATATCAGAGATAGTCAGAACTTAGAAATCTATTGATCCGC	2280
Qy	761	TyrAsnAlaLysHisGlnThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer	780
Db	2281	TATAATGCAAAACACGAAACAGTAAATGTCTAGTACGGGTCTTTATGSCCGCTTTC	2340
Qy	781	ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr	800
Db	2341	GTCCAAGTCCAATCAGAAGTGTGGAAACCGAATCGATCGCGCCACACCTTGAATGG	2400
Qy	801	AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis	820
Db	2401	AATCCTGATCTAGATTGTTCTCGACAGACGGGGAAAAATGTGCACATCATTCGCATCAT	2460
Qy	821	PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal	840
Db	2461	TTCTCTCTGGACATTGATGTTGGATGTACAGACTTAAATAGGACTTAGATGTATGGGTG	2520
Qy	841	IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu	860
Db	2521	ATATTTCAAGATTAAAGACCAAGATGCCATGCCAAGCTAGGAATCTAGAGTTTCTCGAA	2580
Qy	861	GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg	880
Db	2581	GAGAAACCATTAGTCGGGAACCACTAGCTCGTGTGAAAAGACGACAGAAAAAATGGAGA	2640
Qy	881	AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer	900
Db	2641	GATAAAGCTGAAAATTTGGAATTTGAAACAAATATGTTTATAAGAGGCCAAAGAAATCT	2700
Qy	901	ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla	920
Db	2701	GTAGATGCTTTATTGTGAACCTCTCAATATGATCAATTTACAGCGGATACGAATATTGCC	2760
Qy	921	MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu	940
Db	2761	ATGATTCAATCGCGCAGATAACGTGTTTCATAGAATTCGGGAAGCGTATCTTCCAGAGTTA	2820
Qy	941	SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr	960
Db	2821	TCGTGTATTCCGGGTGTAATGTAGACATTTTTCGAAGAATTTAAAGGCGGTATTTTCACT	2880
Qy	961	AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu	980
Db	2881	GCATTTCTCTATATGATCCGGAATGTCAATTAACACGGTGATTTCAATAATGGCTTA	2940

Qy	981	SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal	1000
Db	2941	TCATGCTGGAAAGCGTGAAGAGCATGTAGATGTAGAAGAACAAACACACCGTTCGGTTC	3000
Qy	1001	LeuValValProGluTrpGluAlaGluValSerGlnGluValAlaArgValCysProGlyArg	1020
Db	3001	CTTGTTGTTCCGAATGSGAAGCAGAGTGTACAAAGAAGTTCGTGTCTCCGGGTGCT	3060
Qy	1021	GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle	1040
Db	3061	GGCTATATCCTTCGTGTCCACAGCTACAAAGAGGGATATGGAGAAGTTCGGTAACCAT	3120
Qy	1041	HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal	1060
Db	3121	CATGAGATCGAGACAAATACAGACGAAGTTCAGATTACCACTCGGTAGAGAGAGATC	3180
Qy	1061	TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyTyrGly	1080
Db	3181	TATCCAAACAACACGGTAAACGTGTAAATGATTATCTACTGCAAAATCAAGAAGAATAC	3240
Qy	1081	AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro	1100
Db	3241	CGGTACACTTCCCGTAATCTCGTGATGACGAACCTTATGGAAGCAATCTCTCTGTACA	3300
Qy	1101	AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro	1120
Db	3301	GCTGATTATGCGTTCAGTCTATGAAGAAATTCGTATACAGATGGACGACGAGACAATCCT	3360
Qy	1121	CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys	1140
Db	3361	TGTGAATCTACAGAGNATGCGGATTACACACCCTACCACTGGCGTATGTGNCARAA	3420
Qy	1141	GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly	1160
Db	3421	GAATTAGAGTACTTCCCAAGAACCGGATAAGGTATGATTGATGTAGATCGGAGAACGG	3480
Qy	1161	ThrPheIleValAspSerValGluLeuLeuMetGluGlu	1174
Db	3481	ACATTATCTGGACGCGTGGAAATCTCCTTATGGAGGAA	3522
RESULT	8		
BACCRYIF			
LOCUS	BACCRYIF	3525 bp	DNA linear BCT 26-APR-1993
DEFINITION	Bacillus thuringiensis (cryIF) gene, complete CDS.		
ACCESSION	M73254		
VERSION	M73254.1	GI:142755	
KEYWORDS	insecticidal delta-endotoxin.		
SOURCE	Bacillus thuringiensis (strain PS81I, sub-species aizawai) DNA.		
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.		
REFERENCE	1 (bases 1 to 3525)		
AUTHORS	Feitelson, J.S.		
JOURNAL	Unpublished (1991)		
FEATURES	Location/Qualifiers		
source	1..3525		

gene

CDS

TNRQWARFNRDRDLTLVLDIVALFPNDVRYTPIQTSQTLREIYTSVIEDSPV  
 SYGPNFNGAEPGRVPHLDMFNLSFWTAETVRYSQTVGWHGLVSSRNTAGNRNPP  
 SIVTNGCGAIAWIEDRPFYRTLSDPFVVRGGGNPHYVVLGRLGVAFQCTGNHTR  
 TFRNSGLIDSLDEIPPODNSCAPNDYSHVLNHVTFVRWPEISEIGSDSWRAPMDSWH  
 ASAPTNIIDPERITQPLVKAHLQSGTTVRGPGFTGGDILRLTSGGPFAYTIIVNI  
 NGQLPQRYRARIRYASTNLRIYTVVAGERIFAGQFNKNDTDPFLATFQSFSYATINT  
 AFTFMSQSSVTGADVDFSSNEVYIDRFELIPVTAPEAYDLERAKVNALFTSI  
 NOIGIKTVDTYHIDOVSNLVDCSDFCLDEKRELSKVHAKRLSERNLLODPNF  
 KGINROLDRGRGSTDITIORGDDVFKEVYVLTGCTFDECYPTVLYOKIDESKLPYT  
 RYQOLRGYEDSQDLEILYRYNAKHETVNLVLTGSLPVSQSKCKGECNRCAPHL  
 EWNPDLDCSDEKCAHSHHFSLIDIDVGCTDLNEDLDVWVIFKIQDGHARLGNL  
 EFLPEKLVGALARYAKRAKKWRDKREKLENTNIVYKEAKESYDALFVNSQDLOL  
 ADTNIAHHAADKVRHRIEAYLPELSIPGVNDIFEEELKGRIFTAFPLYDARNVIK  
 NGDNNGLSGVNKHGVDBQNNHRSVLVVPWEAEVSOEVRVCPGRGYILRYTAYK  
 EGYGECVCTIHEIENNTDELKSNCEVEEVYNNVTCTNDYTAQOEYGGAYTSRNG  
 YDEYTGSSNSVPADYASYEKSSTYDGRDNPCESNRGYGDYTFDPAGYVYKELEYFP  
 ETDVWEIGETEGTFIVDSVELLIMEE\*  
 BASE COUNT 1157 a 589 c 783 g 996 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 0 Length: 3525  
 Score: 6244.00 Matches: 1174  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

## US-09-837-961-8 (1-1174) x BACCRIF (1-3525)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20  
 DB 1 ATGGAGAATAATCAAAATCAATCGGTACCTTACAAATGTTAAATAATCCTGAAGTA 60  
 QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40  
 DB 61 GAAATATTAAATGAGAAGAAGTAGTCTGGCAGATTACCGTTAGATATATCCTTATCGCCT 120  
 QY 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60  
 DB 121 ACACGTTTCCTTTTGAGTGAATTTGTTCCAGGTGGGAGTGGCGTTTGGATTATTGTAT 180  
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuGlnIleGluGln 80  
 DB 181 TTAATATGGGGTTTATTAACCTCTGATGGAGCTTATTTCTTTACAGATTGAACAA 240  
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100  
 DB 241 TTGATTGAGCAAGAAGATAGAAACATTTGGAAGAACCCGGGCAATTACTACATTACGAGGG 300  
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120  
 DB 301 TTAGCAGATAGCTATGAAATTTATTTGAAGCACCTAAGACAGTGGGAACCAATCCTAAT 360  
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140  
 DB 361 AATGCACAATTAAGGAAGATGGCGTATTGCTATTGCTAAATACAGCACCGCTTTAATA 420  
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuSerValTyrVal 160  
 DB 421 ACAGCAATAAATAATTTACATTACAGTTTGAATCCCTCTTTTATCGGCTCATGTT 480  
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
 DB 481 CAAGCGCGCAATTTACATTTATCATTATTAGAGACGCTGTATCGTTTGGGCGGGTGG 540  
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200  
 DB 541 GGACTGGATATAGCTACTGTTAATAATCATTTATAATAGATTATTAATCTTATCATAGA 600  
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220  
 DB 601 TATAGAAACATTGTTTGGACACATACAATCAAGGATTAGAAACTTAAAGAGGTACTAAT 660  
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240  
 DB 661 ACTCCACAATGGCAGAGATCAATCAATGTTTACGAGAGATTTACACTTACTGTATTAGAT 720  
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260  
 DB 721 ATCGTTGCTCTTTTCCGAACATACGATGTTAGACATATCCAATCAACAGTCATCCCAA 780  
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280  
 DB 781 TTAACAAGGGAATTTATACAAGTTTCACTAATGAGGATTCCTCCAGTTTCTGCTAATATA 840  
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300  
 DB 841 CTAATGTTTAAATAGGGCGGAATTTGGAGTTAGACCCGCCCACTTATGAGACTTTATG 900  
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320  
 DB 901 AATTCCTTTGTTTAACCTGCAGAGACTGTTAGAAGTCAAACTGTGTGGGAGGACACTTA 960  
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
 DB 961 GTTAGTTTACGAAATACGGCTGTAACCGTATAAAATTCCTAGTTTACGGGCTCTTCAAT 1020  
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360  
 DB 1021 CCTGGTGGCGCCATTGGATTGCAGTAGGATCCACGTCCTTTTTTATCGGACATTATCA 1080  
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
 DB 1081 GATCCTGTTTTTGTCCGAGGAGGATTTGGGAATCCTCATATGATGCTGGGCTTAGGGGA 1140  
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
 DB 1141 GTAGCATTTTCAACAACTGCTAGCAACACACCCGCAACATTTAGAAATATAGTGGACCAT 1200  
 QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyValaProTrpAsnAspTyrSer 420  
 DB 1201 GATTCCTAGATGAATCCACCTCAGGATATATAGTGGGCGACCTTGGAGTATATAGT 1260  
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
 DB 1261 CATGTATTAAATCATGTTACATTTGTACGATGCCAGGTGAGATTTTCAGAACTGATTCA 1320  
 QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
 DB 1321 TGGAGAGCTCCCAATGTTTCTTGGACGCCACCTAGTGCACCCCTACAAATACAATGTAT 1380  
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
 DB 1381 CCGGAGAGATTTACTCAATATACATTTGGTAAAGCACATACACTTCAGTCAGGTACTACT 1440  
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500  
 DB 1441 GTTGTAAAGAGGCGCGGTTTACGGGAGGAGATATTTCTTCGAGAAACAAGTGGAGGACCA 1500  
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520  
 DB 1501 TTTGCTTATATTGTTTAAATGGAATGGAATTAATCCCAAGGTATCCTGCAAGAATA 1560  
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
 DB 1561 CGCTATGCTCTACTACAAATCTAGAAATTTACGTAAACGTTGCAGGTGAACGGATTTT 1620  
 QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
 DB 1621 GCTGGTCAATTTAACAACAAACATGATACCGGTGACCCATTAACATTCCTTTTACT 1680  
 QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
 DB 1681 TAGCAACATTTAATAACAGCTTTTACATTTCCCAATGAGCCAGAGTAGTTTTCACAGTAGT 1740

Qy	581	AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal	600
Db	1741	GCTGATACTTTTAGTTCAGGGAATGAAGTTTATATAGACAGATTTGAATTGATCCAGTT	1800
Qy	601	ThrAlaThrPheGluAlaGluTyrAspLeuGluAArgAlaGluLysAlaValAsnAlaLeu	620
Db	1801	ACTGCAACATTGAAGCAGAAATATGATTTAGAAAGAGCACAAAGAGCGGTGAATCGCGTG	1860
Qy	621	PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln	640
Db	1861	TTTACTTCTATAACCAAAATAGGATATAAAACAGATGTGCGGATATCATATTGATCAA	1920
Qy	641	ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu	660
Db	1921	GTATCCAAATTAGTGGATTGTTTATCAGATGAATTTGTCTGGATGAAAGCAGAAATTG	1980
Qy	661	SerGluLysValLysHisAlaLysArgLeuSerAspGluAArgAsnLeuLeuGlnAspPro	680
Db	1981	TCCGAGAAAGTCAACATCGGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCA	2040
Qy	681	AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr	700
Db	2041	AACTTCAAGGCATCAATAGCCAACATAGACCCTGGTGTGAGAGGAAGTACGATATTACC	2100
Qy	701	IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp	720
Db	2101	ATCCAAAGAGGAGATGACGTATTCAAGAAAAATTTATGCACACTACCAAGTACCTTTGAT	2160
Qy	721	GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr	740
Db	2161	GAGTGCATCCACGATTTTATATCAAAAAATAGATGAGTCGAAATTAACACCTATACT	2220
Qy	741	ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg	760
Db	2221	CGTTATCAATTAAGAGGTATATCGAGGATAGTCAAGACTTAGAAATCTATTTCATCGCG	2280
Qy	761	TyrAsnAlaLysHisGlnThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer	780
Db	2281	TATAATCAAAACACGAACAGTAAATGTGTAGTACCGGTTCTTTATGCGCGCTTCA	2340
Qy	781	ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyrP	800
Db	2341	GTCCAAAGTCCATCAGAAAGTGTGAGAACCGAATCGATGCGCGCCACACCTTGAATGG	2400
Qy	801	AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis	820
Db	2401	AATCCTCATCTAGATTGTTCTCGACAGACGGGAAAAATGTGCACATCATTCGCATCAT	2460
Qy	821	PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal	840
Db	2461	TTCTCCTTGACATCATGTGTGGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG	2520
Qy	841	IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu	860
Db	2521	ATATTCAAGATTAAAGCGCAAGATGGCCATGCCACACTAGGAATTCATAGATTTCTCGAA	2580
Qy	861	GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg	880
Db	2581	GAGAAACCATTAGTCGGGAAGCACTAGTCTCGTGTGAAAGAGCAGAGAAAAATGGAGA	2640
Qy	881	AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer	900
Db	2641	GATAACGTCGAAAAATTTGGAATTTGGAACAAATATTTGTTTATAAGAGGCAAAAAATCT	2700
Qy	901	ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla	920
Db	2701	GTAGATGCTTTATTGTTAAACCTCAATATGATCAATTACAAAGCGGATACCAATATTGCC	2760
Qy	921	MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu	940
Db	2761	ATGATTATCATCGGCAGATAAACGTGTTCATAGAAATTCGGGAGCGGTATCTTCCAGATT	2820
Qy	941	SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr	960

Db	2821	TCTGCGATTCGGGGTAAATCTAGACATTTTCGAGAGATTAAGAGGCGCTATTTTCACT	2880
Qy	961	AlaPhePheLeuTyTAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu	980
Db	2881	GCATCTTCCCTATATGATGCGAGAAATGCTATTAAGACGGTGATTTCATTAATGGCTTA	2940
Qy	981	SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal	1000
Db	2941	TCATGCTGGACGTGAAGAGGCATGTAGATGTAGAAGACAAACACACCGTTCGGTTC	3000
Qy	1001	LeuValValProGluTrpGluAlaGluValSerGlnGlnValArgValValCysProGlyArg	1020
Db	3001	CTTGTTGTTCCGAATGGGAAGCAAGTGTACAAAGAAGTTCGTGTCTGTCGGGTCGT	3060
Qy	1021	GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle	1040
Db	3061	GGCTATATPCCCTCGTGTACACCGCTACAGAGGCGATATGGAGAAGGTTCGTAAACCAT	3120
Qy	1041	HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal	1060
Db	3121	CATGAGATCGAGACAAATACAGACGAACCTGAAGTTTACCACTCGTAGAAGAGGAAGTC	3180
Qy	1061	TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly	1080
Db	3181	TATCCAAACAACAGGTAACTGTAATGATTATCTACTGCATAATCAAGAAGAATACGGGGT	3240
Qy	1081	AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro	1100
Db	3241	CGGTACACTCCCGTAATCGTGGATATACGAACACTTATGGAAGCAATCTCTGTATACA	3300
Qy	1101	AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro	1120
Db	3301	GCTGATTATGCGTCAGTCTATGAAGAAATCGTATACAGATGTCGAGAGAGACATCTCT	3360
Qy	1121	CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys	1140
Db	3361	TGTGAATCTAACAGAGGATATGGGATATACACACACTACCAGCTGGCTATGTGCACAAA	3420
Qy	1141	GluLeuGluTyrPheProGluThrAspLysValThrIleGluIleGlyGluThrGluGly	1160
Db	3421	GAATTAGAGTACTTCCCAAGAACCGATGAAGTATGGATTGAGATCGGAGAACCGAAGGA	3480
Qy	1161	ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174	
Db	3481	ACATTATCGTGGACAGCGTGGATTACTCTTATGGAGGA 3522	
RESULT	9		
BACCRYIFA			
LOCUS		5649 bp DNA linear BCT 26-APR-1993	
DEFINITION		Bacillus thuringiensis insecticidal crystal protein (CryIF) gene, complete cds.	
ACCESSION	M38897		
VERSION	M38897.1	GI:142757	
KEYWORDS		insecticidal crystal protein.	
SOURCE		Bacillus thuringiensis (strain EG6346, sub_species aizawai) DNA.	
ORGANISM		Bacillus thuringiensis	
		Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.	
REFERENCE	1	(bases 1 to 5649)	
AUTHORS		Chambers, J.A., Jelen, A., Gilbert, M.P., Jany, C.S., Johnson, T.B. and Gawron-Burke, C.	
TITLE		Isolation and characterization of a novel insecticidal crystal protein gene from Bacillus thuringiensis subsp. aizawai	
JOURNAL		J. Bacteriol. 173 (13), 3966-3976 (1991)	
MEDLINE		91286178	
PUBMED		2061280	
FEATURES		Location/Qualifiers	
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ORIGIN

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US-09-837-961-8 (1-1174) x BACCRYIFA (1-5649)

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ACCESSION AR050195  
VERSION AR050195.1 GI:5972920  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE  
1 (bases 1 to 3522)  
Unclassified.

AUTHORS Bradfisch,G.A., Thompson,M. and Schwab,G.E.

TITLE Pesticidal compositions

JOURNAL Patent: US 5827514-A 28 27-OCT-1998;

FEATURES Location/Qualifiers

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Best Local Similarity: 97.36% Mismatches: 26  
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US-09-837-961-8 (1-1174) x AR050195 (1-3522)

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DB 2821 TCTGTATTCGGGTGTCATTCGGCTATTTTGAGAAATTAGAACGGCGTATTTTCACT 2880
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
DB 2881 GCATTCCTCCTATATGATCGAGAAATGTCATTAATAAATGGTGATTTAATAATGCTTA 2940
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
DB 2941 TCTGCTGGAACGTGAAGGGCATGTAGATGTAGAAGAACAAACACACCGCTTCGGTC 3000
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
DB 3001 CWTGTGTTCCGGAATGGGAACGACAGAGTGTACAGAAAGTCTCTGTCCGGGTCTG 3060
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
DB 3061 GGTATATCTTCTGTCACAGCTACAGAGGAGGATATGGAGAGGTTCGCTAACCAATT 3120
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
DB 3121 CATGAGATCGAAGAACATACAGCAACTGAAGTTTAGCACTGTGTAGAGAGGAAGTA 3180
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
DB 3181 TATCANAAACACACGCTACGTTATGATTTACTGCCACTCAAGAAAGATATGAGGT 3240
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
DB 3241 ACGTACACTTCTCGTAATCGAGGATATGACGGAGCCTATGAAAGCAATTTCTCTGTACCA 3300
QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
DB 3301 GCTGATATGCTATCGCTATGAAGAAAGCAATATACAGATGGAGAGAGACAACTCT 3360
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
DB 3361 TGTGAATCTAACAGAGGATATGGGATTAACACCACTACAGCTGAGTATGTGACAAAA 3420
QY 1141 GluLeuGlyTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGly 1160
DB 3421 GAATTAGAGTACTTCCAGAAACCGATAAGTATGATTGAGATCGAGAAACGGAAGGA 3480
QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
DB 3481 ACATTATCTGAGACAGCGTGAATTTACTTCTATGGAGGAA 3522
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## RESULT 11

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LOCUS AR060323 3522 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 28 from patent US 5840554.
ACCESSION AR060323
VERSION AR060323.1 GI:5986773
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Thompson,M. and Schwab,G.E.
TITLE .beta.-Endotoxin expression in pseudomonas fluorescens
JOURNAL Patent: US 5840554-A 28 24-NOV-1998;
FEATURES
source Location/Qualifiers
BASE COUNT 1140 a 606 c 795 g 981 t
ORIGIN
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## Alignment Scores:

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Pred. No.: 0 Length: 3522
Score: 6049.00 Matches: 1143
Percent Similarity: 97.79% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 26
Query Match: 96.88% Indels: 0
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US-09-837-961-8 (1-1174) x AR060323 (1-3522)			
QY	1	MetGluAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnProGluVal	20
DB	1	ATGGAARAATAATTCAAAATCAATCGGTACCTTACAATTTGTTAAATAATCTGAAGTA	60
QY	21	GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu	40
DB	61	GAATACTGAACGAAGACGACACCGCGCGCTGCCGCTGGACATCAGCCGTGACCCYT	120
QY	41	ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp	60
DB	121	ACACGTTTCTCTTTTGAGTGAATTTGTTCCAGGTGCGGAGTTGCGTTTGCATTATTGAT	180
QY	61	LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln	80
DB	181	TTAATAATGGGGTTTATACTCCTCTGATTGGAGCTTATTTCTTTACAGATTGAACAA	240
QY	81	LeuIleGluGlnArgIleGluThrLeuGluArgAspAlaIleThrThrLeuArgGly	100
DB	241	TTGATTGACCAAGATAGAAATTTGGAAGAACCGGCAATTTACTATTCAGAGGG	300
QY	101	LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn	120
DB	301	TTAGCAGATAGCTATGAAATTTATATTGAAGCAGCTAAGAGAGTGGGAAGCAATCTTAAT	360
QY	121	AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle	140
DB	361	AATGCACAATTAAGGAAGATGCGGTATTCGATTGCTTAATACAGACGCGCTTAATA	420
QY	141	ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal	160
DB	421	ACAGCAATAAATAATTACACTTACAGTTTGAATCCCTTTTATTCGGTCTATGTT	480
QY	161	GlnAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp	180
DB	481	CAAGCGCGCAATTTACATTTATCACTATTAAAGACGCTGTATCGTTTGGCAGGCTTG	540
QY	181	GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg	200
DB	541	GGACTGGATATAGCTACTGTTTAATAATCAATTAATAGATTAAATAATCTTATTCATAGA	600
QY	201	TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn	220
DB	601	TATACGAACATGTTTGGACATACATCAAGATTAAGAACTTAGAAACTTAGAGGTACTAAT	660
QY	221	ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrValLeuAsp	240
DB	661	ACTCGACAAATGGCAAGATTCAATCAGTTTAGAGAGATTAACTTACTGTATTAGAT	720
QY	241	IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln	260
DB	721	ATCGTGTCTCTTTTCCGAACTACGAGTTTGAACATATCCCAATTCAAACGTCATCCCAA	780
QY	261	LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle	280
DB	781	TTAAACAAGGGAATTTATACAGTTTCAGTAATTGAGGATTCCTCCAGTTTCTGCTAATATA	840
QY	281	ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet	300
DB	841	CCTAATGGTPTTTAATAGGCGGAATTTGAGTTTAGAGTTAGACCGCCCATCTTATGGACTTTATG	900
QY	301	AsnSerLeuPheValThrAlaGluThrValArgSerGluThrValTrpGlyGlyHisLeu	320
DB	901	AATTCCTTTGTTAACTCGACGAGCTGTAGAAGTCAAACTGTGTGGGAGGACACTTA	960
QY	321	ValSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn	340
DB	961	GTTAGTTCACGAATAACGGCTGGTACCGTATAAATTTCCCTAGTTTACGGGGTCTTCAAT	1020
QY	341	ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer	360

DB	1021	CCTGCTGGCGCCATTGGATTGCAGATGAGATCCAGTCTCTTTTATCGGACATATCA	1080
QY	361	AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly	380
DB	1081	GATCCCTGTTTTTTCGAGAGGATTTGGGAATCCTCATTTACTTACTGGGGCTTAGGGGA	1140
QY	381	ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle	400
DB	1141	GTACGATTTCAACAACTGGTACGACACCCGCAACATTAGAATACTGGGACCAT	1200
QY	401	AspSerLeuAspGluIleProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer	420
DB	1201	GATTCTCTAGATGAATCCACCTCAGGATAATAGTGGGCACTCTGGTAATGATTATAGT	1260
QY	421	HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer	440
DB	1261	CATGTATTAAATCATGTTACATTTGACGATGGCCAGGTGAGATTTTCAGGAAGTGATTCA	1320
QY	441	TrpArgAlaProMetPheSerTrpThrHisArgSerAlaIleThrProThrAsnThrIleAsp	460
DB	1321	TGGAGAGCTCCAAATGTTTCTTGGACGCACTGAGTGCACCCCTACAAATACAATTGAT	1380
QY	461	ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr	480
DB	1381	CCGAGAGAGATTACTCAATACCATTTGGTAAAGCACATACACTTCAGTCAGGTACTACT	1440
QY	481	ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgThrSerGlyGlyPro	500
DB	1441	GTGTGAAGAGGCGCGGTTTACGGGAGGAGATATCTTCGACGAACAAGTGGAGGACCA	1500
QY	501	PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle	520
DB	1501	TTTGCTTATACATTGTTAATAATGGCAATTCGCCCAAGGTATCGTCAAGAATA	1560
QY	521	ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe	540
DB	1561	CGCTATGCTCTACTACATAATCTAAGAATTTAGTAACGGTTCGAGGTGAACGGATTTT	1620
QY	541	AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer	560
DB	1621	GCTGGTCAATTTAAACAAAACAATGGATACCGGTGACCCATTAACATTCCAATCTTTAGT	1680
QY	561	TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly	580
DB	1681	TACGCACATTAATAACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGGT	1740
QY	581	AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal	600
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QY	601	ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu	620
DB	1801	ACTGCAACATTTGAAGCAGATATGATTTAGAAAGACACAAAAGCGGTGAATGCGCTG	1860
QY	621	PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspThrHisIleAspGln	640
DB	1861	TTTACTTCTATTAACCAATAGGATTAACACAGATGTGCGGATTTATCATATCGATCGCA	1920
QY	641	ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu	660
DB	1921	GTGTCCAAATTTAGTTACGTATTATTCGGATGAATTTTGTCTGCATGAAAGCCAGATTG	1980
QY	661	SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro	680
DB	1981	TCCGAAAAGTCAACATCGGAAGCACTCAGTGTAGTGAACCAATTTACTCCAAGATTCA	2040
QY	681	AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr	700
DB	2041	AATTTCAAAGACATTAATAGCAACACGAGTGGTGGGGCGGAGTAGTACAGGGATTACC	2100
QY	701	IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp	720

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Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTATCAATAGAGGGTATATCGAAGATAGTCAGACTTAGAAATCTATTAAATTCGC 2280
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780
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Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
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Db 2761 ATGATTCATCGCGACAGATAAACGTGTTCATAGCATTCGAGAACCTTATCGCTGAGCTG 2820
Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
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Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100
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Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
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RESULT 12
LOCUS I19466 3522 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 28 from patent US 5508264.
ACCESSION I19466
VERSION I19466.1 GI:1599821
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3522)
AUTHORS Bradfisch,G.A., Thompson,M. and Schwab,G.E.
TITLE Pesticidal compositions
JOURNAL Patent: US 5508264-A 28 16-APR-1996;
FEATURES
Source 1..3522
Location/Qualifiers
BASE COUNT 1140 a 606 c 795 g 981 t
ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6049.00 Matches: 1143
Percent Similarity: 97.79% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 26
Query Match: 96.88% Indels: 0
DB: 6 Gaps: 0

US-09-837-961-8 (1-1174) x I19466 (1-3522)
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Db 1 ATGGAATAATATTTCAAAATCAATCGTACCTTACAATGTTTAATATTCCTGAGTA 60
Qy 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
Db 61 GAAATATCTGAACGAAGACGACGACGCGCTCGCGCTGGACATCAGCCCTGAGCCT 120
Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
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Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
Db 181 TTAATATGGGTTTATATACTCTTCTGATGGAGCTTATTTCTTTTACAGATTGAACA 240
Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
Db 241 TTGATTGACAAAGAATAGAAACATTGGAAAGAACCGGCAATTACTACATTACGAGG 300
Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
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Qy 141 ThrAlaIleAsnAspPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160  
Db 421 ACAGCAATAAATAATTTACACTTACAAGTTTGAATCCCTCTTTATCGGCTCATGTT 480  
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180  
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Qy 321 ValSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340  
Db 961 GTTACTCACGAATACGGCTGTAACCGTATAATTTCCCTAGTTACGGGCTTTCAT 1020  
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Qy 361 AspProValPheValArgGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380  
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Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400  
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Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420  
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Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440  
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Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460  
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Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480  
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Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540  
Db 1561 CGCTATGCTCTTACACAAATTAAGCAATTAAGTAACGTTGCAGGTGAACGGATTTTT 1620  
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560  
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Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580  
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Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuLeuProVal 600  
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Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640  
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Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660  
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Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680  
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 ACCESSION 122420

VERSION 122420.1 GI:1602774  
 KEYWORDS Unknown.  
 SOURCE Unclassified.  
 ORGANISM Thompson, M. and Schwab, G.E.  
 REFERENCE 1 (bases 1 to 3522)  
 AUTHORS Delta-endoCoxin expression in pseudomonas fluorescens  
 TITLE Patent: US 5527883-A 28 JUN-1996;  
 JOURNAL Location/Qualifiers  
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BASE COUNT 1140 a 506 c 795 g 981 t  
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US-09-837-961-8 (1-1174) x 122420 (1-3522)

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ACCESSION AR050192
VERSION AR050192.1 GI:5972917
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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AUTHORS Bradfisch,G.A., Thompson,M. and Schwab,G.E.
TITLE Pesticidal compositions
JOURNAL Patent: US 5827514-A 22 OCT-1998;
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Location/Qualifiers
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DEFINITION Sequence 26 from patent US 5827514.
ACCESSION AR050194
VERSION AR050194.1 GI:5972919
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3444)
AUTHORS Braafisch,G.A., Thompson,M. and Schwab,G.B.
TITLE Pesticidal compositions
JOURNAL Patent: US 5827514-A 26 27-OCT-1998;
FEATURES Location/Qualifiers
source 1..3444
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BASE COUNT 1119 a 592 c 769 g 964 t
ORIGIN

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Best Local Similarity: 95.49% Mismatches: 20
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Job time : 6715 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 27, 2002, 18:38:09 ; Search time 74 seconds

(without alignments)

252.635 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

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Scoring table:

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Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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7	4745.5	76.0	1177	10	US-09-873-873-28
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#### ALIGNMENTS

##### RESULT 1

US-09-826-660-6

; Sequence 6, Application US/09826660

; Patent No. US20010026940A1

; GENERAL INFORMATION:

; APPLICANT: Cardineau, Guy A.

; APPLICANT: Stelman, Steven J.

; APPLICANT: Narva, Kenneth E.

; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

; FILE REFERENCE: MA-714XC2D1

; CURRENT APPLICATION NUMBER: US/09/826,660

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/178,252

; PRIOR FILING DATE: 1998-10-23

; PRIOR APPLICATION NUMBER: 60/065,215

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/076,445

; PRIOR FILING DATE: 1998-03-02

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 1174

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

; US-09-826-660-6

Query Match 100.0%; Score 6244; DB 10; Length 1174;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIOQCVPYNCLNPEVILNEERSTGRLPLDISLSTRFLLSFVPCGVGVAFLGD 60

Db 1 MENNIOQCVPYNCLNPEVILNEERSTGRLPLDISLSTRFLLSFVPCGVGVAFLGD 60

QY 61 LIWGFITPDSWLSFLLOEQLEIQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120

Db 61 LIWGFITPDSWLSFLLOEQLEIQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120

QY 121 NAQLREDVRIRFANTDALTAINNFILTSFEIPLLSYVQAAANHLISLLRDVSVFGQGW 180

Db 121 NAQLREDVRIRFANTDALTAINNFILTSFEIPLLSYVQAAANHLISLLRDVSVFGQGW 180

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QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDYNQGLNLRGNTQWARFNQFRDLITVLVD 240
Db 181 GLDIATVNNHYNRLINLIHRYTKHCLDYNQGLNLRGNTQWARFNQFRDLITVLVD 240
QY 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVRPPLMDFM 300
Db 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVRPPLMDFM 300
QY 301 NSLFTVTAETVRSQTVGGLHVSRRNTAGNRINFPSPGVFNPGGAIWIADEDPFPYRTLS 360
Db 301 NSLFTVTAETVRSQTVGGLHVSRRNTAGNRINFPSPGVFNPGGAIWIADEDPFPYRTLS 360
QY 361 DPVFRGGGPNHYVLGLRGVAFQQTGTHRTFRNSGTIDSLDEIPPODNSGAPWNDYS 420
Db 361 DPVFRGGGPNHYVLGLRGVAFQQTGTHRTFRNSGTIDSLDEIPPODNSGAPWNDYS 420
QY 421 HVLNHNVTFRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
Db 421 HVLNHNVTFRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
QY 481 VVRGPGFTGGDILRRTSGGPFAYTIIVNINQGLPQRYRARIYASTNLRIVYTVAGERIF 540
Db 481 VVRGPGFTGGDILRRTSGGPFAYTIIVNINQGLPQRYRARIYASTNLRIVYTVAGERIF 540
QY 541 AGQFNKMTDGTDLPTFQSFYSYATINTAFTFPMQSQSFVTGADTFSSGNEVYIDRFELIPV 600
Db 541 AGQFNKMTDGTDLPTFQSFYSYATINTAFTFPMQSQSFVTGADTFSSGNEVYIDRFELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVCLDSEFCLEKREL 660
Db 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVCLDSEFCLEKREL 660
QY 661 SEKVHAKELSDERNLLQDPNFKGINRQLDRGWRGSTDITIQGDDVFKENVYTLPGTGD 720
Db 661 SEKVHAKELSDERNLLQDPNFKGINRQLDRGWRGSTDITIQGDDVFKENVYTLPGTGD 720
QY 721 ECPYLYOKIDESKLPYTRYQLRGYIEDSDLEILYIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYLYOKIDESKLPYTRYQLRGYIEDSDLEILYIRYNAKHETVNVLTGSLWPLS 780
QY 781 VQSPRKCGEPNRCAPHLNPNLDCSRRDGEKCAHSHHFLSDIDVCGTDLNEDLDVWV 840
Db 781 VQSPRKCGEPNRCAPHLNPNLDCSRRDGEKCAHSHHFLSDIDVCGTDLNEDLDVWV 840
QY 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLELTNTIVYKEAKES 900
Db 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLELTNTIVYKEAKES 900
QY 901 VDALFVNSOYDQLOADNTAMIHAADKRVHRIREAYLPBLSVPGVNVDFIPELKGRIFT 960
Db 901 VDALFVNSOYDQLOADNTAMIHAADKRVHRIREAYLPBLSVPGVNVDFIPELKGRIFT 960
QY 961 AFPLDARVNIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCPCR 1020
Db 961 AFPLDARVNIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCPCR 1020
QY 1021 GYLIRVATYKEGEGCVTIHEIENNTDELKFSNCVEEVEYNNVTCTNDYTANOEYGG 1080
Db 1021 GYLIRVATYKEGEGCVTIHEIENNTDELKFSNCVEEVEYNNVTCTNDYTANOEYGG 1080
QY 1081 AYTSNRGYDETYGNSVPADYASYIEKSYTDGRRDNPCSNRGYGDYTPLPAGYVTK 1140
Db 1081 AYTSNRGYDETYGNSVPADYASYIEKSYTDGRRDNPCSNRGYGDYTPLPAGYVTK 1140
QY 1141 ELEYFPETDKVNIETGETGTIVDSVELLME 1174
Db 1141 ELEYFPETDKVNIETGETGTIVDSVELLME 1174

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RESULT 2  
 US-09-826-660-2  
 ; Sequence 2, Application US/09826660  
 ; Patent No. US20010026940A1

```

; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
; US-09-826-660-2

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Query Match 94.2%; Score 5879; DB 10; Length 1148;  
 Best Local Similarity 95.1%; Pred. No. 0;  
 Matches 1117; Conservative 8; Mismatches 23; Indels 26; Gaps 1;

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QY 1 MENNIQOCVPYCNCLNNEVEILNEERSTGRPLDLSLSTRFLLSEFFVGVGVAFGLFD 60
Db 1 MENNIQOCVPYCNCLNNEVEILNEERSTGRPLDLSLSTRFLLSEFFVGVGVAFGLFD 60
QY 61 LWGFTTPSDWSLFLQIEQLIEQRIETLERNAITTLRLGLADSYEIIYIYALREWEANPN 120
Db 61 LWGFTTPSDWSLFLQIEQLIEQRIETLERNAITTLRLGLADSYEIIYIYALREWEANPN 120
QY 121 NACLREDVRIRANTDDALITAINNFTLTSFEPLLSVYVQANLHLSLLRDAVSQGW 180
Db 121 NACLREDVRIRANTDDALITAINNFTLTSFEPLLSVYVQANLHLSLLRDAVSQGW 180
QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDYNQGLNLRGNTQWARFNQFRDLITVLVD 240
Db 181 GLDIATVNNHYNRLINLIHRYTKHCLDYNQGLNLRGNTQWARFNQFRDLITVLVD 240
QY 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVRPPLMDFM 300
Db 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVRPPLMDFM 300
QY 301 NSLFTVTAETVRSQTVGGLHVSRRNTAGNRINFPSPGVFNPGGAIWIADEDPFPYRTLS 360
Db 301 NSLFTVTAETVRSQTVGGLHVSRRNTAGNRINFPSPGVFNPGGAIWIADEDPFPYRTLS 360
QY 361 DPVFRGGGPNHYVLGLRGVAFQQTGTHRTFRNSGTIDSLDEIPPODNSGAPWNDYS 420
Db 361 DPVFRGGGPNHYVLGLRGVAFQQTGTHRTFRNSGTIDSLDEIPPODNSGAPWNDYS 420
QY 421 HVLNHNVTFRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
Db 421 HVLNHNVTFRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
QY 481 VVRGPGFTGGDILRRTSGGPFAYTIIVNINQGLPQRYRARIYASTNLRIVYTVAGERIF 540
Db 481 VVRGPGFTGGDILRRTSGGPFAYTIIVNINQGLPQRYRARIYASTNLRIVYTVAGERIF 540
QY 541 AGQFNKMTDGTDLPTFQSFYSYATINTAFTFPMQSQSFVTGADTFSSGNEVYIDRFELIPV 600
Db 541 AGQFNKMTDGTDLPTFQSFYSYATINTAFTFPMQSQSFVTGADTFSSGNEVYIDRFELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVCLDSEFCLEKREL 660
Db 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVCLDSEFCLEKREL 660
QY 661 SEKVHAKELSDERNLLQDPNFKGINRQLDRGWRGSTDITIQGDDVFKENVYTLPGTGD 720

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Db 661 SEKVHAKRLSDERNLQDPNFRGINRQLDRGWRGSTDITIOGGDDVFKENVYLLIGSTD 720
Qy 721 ECPYTYLQKIDESKLPKTRVQLRGYIEDSDLEYLYIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYTYLQKIDESKLPKTRVQLRGYIEDSDLEYLYIRYNAKHETVNVLTGSLWPLS 780
Qy 781 VQSPIKCGEPCNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840
Db 781 APSPI-----GKCAHSHHFSLDIDVGCTDLNEDLDVWV 814
Qy 841 IFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAEKWKDRKREKLELETNTNIVYKEAKES 900
Db 815 IFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAEKWKDRKREKLEWETNIVYKEAKES 874
Qy 901 VDALFVNSOYDQLOADNTIAMTHAADKRVHRIREAYLPSELVPGVNVNDFIPELKGRIFT 960
Db 875 VDALFVNSOYDQLOADNTIAMTHAADKRVHRIREAYLPSELVPGVNVNDFIPELKGRIFT 934
Qy 961 AFELYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSEVVRVCPGR 1020
Db 935 AFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSEVVRVCPGR 994
Qy 1021 GYLRYTAYKEGEGCVTIHEIENNTDELKFSNCVVEEYVNNVTCNDYTANQEEYGG 1080
Db 995 GYLRYTAYKEGEGCVTIHEIENNTDELKFSNCVVEEYVNNVTCNDYTATQEEYGG 1054
Qy 1081 AYTNRNGYDEYGSNSVSPADYASVYEEKSYTDGRRDNPCSNRGYGDYTPLPAGYVTK 1140
Db 1055 TYTSNRNGYDGAYESNSVSPADYASAYEKKAYTDGRRDNPCSNRGYGDYTPLPAGYVTK 1114
Qy 1141 ELEYFPTDKVWIEIGETGCTFIVDSVELLMEE 1174
Db 1115 ELEYFPTDKVWIEIGETGCTFIVDSVELLMEE 1148
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## RESULT 3

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~ US-09-873-873-26
; Sequence 26, Application US/09873873
; Patent No. US2002008485A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 1999-02-19
; PRIOR FILING DATE: 1997-09-03
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-26
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Query Match 77.1%; Score 4812.5; DB 10; Length 1177;
Best Local Similarity 78.6%; Pred. No. 0;
Matches 933; Conservative 66; Mismatches 165; Indels 23; Gaps 9;
Qy 1 MENNIO-NOCPVPVNCUNNPEVELNFER-STGRPLPDLSLSLTRLSEFVPGVGVAFGL 58
Db 1 MNNPNINCEIPVNCUNSEVEVLGERIETGTPDIDLSLSTQFLSEFVPGVGVAFGL 60
Qy 59 FDLINGFITPDSWLSPLQIQIEQRIETLERNRAITTLRGLADSYEYIYIALREWEAN 118
Db 1131 RDTPLPVGVVTKLEYFPETDKVWIEIGETGCTFIVDSVELLMEE 1177
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Db 61 VDIIMGIFGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAEFSREWEAD 120
Qy 119 PNAQLREDRVIRFANTDDALITAINNFTLTSEFIPLLSVYQAAANLHLSLADAVSFGQ 178
Db 121 PTPALREEMRIQFNDMNSALTAIFLFAVQYQVPLLSVYQAAANLHLSLADAVSFGQ 180
Qy 179 GGLDIATVNNHYNRLNLIHRYTKHCLDYNOGLENLGRTNTROWARENQPERDITLTV 238
Db 181 RGFDAATINSYINDLTRLIGNYTDHAVRWYNTGLERVMGPDROWIRYNQFREUTLTV 240
Qy 239 LDIALFPNDYVRTYP IOTSSOLITREIYTSVIEDSPVSAIPNPGFNRA-----EFGVRPP 294
Db 241 LDIVSLFPNDYRTYPIRTVSQLTIREIYNPVL-----NFDGSPFGSAQGIERSIRSP 294
Qy 295 HLMDFMNSLFTVTAETVRSOTVMGGH--LVSSRNTAGNRINFPYSYGVF--NPGGAIWTADED 351
Db 295 HLMDFMNSLFTVTAETVRSOTVMGGH--LVSSRNTAGNRINFPYSYGVF--NPGGAIWTADED 351
Qy 352 PRPFYRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGNHTRFRNSGTIDSLEIP 407
Db 355 GGGVYRILSTLYRRFPNIGINNQOLSVDLGTFAFXTSSNLPASVYRKSFGVDSLEIP 414
Qy 408 PDNSGAPWNDYSHVLNHHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQI 467
Db 415 PQNNVPPRQGFSHRLSHVSMFSGFSNVSIIIRAPMFSWTHRSATPTNTIDPERITQI 474
Qy 468 PLVKAHTLOSCTTVVRGPGFTGGDILRRTSGGPFATIVNINGQLPQRYRARIYASTIN 527
Db 475 PLVKAHTLOSCTTVVRGPGFTGGDILRRTSGGPFATIVNINGQLPQRYRARIYASTIN 534
Qy 528 LRIYTVVAGERIFAGOFNKMTMDTGDPLTFQSFYSATINTAFPMQSOSTTGVGADTFSSG 587
Db 535 LRIYTVVAGERIFAGOFNKMTMDTGDPLTFQSFYSATINTAFPMQSOSTTGVGADTFSSG 594
Qy 588 NEVYIDRPELIPVATFEAEYDLERAQKAVNALFTSINOIGIKTDYDHIQVSNLVD 647
Db 595 NEVYIDRPELIPVATFEAEYDLERAQKAVNALFTSINOIGIKTDYDHIQVSNLVD 654
Qy 648 LSDEFCLDEKRELSKVKHAKLSDERNLLQDPNFRGINRQLDRGWRGSTDITIOGGDDV 707
Db 655 LSDEFCLDEKRELSKVKHAKLSDERNLLQDPNFRGINRQLDRGWRGSTDITIOGGDDV 714
Qy 708 FKENVYTLPGTFDECYPTLYOKIDESKLPKTRVQLRGYIEDSDLEYLYIRYNAKHET 767
Db 715 FKENVYTLPGTFDECYPTLYOKIDESKLPKTRVQLRGYIEDSDLEYLYIRYNAKHET 774
Qy 768 VNVLTGSLWPLSVAQSPVIRKCGEPCNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDV 827
Db 775 VNVLTGSLWPLSVAQSPVIRKCGEPCNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDV 834
Qy 828 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAEKWKDRKREKLE 887
Db 835 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAEKWKDRKREKLE 894
Qy 888 LETNIVYKEAKESVDALFVNSOYDQLOADNTIAMTHAADKRVHRIREAYLPSELVPGVNV 947
Db 895 WETNIVYKEAKESVDALFVNSOYDQLOADNTIAMTHAADKRVHRIREAYLPSELVPGVNV 954
Qy 948 VDIFEELKGRIETAFPLDYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWE 1007
Db 955 AAIFEELEGRIETAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWE 1014
Qy 1008 AEVSQVRVCPGRGYLLRYTAYKEGEGCVTIHEIENNTDELKFSNCVVEEYVNNVTV 1067
Db 1015 AEVSQVRVCPGRGYLLRYTAYKEGEGCVTIHEIENNTDELKFSNCVVEEYVNNVTV 1074
Qy 1068 CNDYTANQEEYGGAYTSNRNGYDEYGSNSVSPADYASVYEEKSYTDGRRDNPCSNRGY 1127
Db 1075 CNDYTANQEEYGGAYTSNRNGYDEYGSNSVSPADYASVYEEKSYTDGRRDNPCSNRGY 1130
Qy 1128 GYTTPLPAGYVTKLEYFPETDKVWIEIGETGCTFIVDSVELLMEE 1174
Db 1131 RDTPLPVGVVTKLEYFPETDKVWIEIGETGCTFIVDSVELLMEE 1177
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Db 1 MDNPNINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSTQFLSEFVGAGFVGL 60
QY 59 FDLIWTGTFSDWSLFLQIBOLIEORIETLERNRAITTLRGLADSYEIIYEALREWEAN 118
Db 61 VDIWIGFGPSQWDAFLVQIBOLINRIEERFARNAQISRLGLESLNLYQIYAESFREWEAD 120
QY 119 PNAQLREDVIRFANTDDALITAINNFTLSFEIPLLSVYVQAANHLSLRDVAVSFGQ 178
Db 121 PTNPALREEMRIQNDMSALTTPAIPFVAVONYQVPLLSVTVQAANHLSLRDSVFGQ 180
QY 179 GWGLDIATVNNHYNRLINLHRYTKHCLDITYNOGLENLRTNQWAFNQRFRDLTLTV 238
Db 181 RWGFDAAATINSRYNDLTRIGNTDIYAVKNYNTGLERWVGPDSDRWVRYNQFRRLTLTV 240
QY 239 LDIVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSNAPNGFNRA---EFGVRPP 294
Db 241 LDIVALFPNDVRYPIRTVSQTLREIYTNVLE-----NFDGSRFGSAQGIERSIRSP 294
QY 295 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSGVF-NPGGAIWIAD 351
Db 295 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSGVF-NPGGAIWIAD 351
QY 352 PRPFYRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQOQTGTHRTFRNSGTIDSLDEIP 407
Db 355 GQGVYRTLSSLTLYRPPFNIGNNQOLSVDLGTETAYGTSNLPASAVYKSGTVDSLDEIP 414
QY 408 PQDMSGAPNDYSHVLNVITFVRPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQI 467
Db 415 PQDMSGAPNDYSHVLNVITFVRPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQI 474
QY 468 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYARIRYASTN 527
Db 475 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYARIRYASTN 534
QY 528 LRIYTVAGERIFAGQFNKMTDGDPLTFQSFYSYATINTAFTFPMSSQSFYTGADTFSSG 587
Db 535 LRIYTVAGERIFAGQFNKMTDGDPLTFQSFYSYATINTAFTFPMSSQSFYTGADTFSSG 594
QY 588 NEVYIDRELPVPTATFAEYDLERAQAVNALFTSINQIGIKTVDYHIDOVSNLVDC 647
Db 595 NEVYIDRELPVPTATFAEYDLERAQAVNALFTSINQIGIKTVDYHIDOVSNLVDC 654
QY 648 LSDFCLDEKRELSKVKHAKLSERNLLODPNFKGNRLQDRGWRGSTDITIQRGDDV 707
Db 655 LSDFCLDEKRELSKVKHAKLSERNLLODPNFKGNRLQDRGWRGSTDITIQRGDDV 714
QY 708 FKENTVTLPGTFDECYPYLYQKIDESKLKPYTRYQLRGYIEDSDLEIYLRINAKHET 767
Db 715 FKENTVTLPGTFDECYPYLYQKIDESKLKPYTRYQLRGYIEDSDLEIYLRINAKHET 774
QY 768 VNVLTGSLWPLSVQSPTRKGEPRNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDV 827
Db 775 VNVLTGSLWPLSVQSPTRKGEPRNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDV 834
QY 828 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAKWKDRKREKLE 887
Db 835 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAKWKDRKREKLE 894
QY 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIAHADKRYHRIEAYLPELSIPGVN 947
Db 895 WETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIAHADKRYHRIEAYLPELSIPGVN 954
QY 948 VDIPELGRIFTAPFLDARVINKGDPNGLSCWNKVGHDVDEEQNNHRSVLVVPWE 1007
Db 955 AAIFELEGRIFTAPFLDARVINKGDPNGLSCWNKVGHDVDEEQNNHRSVLVVPWE 1014
QY 1008 AEVSQEVRCVPGRGYILRTAYKEGEGCVTHIELENNITDELKTSNCVEEYVYNNVT 1067
Db 1015 AEVSQEVRCVPGRGYILRTAYKEGEGCVTHIELENNITDELKTSNCVEEYVYNNVT 1074
QY 1068 CNDYTANQOEYGGAYTSRNRGYDETYGSSVYPADYASVYEKSYTDGRDNPCSNRGY 1127

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Db 1075 CNDYTANQOEYGGAYTSRNRGYNEA---PSPADYASVYEKSYTDGRRENPCFNRGY 1130
QY 1128 GXYTLPAGYVTKLEYFPETDKVWIEGETEGTFIVDSVELLMEE 1174
Db 1131 RXYTLPAGYVTKLEYFPETDKVWIEGETEGTFIVDSVELLMEE 1177
RESULT 6
US-09-873-873-14
; Sequence 14, Application US/09873873
; Patent NO. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxin
; FILE REFERENCE: MECO-210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 1177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-14

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Query Match 76.9%; Score 4804.5; DB 10; Length 1177;
Best Local Similarity 78.5%; Pred. No. 0;
Matches 932; Conservative 66; Mismatches 166; Indels 23; Gaps 9;
QY 1 MENNIQ-NOCYPNCLNPNPEVILNEER-STGRLPDLISLTRLFLSEFVGVGAVFL 58
Db 1 MDNPNINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSTQFLSEFVGAGFVGL 60
QY 59 FDLIWTGTFSDWSLFLQIBOLIEORIETLERNRAITTLRGLADSYEIIYEALREWEAN 118
Db 61 VDIWIGFGPSQWDAFLVQIBOLINRIEERFARNAQISRLGLESLNLYQIYAESFREWEAD 120
QY 119 PNAQLREDVIRFANTDDALITAINNFTLSFEIPLLSVYVQAANHLSLRDVAVSFGQ 178
Db 121 PTNPALREEMRIQNDMSALTTPAIPFVAVONYQVPLLSVTVQAANHLSLRDSVFGQ 180
QY 179 GWGLDIATVNNHYNRLINLHRYTKHCLDITYNOGLENLRTNQWAFNQRFRDLTLTV 238
Db 181 RWGFDAAATINSRYNDLTRIGNTDIYAVKNYNTGLERWVGPDSDRWVRYNQFRRLTLTV 240
QY 239 LDIVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSNAPNGFNRA---EFGVRPP 294
Db 241 LDIVALFPNDVRYPIRTVSQTLREIYTNVLE-----NFDGSRFGSAQGIERSIRSP 294
QY 295 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSGVF-NPGGAIWIAD 351
Db 295 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSGVF-NPGGAIWIAD 351
QY 352 PRPFYRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQOQTGTHRTFRNSGTIDSLDEIP 407
Db 355 GQGVYRTLSSLTLYRPPFNIGNNQOLSVDLGTETAYGTSNLPASAVYKSGTVDSLDEIP 414
QY 408 PQDMSGAPNDYSHVLNVITFVRPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQI 467
Db 415 PQDMSGAPNDYSHVLNVITFVRPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQI 474
QY 468 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYARIRYASTN 527
Db 475 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYARIRYASTN 534

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QY 528 LRIYVTVAGERIFAGQFNKMTDGLPTFQSPSYATINTAFTFPMQSSQFTVGADTFSSG 587  
DB 535 LRIYVTVAGERIFAGQFNKMTDGLPTFQSPSYATINTAFTFPMQSSQFTVGADTFSSG 594  
QY 588 NEVYIDREFELIPVTATFAEYDLERAQAVNALFTSINOIGIKTDVTDYHIDQVSNLVD 647  
DB 595 NEVYIDREFELIPVTATFAEYDLERAQAVNALFTSINOIGIKTDVTDYHIDQVSNLVD 654  
QY 648 LSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIORGDV 707  
DB 655 LSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIORGDV 714  
QY 708 FKENVYTLPGTFDECYPYLYQKIDESKLPYTRVQLRGYIEDSODLEIYLIRYNAKHET 767  
DB 715 FKENVYTLPGTFDECYPYLYQKIDESKLPYTRVQLRGYIEDSODLEIYLIRYNAKHET 774  
QY 768 VNVLTGSLWPLSVOSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLDIDV 827  
DB 775 VNVLTGSLWPLSVOSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLDIDV 834  
QY 828 GCTDLNEDLDYVWIFKIKTQDGHARGLNLEFLEEKPLVGEALARYKRAEKKWRDKREKLE 887  
DB 835 GCTDLNEDLDYVWIFKIKTQDGHARGLNLEFLEEKPLVGEALARYKRAEKKWRDKREKLE 894  
QY 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIREAYLPELSIPGVN 947  
DB 895 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIREAYLPELSIPGVN 954  
QY 948 VDIPEELKGRIFTAFPLDYDARNVINGDNFNGLSQWNVKGVHDVEEQNNHRSVLVVPWE 1007  
DB 955 AAIPEELEGRIFTAFPLDYDARNVINGDNFNGLSQWNVKGVHDVEEQNNHRSVLVVPWE 1014  
QY 1008 AEVSQEVRCVPCRGYILRVATYKGYGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1067  
DB 1015 AEVSQEVRCVPCRGYILRVATYKGYGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1074  
QY 1068 CNDYTANQEEYGGAYTSRNRGYDETYGNSVPADYASYEESKYTDGRRDNPCEENRGY 1127  
DB 1075 CNDYTANQEEYGGAYTSRNRGYDETYGNSVPADYASYEESKYTDGRRDNPCEENRGY 1130  
QY 1128 GDYTPLPAGYVTKLEYFPETDKVWIEIGETGRTIVDSVELLLMEE 1174  
DB 1131 RDYTPLPAGYVTKLEYFPETDKVWIEIGETGRTIVDSVELLLMEE 1177

## RESULT 7

US-09-873-873-28  
; Sequence 28, Application US/09873873  
; Patent No. US20020064865A1  
; GENERAL INFORMATION:  
; APPLICANT: Malvar, Thomas  
; APPLICANT: Gilmer, Amy Jelen  
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins  
; FILE REFERENCE: MECO:210--2  
; CURRENT APPLICATION NUMBER: US/09/873,873  
; CURRENT FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: US 09/253,341  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: US 08/922,505  
; PRIOR FILING DATE: 1997-09-03  
; PRIOR APPLICATION NUMBER: US 08/754,490  
; PRIOR FILING DATE: 1996-11-20  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 1177  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hybrid Delta-Endotoxin  
US-09-873-873-28

Query Match 76.0%; Score 4745.5; DB 10; Length 1177;  
Best Local Similarity 77.8%; Pred. No. 0;  
Matches 923; Conservative 67; Mismatches 174; Indels 23; Gaps 9;

QY 1 MNNNIQ-NQCVPYCNINPEVEILNEER-STGRPLDIDISLSTRFLSLFVPGVGVAFGL 58  
DB 1 MDNNPNEINCEIPYCNLSNPEVEVLGERLETGYTPIDISLTLQFLSLFVPGVGVAFGL 60  
QY 59 FDLINGFTPPSDNSLFLQIOLIEORITELERNRAITTLRGLADSYETIYIHALREWEAN 118  
DB 61 VDIHWIGTFPSQWDAFLVQIOLINQRIEFARNOAISLEGLSNLYQIYAESFREWEAD 120  
QY 119 PNAOLREDVRREFANTDALTAINNETLTSTFEPILLSVYQOANHLISLIRDAVSFQ 178  
DB 121 PNPALREEMRIQFNDMSALTAIPLFAVQNYQVPLLSVYQOANHLISLIRDAVSFQ 180  
QY 179 GWGLDIAIVNNHYNLNLIIHRYTKHCLDITYNOGLENLRGTNTROWARENQFRRLITLV 238  
DB 181 RWGFAAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRQWRYNQFRRLITLV 240  
QY 239 LDIVALFPNDVRYTPYIQTSSQLTREITTSVIEDSPVSANIPNGFNRA----EFGVRPP 294  
DB 241 LDIVALFPNDVRYTPYIQTSSQLTREITTSVIEDSPVSANIPNGFNRA----EFGVRPP 294  
QY 295 HLMDPMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINRPPSYGVF-NPGGAIWIAED 351  
DB 295 HLMDILNSITTYDAHRGYYWWSGHIWASPVGFGSGPFTFPLYGTMGNAAPQRIVAOL 354  
QY 352 PRPFYRTLSDPVYVRG---GFGNPHY-VLGLRGVAPQQTGTNHTRTFRNSGTFIDSLDEIP 407  
DB 355 GGVYRTLSSTLYRRFPFNIGINNQOLSVLDGTEFAYGTSNLPASVAVYKSGTVDSIDLEIP 414  
QY 408 PDNCSGAPNDYSHVLNHTVYRVWPGETSGSDSWAPMFESWTHRSATPNTTIDPEIRTOI 467  
DB 415 PNNNVPPRQGGSHSLHVSFMSFSGFSNVSIIIRAPMFSWIHRSAEFNIIIASDITOI 474  
QY 468 PLVKAHTLQSGTVVVRGFTGGDILRRTSGPPFAYTIVNINGQLPQRYRARIYASTIN 527  
DB 475 PLVKAHTLQSGTVVVRGFTGGDILRRTSGPPFAYTIVNINGQLPQRYRARIYASTIN 534  
QY 528 LRIYVTVAGERIFAGQFNKMTDGLPTFQSPSYATINTAFTFPMQSSQFTVGADTFSSG 587  
DB 535 LRIYVTVAGERIFAGQFNKMTDGLPTFQSPSYATINTAFTFPMQSSQFTVGADTFSSG 594  
QY 588 NEVYIDREFELIPVTATFAEYDLERAQAVNALFTSINOIGIKTDVTDYHIDQVSNLVD 647  
DB 595 NEVYIDREFELIPVTATFAEYDLERAQAVNALFTSINOIGIKTDVTDYHIDQVSNLVD 654  
QY 648 LSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIORGDV 707  
DB 655 LSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIORGDV 714  
QY 708 FKENVYTLPGTFDECYPYLYQKIDESKLPYTRVQLRGYIEDSODLEIYLIRYNAKHET 767  
DB 715 FKENVYTLPGTFDECYPYLYQKIDESKLPYTRVQLRGYIEDSODLEIYLIRYNAKHET 774  
QY 768 VNVLTGSLWPLSVOSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLDIDV 827  
DB 775 VNVLTGSLWPLSVOSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLDIDV 834  
QY 828 GCTDLNEDLDYVWIFKIKTQDGHARGLNLEFLEEKPLVGEALARYKRAEKKWRDKREKLE 887  
DB 835 GCTDLNEDLDYVWIFKIKTQDGHARGLNLEFLEEKPLVGEALARYKRAEKKWRDKREKLE 894  
QY 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIREAYLPELSIPGVN 947  
DB 895 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIREAYLPELSIPGVN 954  
QY 948 VDIPEELKGRIFTAFPLDYDARNVINGDNFNGLSQWNVKGVHDVEEQNNHRSVLVVPWE 1007  
DB 955 AAIPEELEGRIFTAFPLDYDARNVINGDNFNGLSQWNVKGVHDVEEQNNHRSVLVVPWE 1014  
QY 1008 AEVSQEVRCVPCRGYILRVATYKGYGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1067



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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-30

Query Match          69.1%; Score 4313.5; DB 10; Length 1193;
Best Local Similarity 70.3%; Pred. No. 0;
Matches 844; Conservative 97; Mismatches 226; Indels 33; Gaps 12;

QY 1 MNNNQ-NCVYPNCLNNEVEILNEER-STGRPLDLSLTRFLSEFVPGVAGFL 58
DB 1 MNNPNINEICIPNCLNNEVEILNEER-STGRPLDLSLTRFLSEFVPGVAGFL 60
QY 59 FDLINGFIPSPDWSLFLQIEOLIEQRIETLERNRAITTLRGLADSEYIYIALREWEAN 118
DB 61 VDIWIGIFGSPQWDAPLQIEOLINQRIEFAFNQAIKSLNLYQIYAESFREWEAD 120
QY 119 PNAQOLREVRFRPANTDDALITANNFTLTSTFPLSVYQAAHLNLSLRDVSFGQ 178
DB 121 PTPNALREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYQAAHLNLSLRDVSFGQ 180
QY 179 GGLDIATVNNHYNRLINLHRYTKHCLDYNQGLNLRGTNRQWARENQFRDLTLTV 238
DB 181 RWGFAATINSYNDLTRLIGNYTDYAVRWYNTGLRWGPDSDRWYRNQFRDLTLTV 240
QY 239 LDIVLFPNDYRTPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
DB 241 LDIVLFPNDYRTPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
QY 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINFPYSYGVF-NPGGAIWIADED 351
DB 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINFPYSYGVF-NPGGAIWIADED 351
QY 352 PRPFTLSDPVRG---GFGNPHY-VLGLRGVAFQOQTGTHRTFRNSGTIDSLDEIP 407
DB 352 PRPFTLSDPVRG---GFGNPHY-VLGLRGVAFQOQTGTHRTFRNSGTIDSLDEIP 407
QY 355 GCGVYRTLSLTYRPFNIGINQQLSVLDGTEFAFGTSNLPFSVAYRKSQVSDSLDEIP 414
DB 355 GCGVYRTLSLTYRPFNIGINQQLSVLDGTEFAFGTSNLPFSVAYRKSQVSDSLDEIP 414
QY 408 PDNSGAPNDYSHVNLNHYTVFVRWPCIEISGDSWRAPMFSWTHRSATPTNTIDPERITOI 467
DB 408 PDNSGAPNDYSHVNLNHYTVFVRWPCIEISGDSWRAPMFSWTHRSATPTNTIDPERITOI 467
QY 415 PNNVPPRQGFSHRSLSHVMSFSGNSVSIIIRAPMFSWTHRSATPTNTIDPERINOI 474
DB 415 PNNVPPRQGFSHRSLSHVMSFSGNSVSIIIRAPMFSWTHRSATPTNTIDPERINOI 474
QY 468 PLVKAHTLQSGTVVKGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYARIRYASTTN 527
DB 468 PLVKAHTLQSGTVVKGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYARIRYASTTN 527
QY 475 PLVKGFRVWGGTSVITGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYARIRYASTTN 534
DB 475 PLVKGFRVWGGTSVITGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYARIRYASTTN 534
QY 528 LRIYV-TVAGERIFAGQ-----FNKMTGTGDLPLFQSFYATINTAFTPPMSQSFTV- 579
DB 528 LRIYV-TVAGERIFAGQ-----FNKMTGTGDLPLFQSFYATINTAFTPPMSQSFTV- 579
QY 535 ARVIVLTGAASTGVGGQVSVNNPLOKTMIEIGENLTSRTFRYTDPSNPTFRANPDITIGIS 594
DB 535 ARVIVLTGAASTGVGGQVSVNNPLOKTMIEIGENLTSRTFRYTDPSNPTFRANPDITIGIS 594
QY 580 -----GADTFSSGNEVYIDREELIPVATFEAYDLERAKAVNALFTSINOIGIKTDVT 634
DB 580 -----GADTFSSGNEVYIDREELIPVATFEAYDLERAKAVNALFTSINOIGIKTDVT 634
QY 595 EQPLFGAGSISG-ELYIDKILILADATFEASDLERAKAVNALFTSINOIGIKTDVT 653
DB 595 EQPLFGAGSISG-ELYIDKILILADATFEASDLERAKAVNALFTSINOIGIKTDVT 653
QY 635 DYHDOVSNLVCLEDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWR 694
DB 635 DYHDOVSNLVCLEDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWR 694
QY 654 DYHDOVSNLVCLEDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWR 713
DB 654 DYHDOVSNLVCLEDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWR 713
QY 695 GSTDITIORGDGVFENYVTLPGTDECYPTLYOKIDESKLPKPYTRYLGRYIEDSQDL 754
DB 695 GSTDITIORGDGVFENYVTLPGTDECYPTLYOKIDESKLPKPYTRYLGRYIEDSQDL 754
QY 714 GSTDITIORGDGVFENYVTLPGTDECYPTLYOKIDESKLPKPYTRYLGRYIEDSQDL 773
DB 714 GSTDITIORGDGVFENYVTLPGTDECYPTLYOKIDESKLPKPYTRYLGRYIEDSQDL 773
QY 755 EYLIRYNAKHETVNVGLTSLVQSPFIRKCCPEPNRCAHPLEWNPDLDCSCRGK 814
DB 755 EYLIRYNAKHETVNVGLTSLVQSPFIRKCCPEPNRCAHPLEWNPDLDCSCRGK 814
QY 774 EYLIRYNAKHETVNVGLTSLVQSPFIRKCCPEPNRCAHPLEWNPDLDCSCRGK 833
DB 774 EYLIRYNAKHETVNVGLTSLVQSPFIRKCCPEPNRCAHPLEWNPDLDCSCRGK 833
QY 815 AHHSHFSLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKR 874
DB 815 AHHSHFSLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKR 874
QY 834 AHHSHFSLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKR 893
DB 834 AHHSHFSLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKR 893
QY 875 ABKKWRDKREKLEETNIVYKAKESVDALFVNSQYDQLOADNTNIAHAAKRVHRIE 934
DB 875 ABKKWRDKREKLEETNIVYKAKESVDALFVNSQYDQLOADNTNIAHAAKRVHRIE 934
QY 894 ABKKWRDKREKLEETNIVYKAKESVDALFVNSQYDQLOADNTNIAHAAKRVHRIE 953
DB 894 ABKKWRDKREKLEETNIVYKAKESVDALFVNSQYDQLOADNTNIAHAAKRVHRIE 953

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QY 935 AYLPELSVIPGVNVDIFEELKGRIFTAFLYDARNVKNKGDNNGLSCHNVKGVHVDVEQ 994
DB 935 AYLPELSVIPGVNVDIFEELKGRIFTAFLYDARNVKNKGDNNGLSCHNVKGVHVDVEQ 1013
QY 995 NNHRSVLVPEWEAEVQSVQVPCPGGYILRVTAYKEGYGEGCVTTHEIENNTDELKFSN 1054
DB 995 NNHRSVLVPEWEAEVQSVQVPCPGGYILRVTAYKEGYGEGCVTTHEIENNTDELKFSN 1073
QY 1014 NNHRSVLVPEWEAEVQSVQVPCPGGYILRVTAYKEGYGEGCVTTHEIENNTDELKFSN 1073
DB 1014 NNHRSVLVPEWEAEVQSVQVPCPGGYILRVTAYKEGYGEGCVTTHEIENNTDELKFSN 1073
QY 1055 CVVEEYVYNNVTYNDYTDYANQEEYGGAYTSRNGYDETYGSSNSVPADYASVYEKSYTD 1114
DB 1055 CVVEEYVYNNVTYNDYTDYANQEEYGGAYTSRNGYDETYGSSNSVPADYASVYEKSYTD 1133
QY 1115 GRSDNCPESNRCGYDTPLPAGYVTKELFYFETDKWLEIGETEGCTFFVDSVELLMEE 1174
DB 1115 GRSDNCPESNRCGYDTPLPAGYVTKELFYFETDKWLEIGETEGCTFFVDSVELLMEE 1193
QY 1134 GRSDNCPESNRCGYDTPLPAGYVTKELFYFETDKWLEIGETEGCTFFVDSVELLMEE 1193
DB 1134 GRSDNCPESNRCGYDTPLPAGYVTKELFYFETDKWLEIGETEGCTFFVDSVELLMEE 1193

RESULT 10
US-09-756-643-2
; Sequence 2, Application US/09756643
; Patent No. US20010026939A1
; GENERAL INFORMATION:
; APPLICANT: Rice, Douglas
; APPLICANT: Carozzi, Nadine
; APPLICANT: Anderson, David
; APPLICANT: Rajasekaran, Kanniah
; APPLICANT: Rangan, Thirumale
; APPLICANT: Yemofsky, Richard
; APPLICANT: Lotstein, Richard
; APPLICANT: De Framond, Annick
; TITLE OF INVENTION: Insecticidal Cotton Plant Cells
; FILE REFERENCE: S-16768E
; CURRENT APPLICATION NUMBER: US/09/756,643
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 08/218,697
; PRIOR FILING DATE: 1994-03-28
; PRIOR APPLICATION NUMBER: 07/759,969
; PRIOR FILING DATE: 1991-09-16
; PRIOR APPLICATION NUMBER: 07/274,452
; PRIOR FILING DATE: 1988-11-18
; PRIOR APPLICATION NUMBER: 07/122,109
; PRIOR FILING DATE: 1987-11-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-756-643-2

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Query Match          67.4%; Score 4211.5; DB 10; Length 1155;
Best Local Similarity 70.0%; Pred. No. 0;
Matches 831; Conservative 83; Mismatches 228; Indels 45; Gaps 9;

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QY 1 MNNNQ-NCVYPNCLNNEVEILNEER-STGRPLDLSLTRFLSEFVPGVAGFL 58
DB 1 MNNPNINEICIPNCLNNEVEILNEER-STGRPLDLSLTRFLSEFVPGVAGFL 60
QY 59 FDLINGFIPSPDWSLFLQIEOLIEQRIETLERNRAITTLRGLADSEYIYIALREWEAN 118
DB 59 FDLINGFIPSPDWSLFLQIEOLIEQRIETLERNRAITTLRGLADSEYIYIALREWEAN 120
QY 119 PNAQOLREVRFRPANTDDALITANNFTLTSTFPLSVYQAAHLNLSLRDVSFGQ 178
DB 119 PNAQOLREVRFRPANTDDALITANNFTLTSTFPLSVYQAAHLNLSLRDVSFGQ 180
QY 179 GGLDIATVNNHYNRLINLHRYTKHCLDYNQGLNLRGTNRQWARENQFRDLTLTV 238
DB 179 GGLDIATVNNHYNRLINLHRYTKHCLDYNQGLNLRGTNRQWARENQFRDLTLTV 240
QY 239 LDIVLFPNDYRTPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
DB 239 LDIVLFPNDYRTPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
QY 241 LDIVLFPNDYRTPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
DB 241 LDIVLFPNDYRTPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294

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Qy 295 HLMDFMNSLFVTAETVRSQTVMGH--LVSSRNTAGNRINPFSYGVF-NPGGAIWIADDED 351
Db 295 HLMDFMNSLFVTAETVRSQTVMGH--LVSSRNTAGNRINPFSYGVF-NPGGAIWIADDED 351
Qy 295 HLMDFMNSLFVTAETVRSQTVMGH--LVSSRNTAGNRINPFSYGVF-NPGGAIWIADDED 351
Db 295 HLMDFMNSLFVTAETVRSQTVMGH--LVSSRNTAGNRINPFSYGVF-NPGGAIWIADDED 351
Qy 352 PRPFYRTLSLDPVVRG---GFGNPHY-VLGRGVAFQQTGNHRTFRNSGTIDSLDEIP 407
Db 352 PRPFYRTLSLDPVVRG---GFGNPHY-VLGRGVAFQQTGNHRTFRNSGTIDSLDEIP 407
Qy 355 GQGVYRTLSLTPYRRPFGINNNQOLSVDLGTETAYGTSNNLPSAVYKSGTVDLDEIP 414
Db 355 GQGVYRTLSLTPYRRPFGINNNQOLSVDLGTETAYGTSNNLPSAVYKSGTVDLDEIP 414
Qy 408 PQDMSGAPWNDYSHVNLHVTVFVRWPEIGSGDSWRAPFWSWTHRSATPTNTIDPERITQI 467
Db 408 PQDMSGAPWNDYSHVNLHVTVFVRWPEIGSGDSWRAPFWSWTHRSATPTNTIDPERITQI 467
Qy 415 PQNNVPPRQGFSGHLSHVMSFRSGFSNVSIIIRAPFWSWTHRSAEFNIIISQITQI 474
Db 415 PQNNVPPRQGFSGHLSHVMSFRSGFSNVSIIIRAPFWSWTHRSAEFNIIISQITQI 474
Qy 468 PLVKAHTLQSGTIVVRGPGTGGDILRRTSQGPFFAYTTVINGQLPQYRARIYASTTN 527
Db 468 PLVKAHTLQSGTIVVRGPGTGGDILRRTSQGPFFAYTTVINGQLPQYRARIYASTTN 527
Qy 475 PLTASTNLGSGTSVVGKPGFTGGDLIRTSQGIQSLRVNITAPLSQIRVIRIYASTTN 534
Db 475 PLTASTNLGSGTSVVGKPGFTGGDLIRTSQGIQSLRVNITAPLSQIRVIRIYASTTN 534
Qy 528 LRIYTVVAGERIFAQGNKMTMDTGDPLTFQSFYSYATINTAFTFPMSSQSFVVGADTFSSG 587
Db 528 LRIYTVVAGERIFAQGNKMTMDTGDPLTFQSFYSYATINTAFTFPMSSQSFVVGADTFSSG 587
Qy 535 LQFHTSIDGRPINOGNFSATNNSGSLQSGSFRTVGFTHPFSNGSSVFTLSAHVPNSG 594
Db 535 LQFHTSIDGRPINOGNFSATNNSGSLQSGSFRTVGFTHPFSNGSSVFTLSAHVPNSG 594
Qy 588 NEVYIDRELPVATPAEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVD 647
Db 588 NEVYIDRELPVATPAEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVD 647
Qy 595 NEVYIDRELPVATPAEAYDLERAQKAVNELFTSSNQIGLKTDTVTDYHIDQVSNLVE 654
Db 595 NEVYIDRELPVATPAEAYDLERAQKAVNELFTSSNQIGLKTDTVTDYHIDQVSNLVE 654
Qy 648 LSDEFCLDEKELSEKVKHAKRLSDERNLLQDPNFKGINROLDRGWRGSTDITIQRGDDV 707
Db 648 LSDEFCLDEKELSEKVKHAKRLSDERNLLQDPNFKGINROLDRGWRGSTDITIQRGDDV 707
Qy 655 LSDEFCLDEKELSEKVKHAKRLSDERNLLQDPNFKGINROLDRGWRGSTDITIQRGDDV 714
Db 655 LSDEFCLDEKELSEKVKHAKRLSDERNLLQDPNFKGINROLDRGWRGSTDITIQRGDDV 714
Qy 708 FKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSODLEIYLRINAKHET 767
Db 708 FKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSODLEIYLRINAKHET 767
Qy 715 FKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSODLEIYLRINAKHET 774
Db 715 FKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSODLEIYLRINAKHET 774
Qy 768 VNVLTGSLWPLSVQSPRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHPSLDDIV 827
Db 768 VNVLTGSLWPLSVQSPRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHPSLDDIV 827
Qy 775 VNVLTGSLWPLSVQSPRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHPSLDDIV 808
Db 775 VNVLTGSLWPLSVQSPRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHPSLDDIV 808
Qy 828 GCTDLNEDLVWVIFKIKTQGHARLGNLEFLKPLVGEALARKRAEKWKDRKREKLE 887
Db 828 GCTDLNEDLVWVIFKIKTQGHARLGNLEFLKPLVGEALARKRAEKWKDRKREKLE 887
Qy 809 GCTDLNEDLVWVIFKIKTQGHARLGNLEFLKPLVGEALARKRAEKWKDRKREKLE 868
Db 809 GCTDLNEDLVWVIFKIKTQGHARLGNLEFLKPLVGEALARKRAEKWKDRKREKLE 868
Qy 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIEAYLPSELSVPGVN 947
Db 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIEAYLPSELSVPGVN 947
Qy 869 WETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIEAYLPSELSVPGVN 928
Db 869 WETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIEAYLPSELSVPGVN 928
Qy 948 VDIEELKGRIFTAFPLDYDARNVKNQDFNGLSCWNVKGVHDVDEEQNNHRSVLVVPWE 1007
Db 948 VDIEELKGRIFTAFPLDYDARNVKNQDFNGLSCWNVKGVHDVDEEQNNHRSVLVVPWE 1007
Qy 929 AAIFEELEGRIPTAFSLDYDARNVKNQDFNGLSCWNVKGVHDVDEEQNNHRSVLVVPWE 988
Db 929 AAIFEELEGRIPTAFSLDYDARNVKNQDFNGLSCWNVKGVHDVDEEQNNHRSVLVVPWE 988
Qy 1008 AEVSOEVRVCPGRGYILRVATYKGYGEGCVTIHEIENNTDELKFSNCVEEVEVPNTVT 1067
Db 1008 AEVSOEVRVCPGRGYILRVATYKGYGEGCVTIHEIENNTDELKFSNCVEEVEVPNTVT 1067
Qy 989 AEVSOEVRVCPGRGYILRVATYKGYGEGCVTIHEIENNTDELKFSNCVEEVEVPNTVT 1048
Db 989 AEVSOEVRVCPGRGYILRVATYKGYGEGCVTIHEIENNTDELKFSNCVEEVEVPNTVT 1048
Qy 1068 CNDYTANDEEYGGAYTSNRNGYDYEYGNSSVPADYASVYEEKSYTDGRRDNPCSNRGY 1127
Db 1068 CNDYTANDEEYGGAYTSNRNGYDYEYGNSSVPADYASVYEEKSYTDGRRDNPCSNRGY 1127
Qy 1049 CNDYTATQEEYEGTYSNRNGYDYGAYESSVPADYASVYEEKSYTDGRRDNPCSNRGY 1108
Db 1049 CNDYTATQEEYEGTYSNRNGYDYGAYESSVPADYASVYEEKSYTDGRRDNPCSNRGY 1108
Qy 1128 GDTPLPAGYVTKLEYEPEDTKWIEIETEGTGFIVDSVELLME 1174
Db 1128 GDTPLPAGYVTKLEYEPEDTKWIEIETEGTGFIVDSVELLME 1174
Qy 1109 GDTPLPAGYVTKLEYEPEDTKWIEIETEGTGFIVDSVELLME 1155
Db 1109 GDTPLPAGYVTKLEYEPEDTKWIEIETEGTGFIVDSVELLME 1155

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RESULT 11

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US-09-851-194-2
; Sequence 2, Application US/09851194
; Patent No. US20020048799A1
; GENERAL INFORMATION:
; APPLICANT: Adaug, Michael J
; TITLE OF INVENTION: Insecticidal Protein Fragments
; FILE REFERENCE: MFS17-8304
; CURRENT APPLICATION NUMBER: US/09/851,194
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 06/617,321

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; PRIOR FILING DATE: 1984-06-04
; PRIOR APPLICATION NUMBER: US 08/477,973
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/687,017
; PRIOR FILING DATE: 1996-07-16
; PRIOR APPLICATION NUMBER: US 08/682,169
; PRIOR FILING DATE: 1996-07-16
; PRIOR APPLICATION NUMBER: US 09/422,833
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 09/612,811
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1178
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-09-851-194-2

Query Match      66.4%; Score 4148; DB 10; Length 1178;
Best Local Similarity 69.1%; Pred. No. 0;
Matches 828; Conservative 85; Mismatches 241; Indels 44; Gaps 14;

Qy 1 MNNIQ-NQCVYPYCNLNPEVEILNEER-STGRPLDLSLSTRELLSEFVGVGVAFGL 58
Db 1 MNNPNINECIPYCNLSNPEVEILGRIETGYTPIDISLSLTQELLSEFVGVGVAFGL 60
Qy 59 FDLIWFPTPSDWSLFIQIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLI 118
Db 61 VDIWIGFPGSDWAFVLIQIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLI 120
Qy 119 PNAQLREDVIRFANTDOALITAINNETLTATFEPLLSVYVQAAANLHLSLRDVSFG 178
Db 121 PTNPALEEMKIQFNDMNSALTATPLFAVQNYQVPLLSVYVQAAANLHLSLRDVSFG 180
Qy 179 GGLDIATVNNHYNLNLHRYTKHCLDTYNGQLENLGTNTROWARFNQFRDLTLTV 238
Db 181 RWGFDAAATINSRYNDLRLIGNYTDYAVRWYNTGLRWGPDSDRWYRNPFRRLTLTV 240
Qy 239 LDIVALFNYDVRTYPIQTSQLTREIYTSVIEDSPSVANIPNGFNRA---EFGVRPP 294
Db 241 LDIVALFNYDVRTYPIQTSQLTREIYTNVPLE-----NFDGFRGSAQGIERSIRP 294
Qy 295 HLMDFMNSLFVTAETVRSQTVMGH--LVSSRNTAGNRINPFSYGVF-NPGGAIWIADDED 351
Db 295 HLMDFMNSLFVTAETVRSQTVMGH--LVSSRNTAGNRINPFSYGVF-NPGGAIWIADDED 351
Qy 352 PRPFYRTLSLDPVVRG---GFGNPHY-VLGRGVAFQQTGNHRTFRNSGTIDSLDEIP 407
Db 355 GQGVYRTLSLTPYRRPFGINNNQOLSVDLGTETAYGTSNNLPSAVYKSGTVDLDEIP 414
Qy 408 PQDMSGAPWNDYSHVNLHVTVFVRWPEIGSGDSWRAPFWSWTHRSATPTNTIDPERITQI 467
Db 415 PQNNVPPRQGFSGHLSHVMSFRSGFSNVSIIIRAPFWSWTHRSAEFNIIISQITQI 474
Qy 468 PLVKAHTLQSGTIVVRGPGTGGDILRRTSQGPFFAYTTVINGQLPQYRARIYASTTN 527
Db 475 PAVKGNFLFENG-SVLSGPGFTGGDLVRLNNSGN-----NIQNRGYIEVP IHPSTSPRY 527
Qy 517 RARIRYASTTNLRIVTVVAGERIFAQGNKMTMDTGDPLTFQSFYSYATINTAFTFPMSSQ 576
Db 528 RVRERYASVTPHILNVNMGNSIFSNTPATATSLDNLQSSDFGYFESANAFT---SSLG 584
Qy 577 FTVGADTFSSGNEVYIDRELPVATPAEAYDLERAQKAVNALFTSINOIGIKTDVTDY 636
Db 585 NIVGVNFSGGTAGVIIDRFEPFIPVATLEAEYNLEERAQKAVNALFTSINOIGIKTDVTDY 644
Qy 637 HIDQVSNLVDCLSDDEFCLDEKELSEKVKHAKRLSDERNLLQDPNFKGINROLDRGWRG 696
Db 645 HIDQVSNLVDCLSDDEFCLDEKELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGS 704
Qy 697 TDTIIOGRDDVFKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSODLEI 756
Db 697 TDTIIOGRDDVFKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSODLEI 756

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Db 705 TGITIQGDDVFKENYVTLGTFDFCEPTYLYQKIDESKLAFTRYQLRGYIEDSQDLEI 764  
QY 757 YLIIRYNAKHETVNVULGTSGLWPLSVQSPIRKOGEPNRCAPHLEWNPDLDCSCRDGEKCAH 816  
Db 765 YLIIRYNAKHETVNVVPGTGLWPLSAQSPIGKOGEPNRCAPHLEWNPDLDCSCRDGEKCAH 824  
QY 817 HSHFSDIDVGCITDNLNEDLWVIFKIKTDQGHARLGNLEFLEKPLVGEALARKRAE 876  
Db 825 HSHFSDIDVGCITDNLNEDLWVIFKIKTDQGHARLGNLEFLEKPLVGEALARKRAE 884  
QY 877 KKWRDKREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHRIREAY 936  
Db 885 KKWRDKREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHRIREAY 944  
QY 937 LPELSVIGVNVDFEELKGRIFTAFILYDARNVKNKGDFNGLSCWNVKGVHVDVEBONN 996  
Db 945 LPELSVIGVNAALFEELLEGRIPTAFSLYDARNVKNKGDFNGLSCWNVKGVHVDVEBONN 1004  
QY 997 HRSVLVPEWEAEYSQEVRCVPCGRGYILRVYTAKEGYGEGCVTHIEIENNTDELKFSNCV 1056  
Db 1005 QRSVLVPEWEAEYSQEVRCVPCGRGYILRVYTAKEGYGEGCVTHIEIENNTDELKFSNCV 1064  
QY 1057 BEEVYNNVTVCNDYTANOEEYGGAYTSRNRGYDITYGNSVSPADYASVYEEKSYTDGR 1116  
Db 1065 BEEVYNNVTVCNDYTANOEEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGR 1120  
QY 1117 RDNCESTRNGYDTPPLPAGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLMEE 1174  
Db 1121 RDNCESTRNGYDTPPLPAGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLMEE 1178

RESULT 12  
US-09-826-660-21  
; Sequence 21, Application US/09826660  
; Patent No. US20010026940A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Stelman, Steven J.  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: MA-714XC2D1  
; CURRENT APPLICATION NUMBER: US/09/826,660  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/178,252  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: 60/065,215  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/076,445  
; PRIOR FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 1163  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
US-09-826-660-21

Query Match 64.7%; Score 4042.5; DB 10; Length 1163;  
Best Local Similarity 67.3%; Pred. No. 4.8e-314;  
Matches 814; Conservative 87; Mismatches 226; Indels 83; Gaps 18;

QY 1 MENNQOCVYNNCLNNEVEILNEER-STGRPLDLSLSTRFLLSEFVGVGVAFLG 59  
Db 1 MEENNQOCVYNNCLNNEVEILNEER-STGRPLDLSLSTRFLLSEFVGVGVAFLG 60  
QY 60 DLWGFITPDSWLSPLLOIEQRIETLENRAITTLRGLADSEYIIEALREWEANP 119  
Db 61 DFVWGVGSQWDAFLVQIEQLINERAEFARNAIAINLEGNNFNFIYVEAFKEWEDP 120  
QY 120 NNAQLRDVIRFANTDDALITAINNFITLTSFEIPLLSVYQAAHLHLRLDAYSFGQ 179

Db 121 NNPAITRVIDRFRIDGLLDERIPSFRISEFVEYPLLVSVAQAANLHLAILRDSVIFGER 180  
QY 180 WGLDIATVNNHYNRLINLIHRYTKHCLDITYNOGUENLGTNRWARFNQFRDUTLVLV 239  
Db 181 WGLATTINVENYNRLIRHIDEYADHCANTYNRGLNLPKSYQDWITYNRLRLDTLVL 240  
QY 240 DIVALFPNDVRYPIOTSSOLTRIEYTSVIEDSP---VSANIPNGENRAE-FGVRRPH 295  
Db 241 DIAAFFPNYDNRXPPIQPVQQLTRIEYTDPLINFPNQLQSVAQLPT-FNVMESSAIRPH 299  
QY 296 LMDFNLSLFTAE--TVRSQTWVGWGHLYSSRNTAGNRINFPYSYGVFNPGGAIWIADEP- 352  
Db 300 LFDILNLNLTITDFWFSVGRNFWGCHRYVSSILGGNITSYIG-----REANQRP 351  
QY 353 -----RPFYITLSDPV--FVRGFGNPHYVL-GLRGVAFQOTGTHHTRTFRNSTIDSL 403  
Db 352 RSFTFNGFVFTLNSPTLRLLQCPWAPPPNLRGVEGVEP-STPTN-SFTYRGRCQVDSL 409  
QY 404 DEIPQDNMGAPWNDYSHVLNHTVFRWPGELSGSDSNRAP-----MFSMTHRSATPTN 457  
Db 410 TELPEDNSVPPREGYSHRLCHAFVQRSG-----TFPLTTGVVFSWTHRSATL 460  
QY 458 TIDPERITQIPLVKAHTLQSGTTVVVRGPGFTGGDILRMTSGGPAYTIVNINQLPQRYR 517  
Db 461 TIDPERINQIPLVKGFRVWGCTSVITGFTGGDILRNTFTGDFVSLQVNLNSPITQRYR 520  
QY 518 ARIYASTNLRIVY-TVAGERIFAGQ-----FNKMTDGTGDLPTQFSFVATINTATFF 570  
Db 521 LRFRYASSRDARVILVTGAASTGVGGQSVNMPQLKTMIGEINTLSRTFRYTFDFSNPFSF 580  
QY 571 PMSQSSFTV-----GADTFSSGNEVYIDRELIPVTATFEAEYDLEIRAQKAVNALFTSI 624  
Db 581 RANPDIIIGISQPLFGAGSISG-ELYIDKTEILADATLEAESDLEIRAQKAVNALFTSS 639  
QY 625 NQIGIKTDVTDYHIDQVSNLVDCLSDDEFCLDEKRELSKVKHAKLSDERILLQDPNFKG 684  
Db 640 NQIGLKTDTVTDYHIDRVSNLVECLSDDEFCLDEKRELSKVKHAKLSDBERNLQDPNFRG 699  
QY 685 INQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFDECYPYLYQKIDESKLAFTRYQL 744  
Db 700 INQLDRGWRGSTDITIQGGDVFKENYVTLGLTDECYPTLYQKIDESKLAFTRYQL 759  
QY 745 RGYIEDSQDLEIYLYRNAKHETVNVLCVGLWPLSVQSPIRKOGEPNRCAPHLEWNPDL 804  
Db 760 RGYIEDSQDLEIYLYRNAKHETVNVLCVGLWPLSVQSPIRKOGEPNRCAPHLEWNPDL 800  
QY 805 DCSRDGKCAHSHHSHFSLDIDVGCITDNLNEDLWVIFKIKTDQGHARLGNLEFLEKPL 864  
Db 801 -----GKCAHSHHSHFSLDIDVGCITDNLNEDLWVIFKIKTDQGHARLGNLEFLEKPL 853  
QY 865 VGEALARKRAEKWKWRDKREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNAMTHA 924  
Db 854 VGEALARKRAEKWKWRDKREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNAMTHA 913  
QY 925 ADKRVHRIREAYLPELSVPVGVNVDFEELKGRIFTAFILYDARNVKNKGDFNGLSCW 984  
Db 914 ADKRVHSIREAYLPELSVPVGVNAALFEELLEGRIPTAFSLDARNVKNKGDFNGLSCW 973  
QY 985 VKGHYDVEEQNNHRSVLVPEWEAEYSQEVRCVPCGRGYILRVYTAKEGYGEGCVTHIEI 1044  
Db 974 VKGHYDVEEQNNHRSVLVPEWEAEYSQEVRCVPCGRGYILRVYTAKEGYGEGCVTHIEI 1033  
QY 1045 NNTDELKFSNCVVEEVYNNVTVCNDYTANOEEYGGAYTSRNRGYDITYGNSVSPADYA 1104  
Db 1034 NNTDELKFSNCVVEEVYNNVTVCNDYTANOEEYGGAYTSRNRGYDITYGNSVSPADYA 1093  
QY 1105 SVYEKSYTDGRNRCPCESNRGYDTPPLPAGYVTKLEYFPETDKVWIEIGETGTFIV 1164  
Db 1094 SAYEKAFTDGRNRCPCESNRGYDTPPLPAGYVTKLEYFPETDKVWIEIGETGTFIV 1153  
QY 1165 DSVELLMEE 1174  
Db 1154 DSVELLMEE 1163

```
RESULT 13
US-09-826-660-15
; Sequence 15, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1156
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-15

Query Match      64.7%; Score 4039; DB 10; Length 1156;
Best Local Similarity 67.9%; Pred. No. 9.1e-314;
Matches 813; Conservative 83; Mismatches 236; Indels 66; Gaps 14;

Qy 1 MENNTQ-NOCYPNCLNPEVEILNEER-STGRPLDLSLTRLLSEFFVPGVGVARCL 58
Db 1 MDNNPINECIPIYCLNPEVEVLGGERIETGYTIDISLSTQTLFLLFVPGAGFVLGL 60

Qy 59 FDLINGFITPDSWLSFLQIEQLIQRIETLERNRAITTLRGLADSYEIIYBALREWEAN 118
Db 61 VDIWIGFPGSQWDAFLVQIEQLINRIEFAFNQAISRLGLSNLYQIYAESFREWEAD 120

Qy 119 PNNAQLREDVIRFANTDALTAINNTTLTSTFETPLLSVYVQAAANLHLSLRDAVSFG 178
Db 121 PTNPALREEMRIQFNDMSALTTAIPFAVQYQVPLLSVYVQAAANLHLSLRDAVSFG 180

Qy 179 GWGLDIATVNNHYNRLINLHRYTKECLDTYNOGLENLGTNTROWARNQFRDLTLTV 238
Db 181 RWGFDAAINSRYNDLRLIGNTYAVRWYNTGLERWGPDSRDWRVYNQFRDLTLTV 240

Qy 239 LDVALFPNDVRYTPYIQTSSQLTREIYTSVIEDSPYSANIPNGFNRA---EFGVRPP 294
Db 241 LDVALFPNDYRRYPIRTVSQTLREIYTNVPLE-----NFDGSRGSAQGIERSIRSP 294

Qy 295 HLMDFMNSLFTVTAETVRSCQTVWGGH--LVSSRNTAGNRINFPYSYGVF-NPGGAIWADED 351
Db 295 HLMDFMNSLFTVTAETVRSCQTVWGGH--LVSSRNTAGNRINFPYSYGVF-NPGGAIWADED 351

Qy 352 PRPFYRTLSDPVEVRG---GFGNPHY-VLGLRGVAFQGTGTHRTFRNSGFDISLDEIP 407
Db 353 CGGVYRTLSLSDYRPPNIGINNOQLSDGTGTEFYAGTSNNLPFAVYRKSGFVDSLDEIP 414

Qy 408 FODNSGAPWNDYSHVLNHWTFVRWPGEISGDSWRAPFMSWTHRSATPTNTIDPERITQI 467
Db 415 PONNVVPPRQGFSLHLSVMSFRSGFSNYSVLIIRAPFMSWTHRSAPFMSWTHRSATPTNTIDPERITQI 474

Qy 468 PLVKAHTTQSGTTVVRGCGFTGGDILRTSSGPGFAYTIVNNG-----QIP-----ORY 516
Db 475 PAVKGNFLNG-SVIGSGPGFTGGDLVRLNSSGN-----NIQNRGYIEVPPIHPSTSTRY 527

Qy 517 RARIYASTNLRIYVTVAGERIFAGQENKIMDTGDPITFQSFYSATINTAFTFPMSOSS 576
Db 528 RVRVRYASTPHLNVNNGNSSIFSNTYFATATSLDNLQSSDFGYFESANAFT---SSIG 584
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Qy 577 FTVGADTFSSGNEVYIDREFLIPVTATFEAYDLEPRAQKAVNALETSINOIGIKTDVTDY 636
Db 585 NIVGVNFSGTAGVILDRFEFIPVTATLEAESDLERAQKAVNALETSINOIGIKTDVTDY 644

Qy 637 HIDQVSNLVDCLSDFECLDEKRELSEKVKHAKRLSDERNLLQDPNPKGINRQLDRGWRGS 696
Db 645 HIDRVSNLVECLSDFECLDEKRELSEKVKHAKRLSDERNLLQDPNPKGINRQLDRGWRGS 704

Qy 697 TDITIQGGDDVFKENYVILPGTFDECBYPTLYKQIDESKLYKRYQLRGYIEDSDLEI 756
Db 705 TDITIQGGDDVFKENYVILPGTFDECBYPTLYKQIDESKLYKRYQLRGYIEDSDLEI 764

Qy 757 YLIRYNAKHETVNLGTSLWPLSVQSPIRKCGEPNRCAPHELPNPDLCSCRGKCAH 816
Db 765 YLIRYNAKHETVNLGTSLWPLSVQSPIRKCGEPNRCAPHELPNPDLCSCRGKCAH 798

Qy 817 HSHFSLDIDVGTDLNEDLVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARKRAE 876
Db 799 HSHFSLDIDVGTDLNEDLVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARKRAE 858

Qy 877 KKWDRKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAADKRVHIREAY 936
Db 859 KKWDRKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAADKRVHIREAY 918

Qy 937 LPSELSVPGVNVVDIFEELKGRIFTAFELYDARNVTKNGDFNNGLSWNVKGHVDEEQNN 996
Db 919 LPSELSVPGVNVVDIFEELKGRIFTAFELYDARNVTKNGDFNNGLSWNVKGHVDEEQNN 978

Qy 997 HRSVLVPEWEAEVSOEVRVCPGRGYILRVYKAYKGYGEGCVTIHEIENNTDELKFSNCV 1056
Db 979 HRSVLVPEWEAEVSOEVRVCPGRGYILRVYKAYKGYGEGCVTIHEIENNTDELKFSNCV 1038

Qy 1057 EEEVYNNVTVCNDYTANQEEYGGAYTSNRGYDETYGSSSVPADYASVYEKSTTDGR 1116
Db 1039 EEEVYNNVTVCNDYTANQEEYGGAYTSNRGYDETYGSSSVPADYASVYEKSTTDGR 1098

Qy 1117 RONCESNRGYGDTPLPAGYVTKLEYPPETDKVWIEIGETEGTFIVDSVELLMEE 1174
Db 1099 RONCESNRGYGDTPLPAGYVTKLEYPPETDKVWIEIGETEGTFIVDSVELLMEE 1156

RESULT 14
US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23
```

Query Match 58.1%; Score 3629.5; DB 10; Length 1186;  
Best Local Similarity 62.7%; Pred. No. 4.4e-281;  
Matches 737; Conservative 90; Mismatches 239; Indels 109; Gaps 16;

QY 49 VPCVGVAFGLDILWGFTIP---SDWSLFLLOLEIOLIEQRIETLERNRAITTLRLGLADSY 105  
 DB 72 VFAQIASFYSLVGLWPRGRDWEFLLEHVEQIRIQOQVTEENTRTALARQLQGLGNSEF 131  
 QY 106 EYIFALREWEANPNAOLRDVIRFANTDDALITAINNTLTSTPEIPLLSVYQAANL 165  
 DB 132 RAYQOSLEDWLENRDARTSRVLYQYIALELDFLNAMPFLAIRNQVEPLLMVAQAANL 191  
 QY 166 HLSLRDAVSFCQGLGLDIATVNNHYNRLNLIHRYTKHCLDTYNOGLENLRGTNRQWA 225  
 DB 192 HLLLRDASLFGSEFGLTSQEIQRYERQVETREYSYCARWYNTGLNLRCTRAESWL 251  
 QY 226 RENOQRDLTLVLDVALFPNDVRYTPIOTSSQLTREIYTSVIEDSPVS-ANIPNGF 284  
 DB 252 RYNQFRDLTLGVLDLVALFPDSDYTRVPMNTSAOLTREIYT-----DPIGRTNAPSGF 305  
 QY 285 -----NRABFG-----VRPHPLMDPMNSLFTVA-----ETVRSQTVWGGHLYSSRN 325  
 DB 306 ASTNWFNNAPSFSALEAAVIRPPHLLDPEQOLTIFSVLRSNNTQYMYWVGHRLSEST 365  
 QY 326 TAGNINFPYSYVFNPGGAINTADEDPPEFYRT-----LSDPV-----FVRGGFGNP 372  
 DB 366 IRGS-LSTSTHGNTNTSINPVLTQFTSRDVRTESEFAGINILLTTPVNGVPWAPENRNP 424  
 QY 373 -----HYVLGLRGVAFQQTGNTHTRTFRNSGTIDSLDEIPPDNSGAPWNDYSHVLN 424  
 DB 425 LNSLRGSLLYTIGYGVGTQ-----LFDSETELPPEPTEPNTPEVSYSHRLS 470  
 QY 425 HYTVRWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRG 484  
 DB 471 NURL-----ISG-NTRLAPVSWTHRSADRTNLISSDSITQIPLVKSFNLSGTSVSSG 523  
 QY 485 PGFTGDIILRTSGGFFAYTIWINGQLPQRYRARIYASTNLRIYTVVAGERIFAGOF 544  
 DB 524 PGFTGDIILRTNVGSLVSMGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSGSTTFDQGF 583  
 QY 545 NKTMDIGDPLTFQSPSYATINAFPPMSQS-----SFTVGADTSSGNEVYIDREFELP 599  
 DB 584 PTSMANESLTSQSFRFAEPFVGISAGSQTAGISINNAGQTF-----HFDKTEIFP 637  
 QY 600 VTATPEAEYDLERAOKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLDSDFCLDEKRE 659  
 DB 638 ITATLEAESDLERAOKAVNALFTSSNQIGLKTDTVTDYHIDRVSNLVECLDSDFCLDEKRE 697  
 QY 660 LSEKVKHAKRLSDERNLLQDPNFKGINROLDRGWRGSDITITQRGDDVDFKENYVILPGTF 719  
 DB 698 LSEKVKHAKRLSDERNLLQDPNFRGINROLDRGWRGSDITITQGGDDVDFKENYVILPGTF 757  
 QY 720 DRCYPTYLYOKIDESKLPYTRYQALGYLEDSQDLIEYLIRYNAKHETVNLGTQSLWPL 779  
 DB 758 DRCYPTYLYOKIDESKLPYTRYQALGYLEDSQDLIEYLIRYNAKHETVNLGTQSLWPL 817  
 QY 780 SVOSPTKCGEPNRCAPHLEWNPDLDCSDRCEKCAHSHHFSLDIDVGCTDLNEDLDYV 839  
 DB 818 SAPSPT-----GKCAHSHHFSLDIDVGCTDLNEDLDYV 851  
 QY 840 VIFKIKTQGHARLGNLEFLLEKPLVGEALARKVKAEEKWKROKREKLELETNIVYKEAKE 899  
 DB 852 VIFKIKTQGHARLGNLEFLLEKPLVGEALARKVKAEEKWKROKREKLELETNIVYKEAKE 911  
 QY 900 SYDALFVNSOYQOLQADTNIAHIAADKRVHRIIRAYLPVGLSVIPGVNVDIFPEELKGRIF 959  
 DB 912 SYDALFVNSOYQOLQADTNIAHIAADKRVHRIIRAYLPVGLSVIPGVNVAIPEELEGRIF 971  
 QY 960 TAFILYDARNVKNKNGDFNGLSCWNYKGVHDVVEQONNHRSLVLPVPEWAEVSOEVRVCPG 1019  
 DB 972 TAFILYDARNVKNKNGDFNGLSCWNYKGVHDVVEQONNHRSLVLPVPEWAEVSOEVRVCPG 1031  
 QY 1020 RGYILRVATYKEGYGGCVTIHIEIENNTDELKFSNCVVEEVPNTVTNDYTAQOEYEG 1079  
 DB 1032 RGYILRVATYKEGYGGCVTIHIEIENNTDELKFSNCVVEEVPNTVTNDYTAQOEYEG 1091

QY 1080 GAYTSRNRGYDETYGSSNSVPADYASVYBEKSVTDGRRDNPCESNRGYGDYPLPAGYVT 1139  
 DB 1092 GYTSRNRGYDAYSNSVVPADYASVYBEKAYTIDGRRDNPCESNRGYGDYPLPAGYVT 1151  
 QY 1140 KELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174  
 DB 1152 KELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1186  
 RESULT 15  
 US-09-826-660-4  
 ; Sequence 4, Application US/09826660  
 ; Patent No. US20010026940A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cardineau, Guy A.  
 ; APPLICANT: Stelman, Steven J.  
 ; APPLICANT: Narva, Kenneth E.  
 ; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
 ; FILE REFERENCE: MA-714XC2D1  
 ; CURRENT APPLICATION NUMBER: US/09/826,660  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 09/178,252  
 ; PRIOR FILING DATE: 1998-10-23  
 ; PRIOR APPLICATION NUMBER: 60/065,215  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/076,445  
 ; PRIOR FILING DATE: 1998-03-02  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 605  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
 US-09-826-660-4

Query Match 51.0%; Score 3185; DB 10; Length 605;  
 Best Local Similarity 99.8%; Pred. No. 4.6e-246;  
 Matches 604; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNIQOCVPYCNLNNPEVEILNEERSTGRPLDLSLTLRFLISEFVPGVGVAFGLFD 60  
 DB 1 MENNIQOCVPYCNLNNPEVEILNEERSTGRPLDLSLTLRFLISEFVPGVGVAFGLFD 60

QY 61 LIWGFITPDSWSLFLLOLEIOLIEQRIETLERNRAITTLRLGLADSYEIIYALREWEANPN 120  
 DB 61 LIWGFITPDSWSLFLLOLEIOLIEQRIETLERNRAITTLRLGLADSYEIIYALREWEANPN 120

QY 121 NAOQLREDVIRFANTDDALITAINNFTLSFELIPLLSVYQAANLHLSLRDAVSFGQGW 180  
 DB 121 NAOQLREDVIRFANTDDALITAINNFTLSFELIPLLSVYQAANLHLSLRDAVSFGQGW 180

QY 181 GLDIATVNNHYNRLNLIHRYTKHCLDTYNOGLENLRGTNRQWAFNRFRDLTLTVLD 240  
 DB 181 GLDIATVNNHYNRLNLIHRYTKHCLDTYNOGLENLRGTNRQWAFNRFRDLTLTVLD 240

QY 241 IVALFPNDVRYTPIQTSQTLTREIYTSVIEDSPVSANIPNGFNPAETGVRPPHMDPM 300  
 DB 241 IVALFPNDVRYTPIQTSQTLTREIYTSVIEDSPVSANIPNGFNPAETGVRPPHMDPM 300

QY 301 NSLFTVTAETVRSQTVWGGHLYSSRNAGNIRNPPSVGVNFENPGAGIAWDEDPFPYRILUS 360  
 DB 301 NSLFTVTAETVRSQTVWGGHLYSSRNAGNIRNPPSVGVNFENPGAGIAWDEDPFPYRILUS 360

QY 361 DPFVVRGGFGNPHYVLGLRGVAFQQTGTNHTTFRNSGTIDSLDEIPPDNSGAPWNDYS 420  
 DB 361 DPFVVRGGFGNPHYVLGLRGVAFQQTGTNHTTFRNSGTIDSLDEIPPDNSGAPWNDYS 420

QY 421 HVLNHTVTVRWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480  
 DB 421 HVLNHTVTVRWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480



QY 481 VVRGPGFTGGDILRETSGGPFAYTIVNINGQLPQYRARIYASTTNLRIYVTVAGERIF 540  
 Db 481 VVRGPGFTGGDILRETSGGPFAYTIVNINGQLPQYRARIYASTTNLRIYVTVAGERIF 540  
 QY 541 AGQFNKMTDGTGDLTGFQSFYATINTAFTFPMQSSFTVGADTFSSGNEVYIDREFELIPV 600  
 Db 541 AGQFNKMTDGTGDLTGFQSFYATINTAFTFPMQSSFTVGADTFSSGNEVYIDREFELIPV 600  
 QY 601 TATFE 605  
 Db 601 TATLE 605

Search completed: November 27, 2002, 20:27:48  
 Job time : 80 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 27, 2002, 18:37:19 ; Search time 38 Seconds  
(without alignments)  
909.013 Million cell updates/sec

Title: US-09-837-961-8  
Perfect score: 6244  
Sequence: 1 MENTTONQCVNCLNPEV.....IGTETCTFIVDSVLLMNEE 1174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2.6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2.6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2.6/ptodata/2/iaa/6A\_COMB.pep.\*  
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5: /cgn2.6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6244	100.0	1174	1	US-07-828-788A-10
2	6244	100.0	1174	1	US-08-349-867-25
3	6244	100.0	1174	1	US-08-349-867-32
4	6244	100.0	1174	1	US-08-349-867-25
5	6244	100.0	1174	1	US-08-356-034-8
6	6244	100.0	1174	2	US-08-598-305A-25
7	6244	100.0	1174	2	US-08-598-305A-32
8	6244	100.0	1174	2	US-08-598-305A-25
9	6244	100.0	1174	3	US-08-933-891-8
10	6244	100.0	1174	4	US-09-178-252-6
11	6244	100.0	1174	5	PCT-US91-02560-2
12	6244	100.0	1174	5	PCT-US92-11337-10
13	6244	100.0	1174	5	PCT-US95-05431-25
14	6244	100.0	1174	6	5189960-8
15	6244	100.0	1184	1	US-08-349-867-32
16	6244	100.0	1184	2	US-08-639-923A-32
17	6244	100.0	1184	5	PCT-US95-05431-32
18	6049	96.9	1174	1	US-08-349-867-29
19	6049	96.9	1174	1	US-08-239-476-29
20	6049	96.9	1174	2	US-08-598-305A-29
21	6049	96.9	1174	2	US-08-639-923A-29
22	6049	96.9	1174	5	PCT-US95-05431-29
23	6018.5	96.4	1175	2	US-08-598-305A-36
24	6018.5	96.4	1175	2	US-08-639-923A-36
25	5913	94.7	1148	2	US-08-598-305A-37
26	5913	94.7	1148	2	US-08-639-923A-37
27	5908	94.6	1148	2	US-08-598-305A-38

28	5908	94.6	1148	2	US-08-639-923A-38	Sequence 38, Appl
29	5902	94.5	1148	1	US-08-349-867-23	Sequence 23, Appl
30	5902	94.5	1148	1	US-08-349-867-27	Sequence 27, Appl
31	5902	94.5	1148	1	US-08-239-476-23	Sequence 23, Appl
32	5902	94.5	1148	1	US-08-239-476-27	Sequence 27, Appl
33	5902	94.5	1148	2	US-08-598-305A-23	Sequence 23, Appl
34	5902	94.5	1148	2	US-08-598-305A-27	Sequence 27, Appl
35	5902	94.5	1148	2	US-08-639-923A-23	Sequence 23, Appl
36	5902	94.5	1148	2	US-08-639-923A-27	Sequence 27, Appl
37	5902	94.5	1148	5	PCT-US95-05431-23	Sequence 23, Appl
38	5902	94.5	1148	5	PCT-US95-05431-27	Sequence 27, Appl
39	5889	94.3	1148	2	US-08-598-305A-35	Sequence 35, Appl
40	5889	94.3	1148	2	US-08-639-923A-35	Sequence 35, Appl
41	5879	94.2	1148	4	US-09-178-252-2	Sequence 2, Appl
42	5674	90.9	1150	1	US-08-349-867-21	Sequence 21, Appl
43	5674	90.9	1150	1	US-08-239-476-21	Sequence 21, Appl
44	5674	90.9	1150	2	US-08-598-305A-21	Sequence 21, Appl
45	5674	90.9	1150	2	US-08-639-923A-21	Sequence 21, Appl

## ALIGNMENTS

RESULT 1  
US-07-828-788A-10  
; Sequence 10, Application US/07828788A  
; Patent No. 5273746  
; GENERAL INFORMATION:  
; APPLICANT: PAYNE, JEWEL M.  
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES  
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID R. SALIWANCHIK  
; STREET: 2421 N.W. 41ST STREET, SUITE A-1  
; CITY: GAINESVILLE  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/07/828,788A  
; APPLICATION NUMBER: US/07/828,788A  
; FILING DATE: 19920129  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SALIWANCHIK, DAVID R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA75  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1174 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: BACILLUS THURINGIENSIS  
; STRAIN: AIZAWAI  
; INDIVIDUAL ISOLATE: PS81I  
; IMMEDIATE SOURCE:  
; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK  
; CLONE: 811A  
; US-07-828-788A-10

Query Match 100.0%; Score 6244; DB 1; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 LIWGFTSPDWSLFLQIOLIEQRIETLERNRAITTLRLGLADSYEIIYIETALREWEANPN 120

QY 121 NACLREDVRIRFANTDDALITAINNFTLTSFEIPLSVVYVQAAHLHLSDRLDAVSGQGW 180  
DB 121 NACLREDVRIRFANTDDALITAINNFTLTSFEIPLSVVYVQAAHLHLSDRLDAVSGQGW 180

QY 181 GLDIATVNNHYNRLNLHRYTKHCLDYNQGLENLRTGTQWARFNQFRDLTLTVID 240  
DB 181 GLDIATVNNHYNRLNLHRYTKHCLDYNQGLENLRTGTQWARFNQFRDLTLTVID 240

QY 241 IVALFPNDVRTYPIQTSQLTREIYTSVIEDSPVANIPNGENRAEGVPPHLMDFM 300  
DB 241 IVALFPNDVRTYPIQTSQLTREIYTSVIEDSPVANIPNGENRAEGVPPHLMDFM 300

QY 301 NSLFTVETVRSQTVMGHLYSSRNAGNINFPYGVFNPGATWIADEDPFRYRILS 360  
DB 301 NSLFTVETVRSQTVMGHLYSSRNAGNINFPYGVFNPGATWIADEDPFRYRILS 360

QY 361 DPVFRGFGFNPHYVLGRVAFQQTGTNHTFRPNSGTISLDEIIPQDNGAPWNDYS 420  
DB 361 DPVFRGFGFNPHYVLGRVAFQQTGTNHTFRPNSGTISLDEIIPQDNGAPWNDYS 420

QY 421 HVLNHTVFRWPGELSGSDSNRAPMFWTHRSATNTIDPERIQIPLVKAHTLQSGTT 480  
DB 421 HVLNHTVFRWPGELSGSDSNRAPMFWTHRSATNTIDPERIQIPLVKAHTLQSGTT 480

QY 481 VVRGFTGGDILRTSGGPFAYTIVNINGQLPQYRARIYASTNLRIYTVAGERIF 540  
DB 481 VVRGFTGGDILRTSGGPFAYTIVNINGQLPQYRARIYASTNLRIYTVAGERIF 540

QY 541 AGPNKMTMDTGDPLTFQSFYATINTATFPMSQSFVVGADTFSSGNEVYIDRELIPIV 600  
DB 541 AGPNKMTMDTGDPLTFQSFYATINTATFPMSQSFVVGADTFSSGNEVYIDRELIPIV 600

QY 601 TATFEAEYDLERAKAVNALFTSINQIGIKTDYTHDQVSNLVDCLSDFCLDEKREL 660  
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QY 661 SEKVHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720  
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QY 721 ECPYTYLYQKIDESKLPYTRYOLRGYIEDSDLEIYLIRYNAKHEIVNVLGTSLWPLS 780  
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QY 1081 AYTNRNGYDETYGNSNVPADYASYIEEKSYSYTDGRDNPCESNRGYGYTPLPAGYVTK 1140  
DB 1081 AYTNRNGYDETYGNSNVPADYASYIEEKSYSYTDGRDNPCESNRGYGYTPLPAGYVTK 1140

QY 1141 ELEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174  
DB 1141 ELEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174

RESULT 2

US-08-349-867-25  
; Sequence 25, Application US/08349867  
; Patent No. 5508264  
; GENERAL INFORMATION:  
; APPLICANT: Bradfisch, Gregory A.  
; APPLICANT: Thompson, Mark  
; APPLICANT: Schwab, George E.  
; TITLE OF INVENTION: No. 5508264el Pesticidal Compositions  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/349,867  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: XA86  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1174 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-349-867-25

Query Match 100.0%; Score 6244; DB 1; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 541 AQCFNKMTGDTGDLTFQSFYSATINTATFPMSQSFTVGADTFSSGNEVYIDRELIPIV 600  
Qy 601 TATFAEYDLERAQAVNALFTSINOIGIKTDVTDYHIDOVNLVDCLSDFCLEKREL 660  
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Db 1021 GYLIVTAYKEGSGGCVTIHEIENNTDELKFSNCVVEEYVNNVTCNDYTPANQEEYGG 1080  
Qy 1081 AYTSSNRGYDETYGSSNSVPADYASVYEKSYTDGRONPCSNRGYGDYTPLPAGYVTK 1140  
Db 1081 AYTSSNRGYDETYGSSNSVPADYASVYEKSYTDGRONPCSNRGYGDYTPLPAGYVTK 1140  
Qy 1141 ELEYFPETDKVWIEIGETEGTIFVDSVLELLMEE 1174  
Db 1141 ELEYFPETDKVWIEIGETEGTIFVDSVLELLMEE 1174

## RESULT 3

US-08-349-867-32  
; Sequence 32, Application US/08349867  
; Patent No. 5508264  
; GENERAL INFORMATION:  
; APPLICANT: Bradfisch, Gregory A.

; APPLICANT: Thompson, Mark  
; APPLICANT: Schwab, George E.  
; TITLE OF INVENTION: No. 5508264el Pesticidal Compositions  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL USA  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: US/08/349,867  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA86  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1174 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-349-867-32

Query Match 100.0%; Score 6244; DB 1; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MENNTQNCVPYNCLNNEPEILNEERSTGRPLDLSLSTRFLSEFVPGVGVAFGLFD 60  
Db 1 MENNTQNCVPYNCLNNEPEILNEERSTGRPLDLSLSTRFLSEFVPGVGVAFGLFD 60  
Qy 61 LWGFTIPSDWSLFLQLEQLQETLELRNRAITTLRGLADSVETIYLEARREANEN 120  
Db 61 LWGFTIPSDWSLFLQLEQLQETLELRNRAITTLRGLADSVETIYLEARREANEN 120  
Qy 121 NAQLREDVRIREFANTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDVAFSGQGW 180  
Db 121 NAQLREDVRIREFANTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDVAFSGQGW 180  
Qy 181 GLDIATVNNHYNRLNLHRYTKHCLDVTYNOGLENLRGNTNRQWARFNFQRRDLTLTVLD 240  
Db 181 GLDIATVNNHYNRLNLHRYTKHCLDVTYNOGLENLRGNTNRQWARFNFQRRDLTLTVLD 240  
Qy 241 IVALPNVDVRYPIQTSQSLREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300  
Db 241 IVALPNVDVRYPIQTSQSLREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300  
Qy 301 NSLFTVTAETVRSQTYWGGHLSVSRNAGNINFPSPGVENPGGAIWIADEDPFPYRTLS 360  
Db 301 NSLFTVTAETVRSQTYWGGHLSVSRNAGNINFPSPGVENPGGAIWIADEDPFPYRTLS 360  
Qy 361 DPVFRGGFGNPHYVYLGVAFOQTGTHRTFRNSGTIDSLDEIPPODNGSGAPWNDYS 420  
Db 361 DPVFRGGFGNPHYVYLGVAFOQTGTHRTFRNSGTIDSLDEIPPODNGSGAPWNDYS 420  
Qy 421 HVLNHVTFVRPGEISGDSWRAPFSWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480  
Db 421 HVLNHVTFVRPGEISGDSWRAPFSWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480  
Qy 481 VVRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYTVVAGERIF 540

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Db 481 VVRPGFTGGDIIRRTSGGFAYTIVNINQLPQRARIRYASTNLRIVYTVAGERIF 540
QY 541 AGQFNKTMGTGDLTQSFESYATINTAFPPMSQSFYVAGADTFSSGNEVYIDREFLIPV 600
Db 541 AGQFNKTMGTGDLTQSFESYATINTAFPPMSQSFYVAGADTFSSGNEVYIDREFLIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDOVSLVDCLSDEFCLDEKREL 660
Db 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDOVSLVDCLSDEFCLDEKREL 660
QY 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
Db 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
QY 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSQDLLEYLIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSQDLLEYLIRYNAKHETVNVLTGSLWPLS 780
QY 781 VQSPIKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLDVVV 840
Db 781 VQSPIKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLDVVV 840
QY 841 IFKIKTDQGHARLGNLEFTEKPLVGEALARKVRAEKWKDKREKLELETNIVYKEAKES 900
Db 841 IFKIKTDQGHARLGNLEFTEKPLVGEALARKVRAEKWKDKREKLELETNIVYKEAKES 900
QY 901 VDALFVNSOYDQLOADNTAMTHAADKVRHIREAYLPELSVTPGYNVDFEELKGRIFT 960
Db 901 VDALFVNSOYDQLOADNTAMTHAADKVRHIREAYLPELSVTPGYNVDFEELKGRIFT 960
QY 961 AFPLXDARNVIKNGDFNGLSCWNVKRGHVDVEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020
Db 961 AFPLXDARNVIKNGDFNGLSCWNVKRGHVDVEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020
QY 1021 GYLILWATYKEGEGECVTIHEIENNTDELKFSNCVVEEYVYNNVTYCNQDYANQEEYGG 1080
Db 1021 GYLILWATYKEGEGECVTIHEIENNTDELKFSNCVVEEYVYNNVTYCNQDYANQEEYGG 1080
QY 1081 AYTSNRNGYDEYTGSSNPADYASYEKSXYTDGRDNPCESNRGYGYDTPLPAGYVTK 1140
Db 1081 AYTSNRNGYDEYTGSSNPADYASYEKSXYTDGRDNPCESNRGYGYDTPLPAGYVTK 1140
QY 1141 ELEYFPETDKVWIEIGETGTFIVDSVELLMEE 1174
Db 1141 ELEYFPETDKVWIEIGETGTFIVDSVELLMEE 1174
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## RESULT 4

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US-08-239-476-25
; Sequence 25, Application US/08239476
; Patent No. 552783
; GENERAL INFORMATION:
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; TITLE OF INVENTION: Pseudomonas fluorescens
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,476
; FILING DATE:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-239-476-25
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Query Match 100.0%; Score 6244; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MENNIOQCVPYNCNLANPEVEILNEERSTGRPLDLSLTRELLSEFFVPGVGVAFGLFD 60
Db 1 MENNIOQCVPYNCNLANPEVEILNEERSTGRPLDLSLTRELLSEFFVPGVGVAFGLFD 60
QY 61 LWMGFITPDSWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYEALEWEANPN 120
Db 61 LWMGFITPDSWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYEALEWEANPN 120
QY 121 NAQLREDVIRFANTDDALITAINNETLASFEPILSVVQAANLHLSLLRDVAVSGQW 180
Db 121 NAQLREDVIRFANTDDALITAINNETLASFEPILSVVQAANLHLSLLRDVAVSGQW 180
QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLENLGRNTROWARFNQFRDLTLTVLD 240
Db 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLENLGRNTROWARFNQFRDLTLTVLD 240
QY 241 IVALPNYDVRYPYPIOTSSQLTREIYTSVSSVIEDSPYSANIPNGFNRAEFGVRPHLMDFM 300
Db 241 IVALPNYDVRYPYPIOTSSQLTREIYTSVSSVIEDSPYSANIPNGFNRAEFGVRPHLMDFM 300
QY 301 NSLFTVETVRSQTVWGGHLSVSRNTAGNRINFPSPYGVNPGGAIWIADDPFPYRTLS 360
Db 301 NSLFTVETVRSQTVWGGHLSVSRNTAGNRINFPSPYGVNPGGAIWIADDPFPYRTLS 360
QY 361 DVPVRRGEGNHYVLGLRGVAFQQTGTNHTTFRNSGTIDSLDEIPPODNGAPWNDYS 420
Db 361 DVPVRRGEGNHYVLGLRGVAFQQTGTNHTTFRNSGTIDSLDEIPPODNGAPWNDYS 420
QY 421 HVLNHWTFVRWPGETSGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKARTLOSQT 480
Db 421 HVLNHWTFVRWPGETSGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKARTLOSQT 480
QY 481 VVRGPGFTGGDILRRTSGGPFAYTIVNINQLPQRARIRYASTNLRIVYTVAGERIF 540
Db 481 VVRGPGFTGGDILRRTSGGPFAYTIVNINQLPQRARIRYASTNLRIVYTVAGERIF 540
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Db 541 AGQFNKTMGTGDLTQSFESYATINTAFPPMSQSFYVAGADTFSSGNEVYIDREFLIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDOVSLVDCLSDEFCLDEKREL 660
Db 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDOVSLVDCLSDEFCLDEKREL 660
QY 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
Db 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
QY 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSQDLLEYLIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSQDLLEYLIRYNAKHETVNVLTGSLWPLS 780
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QY 781 VQSPIKCCGPNRCAPHELEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840
Db 781 VQSPIKCCGPNRCAPHELEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840
QY 841 IFKIKTDGCHARLGNLEFELEKPLVGEALARYKRAEKKRDKREKLELETNIVYKEAKES 900
Db 841 IFKIKTDGCHARLGNLEFELEKPLVGEALARYKRAEKKRDKREKLELETNIVYKEAKES 900
QY 901 VDALFVNSQYDQADQNTIAMIHAADKRVHRIREAYLPESLPIGVNVDIFELKGRIFT 960
Db 901 VDALFVNSQYDQADQNTIAMIHAADKRVHRIREAYLPESLPIGVNVDIFELKGRIFT 960
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Db 961 AFPLYDARWIKNGDNGLSCWNVGHVDVBEQNNHRSVLVVPWEAEVQEVRCPCR 1020
QY 1021 GYLIRVAYKEGEGCVTTHETENNTDELKFSNCVVEEYVNNVTVCNDYTANQEEYGG 1080
Db 1021 GYLIRVAYKEGEGCVTTHETENNTDELKFSNCVVEEYVNNVTVCNDYTANQEEYGG 1080
QY 1081 AYTSNRNGYDITYGSSNPADYASVVEEKSYPDGRDRNPCESNRGYDGYTLPAGYVTK 1140
Db 1081 AYTSNRNGYDITYGSSNPADYASVVEEKSYPDGRDRNPCESNRGYDGYTLPAGYVTK 1140
QY 1141 ELEYFETDKWIEIGETEGTFTFVDSVVELLME 1174
Db 1141 ELEYFETDKWIEIGETEGTFTFVDSVVELLME 1174

RESULT 5
US-08-356-034-8
; Sequence 8, Application US/08356034
; Patent No. 5691308
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; TITLE OF INVENTION: Sick, August J.
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,034
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,110
; FILING DATE:
; APPLICATION NUMBER: 07/865,168
; FILING DATE: 09-APR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/451,261
; FILING DATE: 14-DEC-89
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/371,955
; FILING DATE: 27-JUN-89
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; REGISTRATION NUMBER: 21,023
; REFERENCE/DOCKET NUMBER: MA43.C1.D1

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS81I
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811A
; US-08-356-034-8

Query Match 100.0%; Score 6244; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIONQCVYPCYNCLNNEPEVEILNEERSTGRPLDIDSLSTRFLLSEFVPGVGVAFGLFD 60
Db 1 MENNIONQCVYPCYNCLNNEPEVEILNEERSTGRPLDIDSLSTRFLLSEFVPGVGVAFGLFD 60
QY 61 LIWGFITPSDWSLFLLOEQIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120
Db 61 LIWGFITPSDWSLFLLOEQIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120
QY 121 NAQLREDYRIRFANTDDALITAINNFUTLTSFEIPLLSVYVQAAHLHLSDRDAYSFGQGW 180
Db 121 NAQLREDYRIRFANTDDALITAINNFUTLTSFEIPLLSVYVQAAHLHLSDRDAYSFGQGW 180
QY 181 GUDIATVNNHNNRLNLHRTYKHCLOTYNOGLENLRGINTQWARFNQFRDLTLVLD 240
Db 181 GUDIATVNNHNNRLNLHRTYKHCLOTYNOGLENLRGINTQWARFNQFRDLTLVLD 240
QY 241 IVALEPNYDVTYPIQTSQSLTREIYTSVIEDSPVSANIPNGFNRAEFVGRPPHLMDFM 300
Db 241 IVALEPNYDVTYPIQTSQSLTREIYTSVIEDSPVSANIPNGFNRAEFVGRPPHLMDFM 300
QY 301 NSLFTVTAETVRSQTVWGGHLYSSRNNTAGNRRINFPISYGVNFGGAIWADEDPREFYRTLS 360
Db 301 NSLFTVTAETVRSQTVWGGHLYSSRNNTAGNRRINFPISYGVNFGGAIWADEDPREFYRTLS 360
QY 361 DPVFRGGFGPNHYVGLRGVAFQQTGNHTTFPNSGTIDSLDEIPQDNGSGAPWINDY 420
Db 361 DPVFRGGFGPNHYVGLRGVAFQQTGNHTTFPNSGTIDSLDEIPQDNGSGAPWINDY 420
QY 421 HVLNHTVFRWPEGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHLQSGTT 480
Db 421 HVLNHTVFRWPEGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHLQSGTT 480
QY 481 VVRGPGFTGGDILRRTSGGPPAYTIVNINGQLPQYRARIYASTNLRIRYVTVAGERIF 540
Db 481 VVRGPGFTGGDILRRTSGGPPAYTIVNINGQLPQYRARIYASTNLRIRYVTVAGERIF 540
QY 541 AGQFNKTMGTGDLPTQSFYSYATINTAFTFPMSSQSFVSGADTSSSGNEVYIDREFELIPV 600
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QY 601 TATFEAEYDLERAQAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
Db 601 TATFEAEYDLERAQAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
QY 661 SEKVHAKRLSDERNLLODPNFKGINROLDRGWRGSTDTITQRGDDVFKENYVTLPGTFD 720
Db 661 SEKVHAKRLSDERNLLODPNFKGINROLDRGWRGSTDTITQRGDDVFKENYVTLPGTFD 720

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QY 961 AFFLYDARVINKNGDFNGLSCWNVKGVHDVVEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020  
DB 961 AFFLYDARVINKNGDFNGLSCWNVKGVHDVVEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020  
QY 1021 GYILRVATYKGYGEGCVTHIEIENNTDELKFSNCVEEVPNNVTTCNDYTANOEYGG 1080  
DB 1021 GYILRVATYKGYGEGCVTHIEIENNTDELKFSNCVEEVPNNVTTCNDYTANOEYGG 1080  
QY 1081 AYTSRNRGYDITYGSSNVPADYASVYEKSYTDGRRDNPCESNRGYGDYTPPLPAGYVTK 1140  
DB 1081 AYTSRNRGYDITYGSSNVPADYASVYEKSYTDGRRDNPCESNRGYGDYTPPLPAGYVTK 1140  
QY 1141 ELEYFPETDKVWIEIGETEGFFIVDSVELLMEE 1174  
DB 1141 ELEYFPETDKVWIEIGETEGFFIVDSVELLMEE 1174

RESULT 7

US-08-598-305A-32  
; Sequence 32, Application US/08598305A  
; Patent No. 5827514  
; GENERAL INFORMATION:  
; APPLICANT: BRADFISCH, Gregory A.  
; APPLICANT: THOMPSON, Mark  
; TITLE OF INVENTION: SCHWAB, George E.  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/598,305A  
; FILING DATE: 08-FEB-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/349,867  
; FILING DATE: 06-DEC-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA86.D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 352-375-8100  
; TELEFAX: 352-372-5800  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1174 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-598-305A-32

Query Match 100.0%; Score 6244; DB 2; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIQCVNPNCLNNEPEILNEERSTGRPLDLSLTRELLSEFFVPGVGAGLEFD 60  
DB 1 MENNIQCVNPNCLNNEPEILNEERSTGRPLDLSLTRELLSEFFVPGVGAGLEFD 60  
QY 61 LINGFITPSDWSLFLQIQLEQRIETLERNRAITTLRGGLADSYEIIYILEARWEANPN 120

DB 61 LINGFITPSDWSLFLQIQLEQRIETLERNRAITTLRGGLADSYEIIYILEARWEANPN 120  
QY 121 NAQLEDVRIIRFANTDDALITAINNFTLTSTFEIPLLSVVYQAANLHLSLLRDVAFSGQGW 180  
DB 121 NAQLEDVRIIRFANTDDALITAINNFTLTSTFEIPLLSVVYQAANLHLSLLRDVAFSGQGW 180  
QY 181 GLDIATVNVNHNRLNLHRYTKHCLDITYNOGLENLRGNTNQWARFNQFRDRLTLTVLD 240  
DB 181 GLDIATVNVNHNRLNLHRYTKHCLDITYNOGLENLRGNTNQWARFNQFRDRLTLTVLD 240  
QY 241 IVALFPNDVRYPIQTSOLTREIYTSVLEDSVPSANIPNGFNRAEFGVPPHLMDFM 300  
DB 241 IVALFPNDVRYPIQTSOLTREIYTSVLEDSVPSANIPNGFNRAEFGVPPHLMDFM 300  
QY 301 NSLFVTAETVRSQTVWGGHLYSSRNTAGNRFNFPYGVFNPGGAIWIADEDPFPYRILS 360  
DB 301 NSLFVTAETVRSQTVWGGHLYSSRNTAGNRFNFPYGVFNPGGAIWIADEDPFPYRILS 360  
QY 361 DPVFRGFGFNPHVYGLRGVAFQOTGTNHTRTFNSGTIDSLDEIPQDNGSGAPWNDYS 420  
DB 361 DPVFRGFGFNPHVYGLRGVAFQOTGTNHTRTFNSGTIDSLDEIPQDNGSGAPWNDYS 420  
QY 421 HVLNHTVFRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480  
DB 421 HVLNHTVFRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480  
QY 481 VVRGPGTGGDILRRTSGGPFAYTIVNINGQLPQYRARIYASTTNLRIVTVAGERIF 540  
DB 481 VVRGPGTGGDILRRTSGGPFAYTIVNINGQLPQYRARIYASTTNLRIVTVAGERIF 540  
QY 541 AGQFNKMTDGTPLTFQSFYATINTAFTFMSQSSFTVGADTFSSGNEVYIDRELPV 600  
DB 541 AGQFNKMTDGTPLTFQSFYATINTAFTFMSQSSFTVGADTFSSGNEVYIDRELPV 600  
QY 601 TATFEAEYDLERAQKAVNALFTSINQIKTDVTDYHIDQVSNLVDCLSDFCDEKREL 660  
DB 601 TATFEAEYDLERAQKAVNALFTSINQIKTDVTDYHIDQVSNLVDCLSDFCDEKREL 660  
QY 661 SEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVILPGTFD 720  
DB 661 SEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVILPGTFD 720  
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QY 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHPSLDIDVGCCTDLNEDLDVW 840  
DB 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHPSLDIDVGCCTDLNEDLDVW 840  
QY 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLELTNIVYKEAKES 900  
DB 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLELTNIVYKEAKES 900  
QY 901 VDALFVNSQYDQLQADTNIAHIAADKRVHRIREAYLPESLIPGVNVDIFEELKGRIFT 960  
DB 901 VDALFVNSQYDQLQADTNIAHIAADKRVHRIREAYLPESLIPGVNVDIFEELKGRIFT 960  
QY 961 AFFLYDARNVINKNGDFNGLSCWNVKGVHDVVEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020  
DB 961 AFFLYDARNVINKNGDFNGLSCWNVKGVHDVVEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020  
QY 1021 GYILRVATYKGYGEGCVTHIEIENNTDELKFSNCVEEVPNNVTTCNDYTANOEYGG 1080  
DB 1021 GYILRVATYKGYGEGCVTHIEIENNTDELKFSNCVEEVPNNVTTCNDYTANOEYGG 1080  
QY 1081 AYTSRNRGYDITYGSSNVPADYASVYEKSYTDGRRDNPCESNRGYGDYTPPLPAGYVTK 1140  
DB 1081 AYTSRNRGYDITYGSSNVPADYASVYEKSYTDGRRDNPCESNRGYGDYTPPLPAGYVTK 1140  
QY 1141 ELEYFPETDKVWIEIGETEGFFIVDSVELLMEE 1174  
DB 1141 ELEYFPETDKVWIEIGETEGFFIVDSVELLMEE 1174

Db 1141 ELEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174

# RESULT 8

US-08-639-923A-25  
 ; Sequence 25, Application US/08639923A  
 ; Patent No. 5840534  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thompson, Mark  
 ; APPLICANT: Schwab, George E.  
 ; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in  
 ; TITLE OF INVENTION: Pseudomonas fluorescens  
 ; NUMBER OF SEQUENCES: 38  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/639,923A  
 ; FILING DATE: 24-APR-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/239,476  
 ; FILING DATE: 06-MAY-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 31,794  
 ; REFERENCE/DOCKET NUMBER: MA83.D1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (904) 375-8100  
 ; TELEFAX: (904) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1174 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-639-923A-25

Query Match 100.0%; Score 6244; DB 2; Length 1174;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MENNIOQCVPYCLNPNPEVILNEERSTGLPLDLSLTRELLSEFVPGVAGFLED	60
Db	1	MENNIOQCVPYCLNPNPEVILNEERSTGLPLDLSLTRELLSEFVPGVAGFLED	60
Qy	61	LIWGFITPSDWSLFLQIEOLIEQRIETLERNRAITTLRLGLADSYEIIYIEALREWEANPN	120
Db	61	LIWGFITPSDWSLFLQIEOLIEQRIETLERNRAITTLRLGLADSYEIIYIEALREWEANPN	120
Qy	121	NAQLREDVRIRFANTDDALITAINNFTLTSTFEIPLLSVYQAAANLHLSILRDVAVSQGW	180
Db	121	NAQLREDVRIRFANTDDALITAINNFTLTSTFEIPLLSVYQAAANLHLSILRDVAVSQGW	180
Qy	181	GLDITATVNNHYNRLINLHRYTKHCLDTYNOGLENLRCGTNRQWARFNQFRDLTLTVLD	240
Db	181	GLDITATVNNHYNRLINLHRYTKHCLDTYNOGLENLRCGTNRQWARFNQFRDLTLTVLD	240
Qy	241	IVALFPNDVRYTYPIQTSSQLTRIIYTSVIEDSPVSNIPNGFNRAEFGRVPPHLMDFM	300
Db	241	IVALFPNDVRYTYPIQTSSQLTRIIYTSVIEDSPVSNIPNGFNRAEFGRVPPHLMDFM	300

Qy	301	NSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSSYGVFNPGGAIWIADEDPFRFYTL	360
Db	301	NSLFVTAETVRSQTVWGGHLVSSRNTAGNRINFPSSYGVFNPGGAIWIADEDPFRFYTL	360
Qy	361	DPVFRGGFGNPHVYLGIRGVAFOOTGTNHTRTFRNSTIDSLDEIPQNSGAPWNDYS	420
Db	361	DPVFRGGFGNPHVYLGIRGVAFOOTGTNHTRTFRNSTIDSLDEIPQNSGAPWNDYS	420
Qy	421	HVLNHTVFRWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT	480
Db	421	HVLNHTVFRWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT	480
Qy	481	VVRPGFTGGDILRRTSGGPPAYTIVININGQLPORYRARIYASTTNLRIVYVAGRIIF	540
Db	481	VVRPGFTGGDILRRTSGGPPAYTIVININGQLPORYRARIYASTTNLRIVYVAGRIIF	540
Qy	541	AGQFNKMTMDTGDPLTFQSFYSYATINTAFTFPMSSOSTVGVADTFSSGNEVYIDRFELIPV	600
Db	541	AGQFNKMTMDTGDPLTFQSFYSYATINTAFTFPMSSOSTVGVADTFSSGNEVYIDRFELIPV	600
Qy	601	TATFEAEYDLERAKAVNALETSTINQIGIKTDVTDYHIDQVSNLVDCLSDFCLDEREL	660
Db	601	TATFEAEYDLERAKAVNALETSTINQIGIKTDVTDYHIDQVSNLVDCLSDFCLDEREL	660
Qy	661	SEKVKHAKRLSDERNLLQDPNFKGINROLDRGRGSTDITIORGGDDYFKENYVTLPGTFD	720
Db	661	SEKVKHAKRLSDERNLLQDPNFKGINROLDRGRGSTDITIORGGDDYFKENYVTLPGTFD	720
Qy	721	ECYPYLYQKIDESKLPYTRYQLRGYIEDSDLEIYLIRYNAKHETVNLGTSLWPLS	780
Db	721	ECYPYLYQKIDESKLPYTRYQLRGYIEDSDLEIYLIRYNAKHETVNLGTSLWPLS	780
Qy	781	VQSPTRKCGEPNRCAPHLEWNPDDCCSCROGKCAHSHHPSLDIDYDCTDLNEDLVVY	840
Db	781	VQSPTRKCGEPNRCAPHLEWNPDDCCSCROGKCAHSHHPSLDIDYDCTDLNEDLVVY	840
Qy	841	IFPKITQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLELETNIVYKEAKES	900
Db	841	IFPKITQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLELETNIVYKEAKES	900
Qy	901	VDALFVNSQYDQLQADTNIAHAAKVRHIREAYLPELSVIFGVNVDIPEELKGRIFT	960
Db	901	VDALFVNSQYDQLQADTNIAHAAKVRHIREAYLPELSVIFGVNVDIPEELKGRIFT	960
Qy	961	APFLYDARNVKNQDFNNGLSWNVKGVHDVVEEQNNHSSVLVPEWEAEVSQEVAVCPGR	1020
Db	961	APFLYDARNVKNQDFNNGLSWNVKGVHDVVEEQNNHSSVLVPEWEAEVSQEVAVCPGR	1020
Qy	1021	GYILRVTAKEYGEGCVTIHEIENNTDELKFSNCVEEVEYPNNTVTCNDYTANOEEYGG	1080
Db	1021	GYILRVTAKEYGEGCVTIHEIENNTDELKFSNCVEEVEYPNNTVTCNDYTANOEEYGG	1080
Qy	1081	AVTSNRNGYDEYGNSSVPADYASVYEKSYTQGRDRNPCESNRGYDGYTLPAGYVTK	1140
Db	1081	AVTSNRNGYDEYGNSSVPADYASVYEKSYTQGRDRNPCESNRGYDGYTLPAGYVTK	1140
Qy	1141	ELEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174	
Db	1141	ELEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174	

## RESULT 9

US-08-933-891-8  
 ; Sequence 8, Application US/08933891  
 ; Patent No. 6096708  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel M.  
 ; APPLICANT: Sick, August J.  
 ; TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate  
 ; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding  
 ; TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville

STATE: FL  
COUNTRY: US  
ZIP: 32606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,891  
FILING DATE:

CLASSIFICATION:  
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/356,034  
FILING DATE:

APPLICATION NUMBER: US/08/210,110  
FILING DATE:

APPLICATION NUMBER: 07/865,168  
FILING DATE: 09-APR-92

PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/451,261

FILING DATE: 14-DEC-89  
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 07/371,955  
FILING DATE: 27-JUN-89

ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, Roman

REGISTRATION NUMBER: 21,023  
REFERENCE/DOCKET NUMBER: MA43.C1.D1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904)375-8100

TELEFAX: (904)372-5800  
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1174 amino acids

TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: protein

HYPOTHETICAL: YES  
ANTI-SENSE: NO

ORGANISM: BACILLUS THURINGIENSIS  
STRAIN: AIZAWAI

INDIVIDUAL ISOLATE: PS811  
IMMEDIATE SOURCE:

LIBRARY: LAMEDGEM (TM) - 11 LIBRARY OF AUGUST SICK  
CLONE: 811A

US-08-933-891-8

Query Match 100.0%; Score 6244; DB 3; Length 1174;  
Best Local Similarity 100.0%; Pred No. 0;

Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MENNIOQCVPYCLNPNVEILNEERSTGRLPLDISLTLSEFVPGVGVAFLFD 60

Db 1 MENNIOQCVPYCLNPNVEILNEERSTGRLPLDISLTLSEFVPGVGVAFLFD 60

Qy 61 LINGFITPSDWSLFLQIEQLIETLERNRAITLRLGLADSYEYIEALREWEANPN 120

Db 61 LINGFITPSDWSLFLQIEQLIETLERNRAITLRLGLADSYEYIEALREWEANPN 120

Qy 121 NAQLREDVRIRFANTDALLITAINNFITLTFEIPLLSVYVQAANLHLSLLRDVSRGQGW 180

Db 121 NAQLREDVRIRFANTDALLITAINNFITLTFEIPLLSVYVQAANLHLSLLRDVSRGQGW 180

Qy 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRTGTNTROWARNQFRDLTLTVLD 240

Db 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRTGTNTROWARNQFRDLTLTVLD 240

Qy 241 IVALFPNDVTRTYPIQTSSQLTREIYTSSTVEDSPVSANIENGFNRAEFGVRRPPLMDPM 300

Db 241 IVALFPNDVTRTYPIQTSSQLTREIYTSSTVEDSPVSANIENGFNRAEFGVRRPPLMDPM 300

Qy 301 NSLFVTAETVRSQTVWGGHLYSSRNAGNRIFFPSYGFNPGGAIWIADEDPREFYRTLS 360

Db 301 NSLFVTAETVRSQTVWGGHLYSSRNAGNRIFFPSYGFNPGGAIWIADEDPREFYRTLS 360

Qy 361 DPVFRGGFGNPHVYVGLRGVAFQQTGTNHTRTFNSGTIDSLDEIPQDSGAPWMDYS 420

Db 361 DPVFRGGFGNPHVYVGLRGVAFQQTGTNHTRTFNSGTIDSLDEIPQDSGAPWMDYS 420

Qy 421 HVLNHTVFRWPGELISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHLQSGTT 480

Db 421 HVLNHTVFRWPGELISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHLQSGTT 480

Qy 481 VVRGGFTGGDILRTSGGPPAYTIVNINGQLPORIRIYASTTNLRIVTVAGERIF 540

Db 481 VVRGGFTGGDILRTSGGPPAYTIVNINGQLPORIRIYASTTNLRIVTVAGERIF 540

Qy 541 AGOFNKMTDGTPLTFQSFYSATINTAFTFPMSSOSTFTVGADTFSSGNEVYIDRFELIPV 600

Db 541 AGOFNKMTDGTPLTFQSFYSATINTAFTFPMSSOSTFTVGADTFSSGNEVYIDRFELIPV 600

Qy 601 TATFEAYDLERAKAVNALFTSINOIGIKTDVTDYHEDQVSNLVDCLSDFCDEKREL 660

Db 601 TATFEAYDLERAKAVNALFTSINOIGIKTDVTDYHEDQVSNLVDCLSDFCDEKREL 660

Qy 661 SEKVKAHRLSDERNLLODPNFKGINROLDRGWRGSTDITIQRGDDVFKENVTLPGTFD 720

Db 661 SEKVKAHRLSDERNLLODPNFKGINROLDRGWRGSTDITIQRGDDVFKENVTLPGTFD 720

Qy 721 EGYPTLYKQIDESKLPYTRYQLRGYIEDSODLEIYLIRYNNAKHETVNLGTGSLWPLS 780

Db 721 EGYPTLYKQIDESKLPYTRYQLRGYIEDSODLEIYLIRYNNAKHETVNLGTGSLWPLS 780

Qy 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVCGTDLNEDLDVWV 840

Db 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVCGTDLNEDLDVWV 840

Qy 841 IFKIKTQDGHARLGNLEFLKPLVGEALARKVRAEKWKROKREKLELETNIVYKEAKES 900

Db 841 IFKIKTQDGHARLGNLEFLKPLVGEALARKVRAEKWKROKREKLELETNIVYKEAKES 900

Qy 901 VDALEFVNSQYDQLOQADTNIAHAAKRVHRIREAYLPSELSVPGVNVVDIEELKGRIFT 960

Db 901 VDALEFVNSQYDQLOQADTNIAHAAKRVHRIREAYLPSELSVPGVNVVDIEELKGRIFT 960

Qy 961 AFFLYDARNVKNKGFNNGLSQWNVKGVHVDVEEQNNHSSVLVWPEWEAEVSQEVRCVGR 1020

Db 961 AFFLYDARNVKNKGFNNGLSQWNVKGVHVDVEEQNNHSSVLVWPEWEAEVSQEVRCVGR 1020

Qy 1021 GYLIRVTAYKEGYGECVYTHIENNTDELKFSNCVEEVPNNVTTCNDYTANOEYGG 1080

Db 1021 GYLIRVTAYKEGYGECVYTHIENNTDELKFSNCVEEVPNNVTTCNDYTANOEYGG 1080

Qy 1081 ATTSNRGDETYGNSVYPADYASVYEKSYTDGRRNPNCPESNRGYGDTYPLPAGYTK 1140

Db 1081 ATTSNRGDETYGNSVYPADYASVYEKSYTDGRRNPNCPESNRGYGDTYPLPAGYTK 1140

Qy 1141 ELEYFPETDKVWEIETEGTGTIVDSVELLMEE 1174

Db 1141 ELEYFPETDKVWEIETEGTGTIVDSVELLMEE 1174

RESULT 10  
US-09-178-252-6

; Sequence 6, Application US/09178252

; Patent No. 6218188

; GENERAL INFORMATION:

; APPLICANT: Cardineau, Guy A.

; APPLICANT: Steilman, Steven J.

; APPLICANT: Narva, Kenneth E.



QY 1 MENNIONQVPCVNCNNPEVEILNEERSTGRPLDLSLTLRFLLSRVPVGVAFGLFD 60  
DB 1 MENNIONQVPCVNCNNPEVEILNEERSTGRPLDLSLTLRFLLSRVPVGVAFGLFD 60  
QY 61 LWGFITPDSWLSFLQLBOLQEIOETLERNRAITTLRGLADSYEIIYIEALREWEANPN 120  
DB 61 LWGFITPDSWLSFLQLBOLQEIOETLERNRAITTLRGLADSYEIIYIEALREWEANPN 120  
QY 121 NAQLRDEVRIRFANTDDALITAINFTLTSFEIPLSVYVQAANHLSLRDVAFSGGW 180  
DB 121 NAQLRDEVRIRFANTDDALITAINFTLTSFEIPLSVYVQAANHLSLRDVAFSGGW 180  
QY 181 GDIATVNNHYNRLNLIHRYTKHCLDYNQGLNRTGNTQWARFQFRDLTLTVLD 240  
DB 181 GDIATVNNHYNRLNLIHRYTKHCLDYNQGLNRTGNTQWARFQFRDLTLTVLD 240  
QY 241 IVALFPNDVRYPIQTSOLTRFYTSSVIEDSPVSANIPNGFNRAEFGVRPPLHDMFM 300  
DB 241 IVALFPNDVRYPIQTSOLTRFYTSSVIEDSPVSANIPNGFNRAEFGVRPPLHDMFM 300  
QY 301 NSLFTVTAETVRSQTVWGHLVSSRTAGNINFPVGVFNGGATWIADEDPPEYRTLS 360  
DB 301 NSLFTVTAETVRSQTVWGHLVSSRTAGNINFPVGVFNGGATWIADEDPPEYRTLS 360  
QY 361 DPFVVRGFGFNHYVLGRVAFQQTGNTNRTFRNSGTIDSLDEIPQDNSGAPWNDYS 420  
DB 361 DPFVVRGFGFNHYVLGRVAFQQTGNTNRTFRNSGTIDSLDEIPQDNSGAPWNDYS 420  
QY 421 HVLNHTVFRVWGEISGDSWAPFWSWTHRSATPTNTIDPERITQIPLVKAHTLOSITT 480  
DB 421 HVLNHTVFRVWGEISGDSWAPFWSWTHRSATPTNTIDPERITQIPLVKAHTLOSITT 480  
QY 481 VVRGPGTGDILRTSGGPFAYTIVNINQQLPQRYRARIYASTNRIYVTVAGERIF 540  
DB 481 VVRGPGTGDILRTSGGPFAYTIVNINQQLPQRYRARIYASTNRIYVTVAGERIF 540  
QY 541 AQGFNTMTDGPDLTQSFYSYATINTAFTFPMSSQSFVGAOTFSSGNEVYIDREFLAPV 600  
DB 541 AQGFNTMTDGPDLTQSFYSYATINTAFTFPMSSQSFVGAOTFSSGNEVYIDREFLAPV 600  
QY 601 TATFEAYDLERAKAVNALETSINOIGTKTDVTDVHIDQVNLVDCLEDFCLDEKREL 660  
DB 601 TATFEAYDLERAKAVNALETSINOIGTKTDVTDVHIDQVNLVDCLEDFCLDEKREL 660  
QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQDRGWRGSTDTIQGGDDVFKENYVTLPGTFD 720  
DB 661 SEKVKHAKRLSDERNLLQDPNFKGINRQDRGWRGSTDTIQGGDDVFKENYVTLPGTFD 720  
QY 721 ECVPTVLYOKIDESKLPYTRYQLRGYIEDSODLEIYLYRYNAKHETVNLGTSWLPIS 780  
DB 721 ECVPTVLYOKIDESKLPYTRYQLRGYIEDSODLEIYLYRYNAKHETVNLGTSWLPIS 780  
QY 781 VQSPIRKGEPNRCAPHEWNPDLDCSRRGKCAHSHHFLDIDVGCTDLNEDLDVWV 840  
DB 781 VQSPIRKGEPNRCAPHEWNPDLDCSRRGKCAHSHHFLDIDVGCTDLNEDLDVWV 840  
QY 841 IFKIKTDGCHARLGNLEFLEKPLVGEALARYKRAEKKWRDRKREKLEETNIVYKEAKES 900  
DB 841 IFKIKTDGCHARLGNLEFLEKPLVGEALARYKRAEKKWRDRKREKLEETNIVYKEAKES 900  
QY 901 VDALFVNSQVQDQADNTAMIAHAAKRVHRIEAYLPEISVIPGVNVDIFPEELKGRIFT 960  
DB 901 VDALFVNSQVQDQADNTAMIAHAAKRVHRIEAYLPEISVIPGVNVDIFPEELKGRIFT 960  
QY 961 AFFLYDARNYIKNGDFNNGLSKNVKGHDVBEQNNHRSVLYVPEWEAEVSQEVRCPCR 1020  
DB 961 AFFLYDARNYIKNGDFNNGLSKNVKGHDVBEQNNHRSVLYVPEWEAEVSQEVRCPCR 1020  
QY 1021 GYLIRVTAYKEGEGCVTTHETENNTDELKFSNCVBEVEYVNNVTVCNDYTANQOEYGG 1080  
DB 1021 GYLIRVTAYKEGEGCVTTHETENNTDELKFSNCVBEVEYVNNVTVCNDYTANQOEYGG 1080  
QY 1081 AYTSRNRGYDETYGSSNPADYASVYEESYTDGRRDNPCESNRGYGDTPLPAGVYTK 1140

DB 1081 AYTSRNRGYDETYGSSNPADYASVYEESYTDGRRDNPCESNRGYGDTPLPAGVYTK 1140  
QY 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLME 1174  
DB 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLME 1174

## RESULT 12

PCT-US92-11337-10  
; Sequence 10, Application PC/TUS9211337  
; GENERAL INFORMATION:  
; APPLICANT: PAYNE, JEWEL M.  
; APPLICANT: HICKLE, LESLIE A.  
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES  
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID R. SALIWANCHIK  
; STREET: 2421 N.W. 41st STREET, SUITE A-1  
; CITY: GAINESVILLE  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/11337  
; FILING DATE: 19921231  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 97/828,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SALIWANCHIK, DAVID R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA75  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1174 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEetical: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: BACILLUS THURINGIENSIS  
; STRAIN: AIZAWAI  
; INDIVIDUAL ISOLATE: PS811  
; IMMEDIATE SOURCE:  
; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK  
; CLONE: 811A  
PCT-US92-11337-10

Query Match 100.0%; Score 6244; DB 5; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MENNIONQVPCVNCNNPEVEILNEERSTGRPLDLSLTLRFLLSRVPVGVAFGLFD 60  
DB 1 MENNIONQVPCVNCNNPEVEILNEERSTGRPLDLSLTLRFLLSRVPVGVAFGLFD 60  
QY 61 LWGFITPDSWLSFLQLBOLQEIOETLERNRAITTLRGLADSYEIIYIEALREWEANPN 120  
DB 61 LWGFITPDSWLSFLQLBOLQEIOETLERNRAITTLRGLADSYEIIYIEALREWEANPN 120

QY 121 NAQLREDVIRFANTDDALITAINNNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSGQW 180  
DB 121 NAQLREDVIRFANTDDALITAINNNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSGQW 180  
QY 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENLRTNQWAFNQFRDLTLTVID 240  
DB 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENLRTNQWAFNQFRDLTLTVID 240  
QY 241 IVALFPNDVRYPIOTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300  
DB 241 IVALFPNDVRYPIOTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300  
QY 301 NSLFTVTAETVRSQVWGGHLVSSRNAGNINFPSPYGVNPGGAIWAIEDPRPYRTLS 360  
DB 301 NSLFTVTAETVRSQVWGGHLVSSRNAGNINFPSPYGVNPGGAIWAIEDPRPYRTLS 360  
QY 361 DPVFEVGGFNGPHYVGLRGVAFQQTGNTHTFRNSGTIDSLDETPDONGSGAPWNYD 420  
DB 361 DPVFEVGGFNGPHYVGLRGVAFQQTGNTHTFRNSGTIDSLDETPDONGSGAPWNYD 420  
QY 421 HVLNHTVFRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480  
DB 421 HVLNHTVFRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480  
QY 481 VVRPGFTGDDILRRISGPPFAYTIVNIGQLPQRYARIRVASTNLIYVTVAGERIF 540  
DB 481 VVRPGFTGDDILRRISGPPFAYTIVNIGQLPQRYARIRVASTNLIYVTVAGERIF 540  
QY 541 AGQFNKMTDGTPLTQSFYSYATINTAFTFPMQSQSFVTCGADTFSSGNEVYIDRELIPV 600  
DB 541 AGQFNKMTDGTPLTQSFYSYATINTAFTFPMQSQSFVTCGADTFSSGNEVYIDRELIPV 600  
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDQVNLVDCLDFCLDEKREL 660  
DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDQVNLVDCLDFCLDEKREL 660  
QY 661 SEKVAKRLSDERNLQDPNFKGINRQLDRGWRGSTDITIOGDDVFNKVTVLPGFDF 720  
DB 661 SEKVAKRLSDERNLQDPNFKGINRQLDRGWRGSTDITIOGDDVFNKVTVLPGFDF 720  
QY 721 ECPYTYLYOKIDESKLPKPYRYOLRGYIEDSDQLEYLYRYNAKHETVNLGTSLWPLS 780  
DB 721 ECPYTYLYOKIDESKLPKPYRYOLRGYIEDSDQLEYLYRYNAKHETVNLGTSLWPLS 780  
QY 781 VQSPIRKCGPNPCAPHEWNPDLDCSDRGKCAHSHHFSLDIDVCGTDLNEEDLVWV 840  
DB 781 VQSPIRKCGPNPCAPHEWNPDLDCSDRGKCAHSHHFSLDIDVCGTDLNEEDLVWV 840  
QY 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKES 900  
DB 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKES 900  
QY 901 VDALFVNSQVDDOQADNTAMIAHAKRVHRIEAYVLPESLYTPGVNVDIFELKGRIFT 960  
DB 901 VDALFVNSQVDDOQADNTAMIAHAKRVHRIEAYVLPESLYTPGVNVDIFELKGRIFT 960  
QY 961 AFELYDARNYIKNGDFNNGLSWNVKGVHDVVEEQNNHRSVLYVPEWAEVSGEVRVCPGR 1020  
DB 961 AFELYDARNYIKNGDFNNGLSWNVKGVHDVVEEQNNHRSVLYVPEWAEVSGEVRVCPGR 1020  
QY 1021 GYLIRVTAKEGEGECVTIHEJNTNDELKFSNCVEEYVNNVTTCNDYTANOEYGG 1080  
DB 1021 GYLIRVTAKEGEGECVTIHEJNTNDELKFSNCVEEYVNNVTTCNDYTANOEYGG 1080  
QY 1081 AYTSSRNGYDETYGSSNVPADYASVYEEKSYTDGRRDNPCESNRGYGDYTPLPAGYVTK 1140  
DB 1081 AYTSSRNGYDETYGSSNVPADYASVYEEKSYTDGRRDNPCESNRGYGDYTPLPAGYVTK 1140  
QY 1141 ELEYFPDOKWIEIGTEGTFTFVDSVELLME 1174  
DB 1141 ELEYFPDOKWIEIGTEGTFTFVDSVELLME 1174

RESULT 13  
PCT-US95-05431-25  
: Sequence 25, Application PC/TUS95050431  
: GENERAL INFORMATION:  
: APPLICANT: Street address: 5501 Oberlin Drive  
: APPLICANT: City: San Diego California  
: APPLICANT: State/Province: California  
: APPLICANT: Country: US  
: APPLICANT: Postal code/zip: 92121  
: APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991  
: APPLICANT: Telex number:  
: TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in  
: Pseudomonas fluorescens  
: NUMBER OF SEQUENCES: 34  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: David R. Saliwanchik  
: STREET: 2421 N.W. 41st Street, Suite A-1  
: CITY: Gainesville  
: STATE: Florida  
: COUNTRY: USA  
: ZIP: 32606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: PCT/US95/05431  
: FILING DATE:  
: CLASSIFICATION:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Saliwanchik, David R.  
: REGISTRATION NUMBER: 31,794  
: REFERENCE/DOCKET NUMBER: MA83  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (904) 375-8100  
: TELEFAX: (904) 372-5800  
: INFORMATION FOR SEQ ID NO: 25:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1174 amino acids  
: TYPE: amino acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
PCT-US95-05431-25

Query Match 100.0%; Score 6244; DB 5; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MENNIOQCPVNCNNPEVEILNEERSTGRPLDLSLSTRFLLSEFVPGVGVAFGLFD 60  
QY 61 LIWGFITPDSWLSFLLOEQLEIQRITELERNRAITTLRGLADSYEYIEALREWEANPN 120  
DB 61 LIWGFITPDSWLSFLLOEQLEIQRITELERNRAITTLRGLADSYEYIEALREWEANPN 120  
QY 121 NAQLREDVIRFANTDDALITAINNNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSGQW 180  
DB 121 NAQLREDVIRFANTDDALITAINNNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSGQW 180  
QY 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENLRTNQWAFNQFRDLTLTVID 240  
DB 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENLRTNQWAFNQFRDLTLTVID 240  
QY 241 IVALFPNDVRYPIOTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300  
DB 241 IVALFPNDVRYPIOTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300  
QY 301 NSLFTVTAETVRSQVWGGHLVSSRNAGNINFPSPYGVNPGGAIWAIEDPRPYRTLS 360  
DB 301 NSLFTVTAETVRSQVWGGHLVSSRNAGNINFPSPYGVNPGGAIWAIEDPRPYRTLS 360

Db 301 NSLFVTAETVRSQTVWGCHLVSSRNTAGNRRNFPISYGVNPGGAIWIADDEPRPFYRTLS 360  
QY 361 DPVVRGSGFNGPHYVLGRGVAFOQTGTHHTRTFRNSGTIDSLDEIPPDNSGAPWNDYS 420  
Db 361 DPVVRGSGFNGPHYVLGRGVAFOQTGTHHTRTFRNSGTIDSLDEIPPDNSGAPWNDYS 420  
QY 421 HVLNHVTFVRWPGGELSGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480  
Db 421 HVLNHVTFVRWPGGELSGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480  
QY 481 VVRGPGTGGDILARTSGGPAYITVNLINGOLPQYRARIYASTNRIYVTVAGERIF 540  
Db 481 VVRGPGTGGDILARTSGGPAYITVNLINGOLPQYRARIYASTNRIYVTVAGERIF 540  
QY 541 AGQFNKMTDGTGDLPTFQSFYSATINTAFTFPMQSSSFVGGADTFSSGNEVIDRFEPLPV 600  
Db 541 AGQFNKMTDGTGDLPTFQSFYSATINTAFTFPMQSSSFVGGADTFSSGNEVIDRFEPLPV 600  
QY 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660  
Db 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660  
QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDGRGSGTDTITQRGDDVFKENYVTLPGTFD 720  
Db 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDGRGSGTDTITQRGDDVFKENYVTLPGTFD 720  
QY 721 ECTPTLYQKIDESKLPYTRYQLRGYIEDSQDLLEIYLIRYNAKHETVNLVGTGSLWPLS 780  
Db 721 ECTPTLYQKIDESKLPYTRYQLRGYIEDSQDLLEIYLIRYNAKHETVNLVGTGSLWPLS 780  
QY 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
Db 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
QY 841 IFKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLETNIVYKAKES 900  
Db 841 IFKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLETNIVYKAKES 900  
QY 901 VDALFVNSQVDQLOADNTAMIHAADKRVHRIREAYLPESLIPGVNVDIPEELKGRIFT 960  
Db 901 VDALFVNSQVDQLOADNTAMIHAADKRVHRIREAYLPESLIPGVNVDIPEELKGRIFT 960  
QY 961 AFPLYDARNVKNKGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCPCR 1020  
Db 961 AFPLYDARNVKNKGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCPCR 1020  
QY 1021 GYLIRVTAAYKEGYEGCVTTHEIENNTDELKFSNCVREEVYPNNVTVCNDYTANQEEYGG 1080  
Db 1021 GYLIRVTAAYKEGYEGCVTTHEIENNTDELKFSNCVREEVYPNNVTVCNDYTANQEEYGG 1080  
QY 1081 AVTSRNRGYDETYGSSNSVPADYASVYEKSYTDGRRDNPCESNRGYGDXTPPLPAGVYTK 1140  
Db 1081 AVTSRNRGYDETYGSSNSVPADYASVYEKSYTDGRRDNPCESNRGYGDXTPPLPAGVYTK 1140  
QY 1141 ELEYFETDKVWIEIGETGTFIVDSVELLLMEE 1174  
Db 1141 ELEYFETDKVWIEIGETGTFIVDSVELLLMEE 1174

## RESULT 14

5188960-8

; Patent No. 5188960

; APPLICANT: PAYNE, JEWEL; SICK, AUGUST J.

; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE

; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL

; LEPIDOPTERAN-ACTIVE TOXINS

; NUMBER OF SEQUENCES: 8

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/451,261

; FILING DATE: 14-DEC-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 371,955

; FILING DATE: 27-JUN-1989

; SEQ ID NO: 8:

; LENGTH: 1174

5188960-8

## Query Match

100.0%; Score 6244; DB 6; Length 1174;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIONCVYPNCLNNEPVEILLNEERSTGRPLDLSLSTRFLLSSEVPVGVAGFLPD 60

Db 1 MENNIONCVYPNCLNNEPVEILLNEERSTGRPLDLSLSTRFLLSSEVPVGVAGFLPD 60

QY 61 LIWGFITPDSKSLFQLEQLEQRIETLERNRAITTLRGGLADSYEIIYIEARWEANPN 120

Db 61 LIWGFITPDSKSLFQLEQLEQRIETLERNRAITTLRGGLADSYEIIYIEARWEANPN 120

QY 121 NAQLREDVRIREFANTDDALITAINNFTLTSPFIPLLSYVQAANLHLSLLRDVAVSFGOGW 180

Db 121 NAQLREDVRIREFANTDDALITAINNFTLTSPFIPLLSYVQAANLHLSLLRDVAVSFGOGW 180

QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDITYNOGLENLNRCNTROWARFNQFRDLTLTVID 240

Db 181 GLDIATVNNHYNRLINLIHRYTKHCLDITYNOGLENLNRCNTROWARFNQFRDLTLTVID 240

QY 241 IVALFPNDVRYTPIQTSSQLTRIIYTSVIEDSPVSIPIGNFNRAEFGVRPPLMDFM 300

Db 241 IVALFPNDVRYTPIQTSSQLTRIIYTSVIEDSPVSIPIGNFNRAEFGVRPPLMDFM 300

QY 301 NSLFVTAETVRSQTVWGCHLVSSRNTAGNRRNFPISYGVNPGGAIWIADDEPRPFYRTLS 360

Db 301 NSLFVTAETVRSQTVWGCHLVSSRNTAGNRRNFPISYGVNPGGAIWIADDEPRPFYRTLS 360

QY 361 DPVVRGSGFNGPHYVLGRGVAFOQTGTHHTRTFRNSGTIDSLDEIPPDNSGAPWNDYS 420

Db 361 DPVVRGSGFNGPHYVLGRGVAFOQTGTHHTRTFRNSGTIDSLDEIPPDNSGAPWNDYS 420

QY 421 HVLNHVTFVRWPGGELSGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480

Db 421 HVLNHVTFVRWPGGELSGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480

QY 481 VVRGPGTGGDILARTSGGPAYITVNLINGOLPQYRARIYASTNRIYVTVAGERIF 540

Db 481 VVRGPGTGGDILARTSGGPAYITVNLINGOLPQYRARIYASTNRIYVTVAGERIF 540

QY 541 AGQFNKMTDGTGDLPTFQSFYSATINTAFTFPMQSSSFVGGADTFSSGNEVIDRFEPLPV 600

Db 541 AGQFNKMTDGTGDLPTFQSFYSATINTAFTFPMQSSSFVGGADTFSSGNEVIDRFEPLPV 600

QY 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660

Db 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660

QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDGRGSGTDTITQRGDDVFKENYVTLPGTFD 720

Db 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDGRGSGTDTITQRGDDVFKENYVTLPGTFD 720

QY 721 ECTPTLYQKIDESKLPYTRYQLRGYIEDSQDLLEIYLIRYNAKHETVNLVGTGSLWPLS 780

Db 721 ECTPTLYQKIDESKLPYTRYQLRGYIEDSQDLLEIYLIRYNAKHETVNLVGTGSLWPLS 780

QY 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLDVWV 840

Db 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLDVWV 840

QY 841 IFKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLETNIVYKAKES 900

Db 841 IFKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLETNIVYKAKES 900

QY 901 VDALFVNSQVDQLOADNTAMIHAADKRVHRIREAYLPESLIPGVNVDIPEELKGRIFT 960

Db 901 VDALFVNSQVDQLOADNTAMIHAADKRVHRIREAYLPESLIPGVNVDIPEELKGRIFT 960

QY 961 AFPLYDARNVKNKGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCPCR 1020

Db 961 AFFLYDARNVKNKNGDFNGLSCWNRKGVHDVEBQNNHRSVLVVPWEAEVSQEVRCPCR 1020  
Qy 1021 GYLRTVAYKEGEGCVTTHEIENNTDELKPSNCVEEVEYPPNNTVTCNDYTANQEEYGG 1080  
Db 1021 GYLRTVAYKEGEGCVTTHEIENNTDELKPSNCVEEVEYPPNNTVTCNDYTANQEEYGG 1080  
Qy 1081 AYTSRNRGYDETYGNSVSPADYASVYEKSYTDGRRDNPCESTRNGYGYDTPLPAGYVTK 1140  
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Qy 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174  
Db 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174

## RESULT 15

US-08-239-476-32  
; Sequence 32, Application US/08239476  
; Patent No. 5527883  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Mark  
; APPLICANT: Schwab, George E.  
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in  
; TITLE OF INVENTION: Pseudomonas fluorescens  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/239,476  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: M83  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1184 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-239-476-32

Query Match 100.0%; Score 6244; DB 1; Length 1184;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 11 MENNIOQCVNCLNPEVILNEERSTGRPLDLSLSTRLLSEFFVPGVGFALFLD 70  
Qy 61 LIWGFITPSDWSLFLQIEQLIEQRIETLRNRAITTLRLGLADSYEYIYIYALREWEANPN 120  
Db 71 LIWGFITPSDWSLFLQIEQLIEQRIETLRNRAITTLRLGLADSYEYIYIYALREWEANPN 130  
Qy 121 NAOLREDVRIRFANTDALTAINNFTLTSTFEIPLLSVYVQAAMHLSLRLDRAVSFGQW 180  
Db 131 NAOLREDVRIRFANTDALTAINNFTLTSTFEIPLLSVYVQAAMHLSLRLDRAVSFGQW 190

Qy 181 GLDIATVNNHYNRLINLHRYTKHCLDLYNQGLNENLGTNTKQWAFNQFRRDLTIVLD 240  
Db 191 GLDIATVNNHYNRLINLHRYTKHCLDLYNQGLNENLGTNTKQWAFNQFRRDLTIVLD 250  
Qy 241 IVALFPNVDTYPIQTSQTLREIYTSSTVEDSPVSGANIPNGFNRAEFGVRPPLHMDFM 300  
Db 251 IVALFPNVDTYPIQTSQTLREIYTSSTVEDSPVSGANIPNGFNRAEFGVRPPLHMDFM 310  
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Db 311 NSLFTVTAETVSQVWVGHLVSSRNTAGNINPSPYGVNPGGAIWIAEDDPPFPYRTLS 370  
Qy 361 DPVFRGFGNPHYVLGLRGVAFQQTGTNHTFRNRSSTIDSLDEIPPOQNSGAPNDYS 420  
Db 371 DPVFRGFGNPHYVLGLRGVAFQQTGTNHTFRNRSSTIDSLDEIPPOQNSGAPNDYS 430  
Qy 421 HVLNHTVFRWPGELSGSDSHRAPMFWSHRSATPTTIDPERITQIPLKAKHTLQSGTT 480  
Db 431 HVLNHTVFRWPGELSGSDSHRAPMFWSHRSATPTTIDPERITQIPLKAKHTLQSGTT 490  
Qy 481 VVRGPGFTGGDILRRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYTVVAGERIF 540  
Db 491 VVRGPGFTGGDILRRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYTVVAGERIF 550  
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Db 551 AGQPNKMTMDTGDTLTFQSFYSATINTAFTPPMSOSSFTVGADTFSSGNEVYIDREFELIPV 610  
Qy 601 TATPEAYDLERAOKAVNALFTSINOIGIKTDVTDYHDOVSNLVDCLSDFCLDKREL 660  
Db 611 TATPEAYDLERAOKAVNALFTSINOIGIKTDVTDYHDOVSNLVDCLSDFCLDKREL 670  
Qy 661 SEKVHAKRLSDERNLQDPNFKGINQLDRGWSGSDITIIQRGDDVFKENYVTLPGTFD 720  
Db 671 SEKVHAKRLSDERNLQDPNFKGINQLDRGWSGSDITIIQRGDDVFKENYVTLPGTFD 730  
Qy 721 ECPYPLYQKIDESKLPYTRYQLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLWPLS 780  
Db 731 ECPYPLYQKIDESKLPYTRYQLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLWPLS 790  
Qy 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
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Qy 841 IFKIKTODGHARLGNLELEKPLVGEALARYKRAEKWRDKREKLELTNIVYKRAES 900  
Db 851 IFKIKTODGHARLGNLELEKPLVGEALARYKRAEKWRDKREKLELTNIVYKRAES 910  
Qy 901 VDLEFVNSQYDQLQADTNIAHAAKRVHRIEAYLPESLVIQVNVVDIFEELKGRIFT 960  
Db 911 VDLEFVNSQYDQLQADTNIAHAAKRVHRIEAYLPESLVIQVNVVDIFEELKGRIFT 970  
Qy 961 AFFLYDARNVKNKNGDFNGLSCWNRKGVHDVEBQNNHRSVLVVPWEAEVSQEVRCPCR 1020  
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Db 1031 GYLRTVAYKEGEGCVTTHEIENNTDELKPSNCVEEVEYPPNNTVTCNDYTANQEEYGG 1090  
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Qy 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174  
Db 1151 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1184

Search completed: November 27, 2002, 20:26:20  
Job time : 43 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 27, 2002, 13:01:49 ; Search time 83 Seconds

(without alignments)  
1884.774 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MNNIQNQCVPYCNLNPEV.....IGTEGTFIVDSVELLMEE 1174

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
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- 5: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
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- 7: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
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- 10: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
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- 21: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6244	100.0	1174	12 AAR10131	Lepidopteran-activ
2	6244	100.0	1174	12 AAR14856	CryIF protein. Ba
3	6244	100.0	1174	14 AAR39754	Delta endotoxin.
4	6244	100.0	1174	19 AAW76708	Plasmid pMYC2243 B
5	6244	100.0	1174	19 AAW76712	B.thuringiensis c
6	6244	100.0	1174	20 AAY16792	Wild-type B.t cryI
7	6244	100.0	1174	22 AAU00533	B. thuringiensis t
8	6244	100.0	1184	16 AAR84737	Native cryIF toxin
9	6238	99.9	1174	16 AAR84735	CryIF toxin with l
10	6237	99.9	1174	17 AAR94914	CryIF toxin encode

11	6236	99.9	1174	17 AAR94916	Native CryIF/CryIA
12	6049	96.9	1174	16 AAR84732	CryIF/436 chimeric
13	6049	96.9	1174	17 AAR94908	CryIF/436 chimeric
14	6049	96.9	1174	19 AAW76710	Plasmid pMYC2254 c
15	6018.5	96.4	1175	19 AAW76716	Alternative cryIF/
16	5913	94.7	1148	19 AAW76717	Alternative cryIF/
17	5908	94.6	1148	19 AAW76718	Alternative cryIF/
18	5902	94.5	1148	16 AAR84731	CryIF/CryIA(b) chi
19	5902	94.5	1148	16 AAR84733	CryIF/CryIA(b) chi
20	5902	94.5	1148	17 AAR94907	Plasmid pMYC2244 c
21	5902	94.5	1148	19 AAW76709	Plasmid pMYC2523 c
22	5889	94.3	1148	19 AAW76715	Consensus cryIF/cr
23	5889	94.3	1148	19 AAW76715	Plant-optimised cr
24	5879	94.2	1148	20 AAY16790	CryIF/CryIA chimera
25	5879	94.2	1148	22 AAU00531	CryIA(c)/CryIF/cry
26	5674	90.9	1150	16 AAR84734	CryIA(c)/CryIF/cry
27	5674	90.9	1150	17 AAR94913	Plasmid pMYC2239 b
28	5674	90.9	1150	19 AAW76706	Bacillus thuringie
29	5595	89.6	1186	22 AAU00419	Bacillus thuringie
30	5409	86.6	1168	17 AAR89493	CryIF class toxin
31	5141	82.3	1174	17 AAR89483	Generic formula fo
32	4815.5	77.1	1177	19 AAW58558	Bacillus thuringie
33	4815.5	77.1	1177	23 AAU77239	Bacillus thuringie
34	4812.5	77.1	1177	19 AAW58559	Bacillus thuringie
35	4812.5	77.1	1177	23 AAU77240	Bacillus thuringie
36	4804.5	76.9	1177	19 AAW58556	Bacillus thuringie
37	4804.5	76.9	1177	23 AAU77237	Bacillus thuringie
38	4745.5	76.0	1177	19 AAW58560	Bacillus thuringie
39	4745.5	76.0	1177	23 AAU77241	Bacillus thuringie
40	4706.5	75.4	1177	19 AAW58557	Bacillus thuringie
41	4706.5	75.4	1177	23 AAU77238	Bacillus thuringie
42	4647.5	74.4	1177	23 AAU77243	Bacillus thuringie
43	4636.5	74.3	1177	19 AAW58562	Bacillus thuringie
44	4391.5	70.3	1202	10 AAP90717	Bacillus thuringie
45	4380.5	70.2	1180	12 AAR13309	Modified thermosta

## ALIGNMENTS

RESULT 1	
AAR10131	
ID AAR10131 standard; Protein; 1174 AA.	
XX AAR10131;	
XX AC	
XX 20-MAR-1991 (first entry)	
DT XX	
XX Lepidopteran-active toxin D.	
DE XX	
XX Lepidopteran-active toxin D; pest control.	
XX	
XX Bacillus thuringiensis PS8LL (NRRL B-18484).	
XX	
PN EP405810-A.	
XX	
XX 02-JAN-1991.	
PD XX	
XX 18-JUN-1990; 90EP-0306594.	
XX	
PR 14-DEC-1989; 89US-0451261.	
PR 27-JUN-1989; 89US-0371955.	
XX	
XX (MYCO-) MYCOGEN CORP.	
PA Payne J, Sick AJ;	
XX	
PI WPI; 1991-009132/02.	
DR Q-PSDB; Q10182.	
DR	
PT Bacillus thuringiensis contg. DNA encoding lepidopteran-active	
PT toxin - use of microorganisms transformed with the toxin gene	
PT in pest control	

XX  
PS Claim 6; Page 24-27; 28pp; English.  
XX Expression of the toxin gene by a host results, directly or  
CC indirectly, in the intracellular prodn. and maintenance of the  
CC pesticide.  
CC See also AAQ10179-82.  
XX  
XX Sequence 1174 AA;  
SQ

Query Match 100.0%; Score 6244; DB 12; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIONQCVNCLNNEVEILNEERSTGRPLDLSLSTRLLSEFFVGVGVAFLFD 60  
Db 1 MENNIONQCVNCLNNEVEILNEERSTGRPLDLSLSTRLLSEFFVGVGVAFLFD 60

QY 61 LIWGFITPDSWSLFLQIEQLIBQRIETLERNAITLRLGLADSYEYIEALREWEANPN 120  
Db 61 LIWGFITPDSWSLFLQIEQLIBQRIETLERNAITLRLGLADSYEYIEALREWEANPN 120

QY 121 NAQLRDVRIRFANTDALLTAINNTLTSTFEIPLSVYVQAAANLHLSLLRDVAVSQGW 180  
Db 121 NAQLRDVRIRFANTDALLTAINNTLTSTFEIPLSVYVQAAANLHLSLLRDVAVSQGW 180

QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENGTNTROWARFNQFRDLTLTVLD 240  
Db 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENGTNTROWARFNQFRDLTLTVLD 240

QY 241 IVALFPNDVRYTPIOTSSOLTEIYTSVIEDSPVSANIPNGFNRAEFGVRPPLHMDFM 300  
Db 241 IVALFPNDVRYTPIOTSSOLTEIYTSVIEDSPVSANIPNGFNRAEFGVRPPLHMDFM 300

QY 301 NSLFVTAETVRSQTVGGHVLSSRNTAGNINPSPYGVFNPGGAIWIADEDPPEYRTLS 360  
Db 301 NSLFVTAETVRSQTVGGHVLSSRNTAGNINPSPYGVFNPGGAIWIADEDPPEYRTLS 360

QY 361 DPVVRGGFGNPHVVLGRVAFQOQGTNHTFRFRSGTIDSLDEIPPOQNSGAPNDYS 420  
Db 361 DPVVRGGFGNPHVVLGRVAFQOQGTNHTFRFRSGTIDSLDEIPPOQNSGAPNDYS 420

QY 421 HVLNHYTFVRWPGIEISGSDSWRAPMFSWTHRSATPNTIDPERITOPLVKAHTLOSGET 480  
Db 421 HVLNHYTFVRWPGIEISGSDSWRAPMFSWTHRSATPNTIDPERITOPLVKAHTLOSGET 480

QY 481 VVRPGFTGGDILRRTSGGPFATYVINGQLPQYRARIYASTNLRIYTVAGERIF 540  
Db 481 VVRPGFTGGDILRRTSGGPFATYVINGQLPQYRARIYASTNLRIYTVAGERIF 540

QY 541 AGQFNKMTDGLTTFQSPSYATINFTAFPMSSQSTYVAGDTFSSGNEVYIDRFELIPV 600  
Db 541 AGQFNKMTDGLTTFQSPSYATINFTAFPMSSQSTYVAGDTFSSGNEVYIDRFELIPV 600

QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDQVSNLVCLSDFCFLDEKREL 660  
Db 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDQVSNLVCLSDFCFLDEKREL 660

QY 661 SEKVHAKLSBERNLQDPNFKGINRQDRGRGSTDITIQRGDDVFKENYVTLPGTFD 720  
Db 661 SEKVHAKLSBERNLQDPNFKGINRQDRGRGSTDITIQRGDDVFKENYVTLPGTFD 720

QY 721 ECVPTLYOKIDESKLPYTRVLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLWPLS 780  
Db 721 ECVPTLYOKIDESKLPYTRVLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLWPLS 780

QY 781 VQSPIRKCEPNRCAHLEWNPDLDCSRRGCKAHHSHFSLDIDVGCTDLNEDLDVWV 840  
Db 781 VQSPIRKCEPNRCAHLEWNPDLDCSRRGCKAHHSHFSLDIDVGCTDLNEDLDVWV 840

QY 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKEAKES 900  
Db 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKEAKES 900

QY 901 VDALFVNSQYDQLOADTNIAIMIHAADKRVHRIRIAYLPILSVIPGVNVDIFEELKGRIFT 960  
Db 901 VDALFVNSQYDQLOADTNIAIMIHAADKRVHRIRIAYLPILSVIPGVNVDIFEELKGRIFT 960

QY 961 AFFLYDARNVIKNGDFNNGLSKNVKGHDVEEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020  
Db 961 AFFLYDARNVIKNGDFNNGLSKNVKGHDVEEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020

QY 1021 GYLRTVAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYYPNNTVTCNDYTANQEEYGG 1080  
Db 1021 GYLRTVAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYYPNNTVTCNDYTANQEEYGG 1080

QY 1081 AYTSSRNGYDETYGSSSVPADYASVYEKSYTDGRDNPCESNRGYDITPLPAGVYTK 1140  
Db 1081 AYTSSRNGYDETYGSSSVPADYASVYEKSYTDGRDNPCESNRGYDITPLPAGVYTK 1140

QY 1141 ELEYFFETDKVWIEIGETEGTFIVDSVELLMEE 1174  
Db 1141 ELEYFFETDKVWIEIGETEGTFIVDSVELLMEE 1174

RESULT 2  
AAR14856  
ID AAR14856 standard; Protein; 1174 AA.  
XX AAR14856;  
AC AAR14856;  
XX 31-JAN-1992 (first entry)  
DT 31-JAN-1992 (first entry)  
XX CryIF protein.  
XX Insecticide; Lepidoptera control; ss.  
XX Bacillus thuringiensis.  
XX WO9116434-A.  
XX 31-OCT-1991.  
XX 15-APR-1991; 91WO-US02560.  
XX 16-APR-1990; 90US-0510327.  
XX (ECOG-) ECOGEN INC.  
XX Gawron-Burke CM, Chambers JA, Gonzalez JM;  
XX WPI: 1991-339822/46.  
XX N-PSDB; AAR14848.  
XX Purifying and isolating CRY-I type genes - from novel Bacillus  
XX thuringiensis strain as insecticides  
XX Claim 3; Fig 1A-E; 100pp; English.  
XX The sequence is that of the CryIF protein produced by Bacillus  
XX thuringiensis strains EG6845 and EG6346 obtd. from a maize grain  
XX dust sample. The CryIF protein is a toxin produced by the cryIF  
XX gene can be used in insecticide compns. to control lepidoptera.  
XX esp. Ostrinia nubilalis, Spodoptera exigua, and Plutella xylostella.  
XX See also AAR14857.

SQ Sequence 1174 AA;  
Query Match 100.0%; Score 6244; DB 12; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIONQCVNCLNNEVEILNEERSTGRPLDLSLSTRLLSEFFVGVGVAFLFD 60  
Db 1 MENNIONQCVNCLNNEVEILNEERSTGRPLDLSLSTRLLSEFFVGVGVAFLFD 60

QY 61 LINGFITPSDWSLFLILQIQEIQRIETERNPAITTLRGLADSYEIIYIEALREWEANPN 120  
DB 61 LINGFITPSDWSLFLILQIQEIQRIETERNPAITTLRGLADSYEIIYIEALREWEANPN 120  
QY 121 NAQLREDVIRANTDDALITAINNFTLSFEIPILSVVQAAHLHLSLLRDVAFSGQGW 180  
DB 121 NAQLREDVIRANTDDALITAINNFTLSFEIPILSVVQAAHLHLSLLRDVAFSGQGW 180  
QY 181 GDIATVNNHYNRLNLHRYTKHCLDITYNOGLENURGTNTROWARFNQFRDLTLTVLD 240  
DB 181 GDIATVNNHYNRLNLHRYTKHCLDITYNOGLENURGTNTROWARFNQFRDLTLTVLD 240  
QY 241 IVALFPNDVRYPIQTSOLTRIEIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300  
DB 241 IVALFPNDVRYPIQTSOLTRIEIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300  
QY 301 NSLFTVTAETVRSQTVMGHLSVSRNAGNINFPSPVSGVFNPGGAIWIADDEPRFVRLS 360  
DB 301 NSLFTVTAETVRSQTVMGHLSVSRNAGNINFPSPVSGVFNPGGAIWIADDEPRFVRLS 360  
QY 361 DPVFRGGFGNHYVLGLRGVAFQQTGTHRTFRNSGTHIDSLEIPPODNSGAPWNDYS 420  
DB 361 DPVFRGGFGNHYVLGLRGVAFQQTGTHRTFRNSGTHIDSLEIPPODNSGAPWNDYS 420  
QY 421 HVLNHTVFEVRWCEISGDSWRAPMSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480  
DB 421 HVLNHTVFEVRWCEISGDSWRAPMSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480  
QY 481 VVRGPGFTGDIILRRYSGGFFAYTIWINGQLPQRYRARIYASTNNLIYVTVAGERIF 540  
DB 481 VVRGPGFTGDIILRRYSGGFFAYTIWINGQLPQRYRARIYASTNNLIYVTVAGERIF 540  
QY 541 AGQFNKMTDMDGLTQFSYSYATINFTAFPMSSQSFYVADTFSSGNEVYIDRPELIV 600  
DB 541 AGQFNKMTDMDGLTQFSYSYATINFTAFPMSSQSFYVADTFSSGNEVYIDRPELIV 600  
QY 601 TATFEAYDLERAQKAVNALFTSINGIKTDVTDVHIDOVSNLVDCLSDFCLEKREL 660  
DB 601 TATFEAYDLERAQKAVNALFTSINGIKTDVTDVHIDOVSNLVDCLSDFCLEKREL 660  
QY 661 SEVKHAKRLSDERNLQDPNFGINRLDGRWGSGTDTIQRGDDVFKENYVTLPGTFD 720  
DB 661 SEVKHAKRLSDERNLQDPNFGINRLDGRWGSGTDTIQRGDDVFKENYVTLPGTFD 720  
QY 721 EGYPTLYQXIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLWPLS 780  
DB 721 EGYPTLYQXIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLWPLS 780  
QY 781 VQSPIRKCGEPNRCAPHLNPNLDCSRRGCKCAHSHHFLDIDVGTDLNEDLDVWV 840  
DB 781 VQSPIRKCGEPNRCAPHLNPNLDCSRRGCKCAHSHHFLDIDVGTDLNEDLDVWV 840  
QY 841 IFKIKTODGHARLGNLEFLEEKPLVGEALARVARAEKWRDKREKLELENTIYVKEAKES 900  
DB 841 IFKIKTODGHARLGNLEFLEEKPLVGEALARVARAEKWRDKREKLELENTIYVKEAKES 900  
QY 901 VDALFVNSQVQDQADTNIAHIAAOKRVHRIREAVLPESLVPGVNVDIFELKGRIFT 960  
DB 901 VDALFVNSQVQDQADTNIAHIAAOKRVHRIREAVLPESLVPGVNVDIFELKGRIFT 960  
QY 961 AFFLYDARNVYKNGDFNGLSCWNKGVHVDVEQNNHRSVLVVPENAEVSQEVRYCPCR 1020  
DB 961 AFFLYDARNVYKNGDFNGLSCWNKGVHVDVEQNNHRSVLVVPENAEVSQEVRYCPCR 1020  
QY 1021 GYLRLVTAKEYGEGCVTTHEIENNTDELKFSNCVEEYYPNTVTCNDYTANQOEYGG 1080  
DB 1021 GYLRLVTAKEYGEGCVTTHEIENNTDELKFSNCVEEYYPNTVTCNDYTANQOEYGG 1080  
QY 1081 AYTSRNGYDETYGNSSVFADYASVTEKSYTDGRDNPCESNRGYGDYTPLPAGYVTK 1140  
DB 1081 AYTSRNGYDETYGNSSVFADYASVTEKSYTDGRDNPCESNRGYGDYTPLPAGYVTK 1140  
QY 1141 ELEYFPETDKVWIEIGETGTFIVDSVELLMEE 1174

DB 1141 ELEYFPETDKVWIEIGETGTFIVDSVELLMEE 1174  
RESULT 3  
RAR39754  
ID AAR39754 standard; Protein: 1174 AA.  
XX AAR39754;  
XX 28-JAN-1994 (first entry)  
XX Delta endotoxin.  
XX Endotoxin; Bacillus; lice; insecticide; sheep.  
XX Bacillus thuringiensis PS81I (Clone 81IA).  
XX WO9314641-A.  
XX 05-AUG-1993.  
XX 31-DEC-1992; 92WO-US11337.  
XX 29-JAN-1992; 92US-0828788.  
XX (MYCO ) MYCOGEN CORP.  
XX Hickle LA, Payne J;  
XX WPI; 1993-258266/32.  
XX N-PSDB; AAQ47291.  
XX Controlling biting lice on sheep - comprises administering  
XX Bacillus thuringiensis toxins to host  
XX Disclosure; Page 43-46; 64pp; English.  
XX Many strains of Bacillus thuringiensis (B.t) produce insecticidal  
XX delta endotoxins. A number of these endotoxins have been found to  
XX be toxic to Damlinia ovis, the biting louse of sheep. The B.T.  
XX isolates which produce these toxins can be grown and the delta  
XX endotoxin which is produced can be recovered by standard procedures.  
XX The genes encoding these endotoxins can also be transferred to a  
XX suitable host via a recombinant vector and the resulting  
XX transformants used in methods to control lice.  
SQ Sequence 1174 AA;  
Query Match 100.0%; Score 6244; DB 14: Length 1174;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MENNTQNCVPCVNCNNPEVELNEERSTGRPLDLSLTRLFLLSPVPGVAGFLFD 60  
DB 1 MENNTQNCVPCVNCNNPEVELNEERSTGRPLDLSLTRLFLLSPVPGVAGFLFD 60  
QY 61 LINGFITPSDWSLFLILQIQEIQRIETERNPAITTLRGLADSYEIIYIEALREWEANPN 120  
DB 61 LINGFITPSDWSLFLILQIQEIQRIETERNPAITTLRGLADSYEIIYIEALREWEANPN 120  
QY 121 NAQLREDVIRANTDDALITAINNFTLSFEIPILSVVQAAHLHLSLLRDVAFSGQGW 180  
DB 121 NAQLREDVIRANTDDALITAINNFTLSFEIPILSVVQAAHLHLSLLRDVAFSGQGW 180  
QY 181 GDIATVNNHYNRLNLHRYTKHCLDITYNOGLENURGTNTROWARFNQFRDLTLTVLD 240  
DB 181 GDIATVNNHYNRLNLHRYTKHCLDITYNOGLENURGTNTROWARFNQFRDLTLTVLD 240  
QY 241 IVALFPNDVRYPIQTSOLTRIEIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300  
DB 241 IVALFPNDVRYPIQTSOLTRIEIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300

301 NSLFVTAETVRSQTVWGCHLVSSRNATAGNRINPESYGVNPGGAIWIADEDPPEFYRTLS 360  
 301 NSLFVTAETVRSQTVWGCHLVSSRNATAGNRINPESYGVNPGGAIWIADEDPPEFYRTLS 360  
 361 DPVFRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPPDNSGAPWNDYS 420  
 361 DPVFRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPPDNSGAPWNDYS 420  
 421 HVLNHTVFRWPGEISGDSWRAPMSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480  
 421 HVLNHTVFRWPGEISGDSWRAPMSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480  
 481 VVRGPGFTGDIILRRSTSGGPFATIVNINGQLPQRYARIRYASTNLRIVYTVAGERIF 540  
 481 VVRGPGFTGDIILRRSTSGGPFATIVNINGQLPQRYARIRYASTNLRIVYTVAGERIF 540  
 541 AGQFNKTMGTGDLTQSFYSATINTAFTPPMSQSSTFGADTFSSGNEVYIDRFELIPV 600  
 541 AGQFNKTMGTGDLTQSFYSATINTAFTPPMSQSSTFGADTFSSGNEVYIDRFELIPV 600  
 601 TATFEAYDLERAQAVNALFTSINOIGIKTDVTDYHIDOVSNLVDCLSDFECLDEKREL 660  
 601 TATFEAYDLERAQAVNALFTSINOIGIKTDVTDYHIDOVSNLVDCLSDFECLDEKREL 660  
 661 SEKVHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVTLPGCTD 720  
 661 SEKVHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVTLPGCTD 720  
 721 ECVPTLYQKIDBSKLPKPYTRYOLRGYIEDSQBLEYLIRYNAKHETVNVGLTGSWLPLS 780  
 721 ECVPTLYQKIDBSKLPKPYTRYOLRGYIEDSQBLEYLIRYNAKHETVNVGLTGSWLPLS 780  
 781 VOSPIRKCEPNRCAPHELNWPDLCSDRGKCAHSHHFDIDVCGTDLNEDLDVWV 840  
 781 VOSPIRKCEPNRCAPHELNWPDLCSDRGKCAHSHHFDIDVCGTDLNEDLDVWV 840  
 841 IFKIKTDQGHARLGNLEFLEKPLVGEALARYKRAEKKWRDKREKLELETINIVYKEAKES 900  
 841 IFKIKTDQGHARLGNLEFLEKPLVGEALARYKRAEKKWRDKREKLELETINIVYKEAKES 900  
 901 VDALFVNSQYDQADNTAMIAHAKRVHRIEAYLPVLPVGVNVDIFEELKGRIFT 960  
 901 VDALFVNSQYDQADNTAMIAHAKRVHRIEAYLPVLPVGVNVDIFEELKGRIFT 960  
 961 APFLYDARNVINGDFNGLSCWNVKGVHDVEQNNHRSVLVVPWEAEVQSQRVCPGR 1020  
 961 APFLYDARNVINGDFNGLSCWNVKGVHDVEQNNHRSVLVVPWEAEVQSQRVCPGR 1020  
 1021 GYLIRVTAYKEGEGECVTIHEIENNTDELKFSNCVEEVEEYVNTVTCNDYTANQEYGG 1080  
 1021 GYLIRVTAYKEGEGECVTIHEIENNTDELKFSNCVEEVEEYVNTVTCNDYTANQEYGG 1080  
 1081 AYTSNRNGYDETYGNSNPADYASYEBSKYTDGRDRNPNCSNRGYGDTPLPAGYVTK 1140  
 1081 AYTSNRNGYDETYGNSNPADYASYEBSKYTDGRDRNPNCSNRGYGDTPLPAGYVTK 1140  
 1141 ELEYPPETDKVWEIGETEGTFTVDSVEILLMEE 1174  
 1141 ELEYPPETDKVWEIGETEGTFTVDSVEILLMEE 1174

RESULT 4  
 AA76708  
 ID AA76708 standard; Protein; 1174 AA.  
 AC AA76708;  
 XX  
 XX  
 XX 13-JAN-1999 (first entry)  
 DE Plasmid pMYC2243 Bt endotoxin protein fragment.  
 XX Bt toxin; lepidoptera; pest; cryIF; chimeric; core toxin; cryIA(c);  
 KW synergism; plant; primer; endotoxin.

XX Synthetic.  
 OS US5827514-A.  
 PN 27-OCT-1998.  
 XX 08-FEB-1996; 96US-0598305.  
 XX 06-DEC-1994; 94US-0349867.  
 PR 08-FEB-1996; 96US-0598305.  
 XX (MYCO ) MYCOGEN CORP.  
 PA Bradfisch GA, Schwab GE, Thompson M;  
 PI WPI; 1998-593944/50.  
 XX DR N-PSDB; AAV62081.  
 XX PT Composition for biological control of lepidopteran pests -  
 PT comprising cells expressing two chimeric Bacillus thuringiensis  
 PT crystal proteins  
 XX Example 5; Column 57-64; 75pp; English.  
 PS This sequence represents a Bt endotoxin which is used in a method for  
 CC controlling lepidopteran pests. The method involves the use of cells  
 CC that express the Bacillus thuringiensis delta-endotoxin cryIF chimeric  
 CC core toxin-containing protein and CryIA(c) chimeric core toxin-containing  
 CC protein in a combination that have synergistically enhanced activity,  
 CC against e.g. corn earworm (Heliothis zea).  
 XX Sequence 1174 AA;  
 SQ Query Match 100.0%; Score 6244; DB 19; Length 1174;  
 Best Local Similarity 100.0%; Pred No. 0;  
 Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIOQCVPVNCNNPEVEILNEERSTGRPLDLSLSLTRELLSEFVPGVGVAFGLFD 60  
 DB 1 MENNIOQCVPVNCNNPEVEILNEERSTGRPLDLSLSLTRELLSEFVPGVGVAFGLFD 60  
 QY 61 LWGFTTPSDWSLFLQIEQLTEORITLERNRAITTLRGLADSYEIIYEALEWEANPN 120  
 DB 61 LWGFTTPSDWSLFLQIEQLTEORITLERNRAITTLRGLADSYEIIYEALEWEANPN 120  
 QY 121 NQALREDVIRFANTDDALITAINNFTLTSFEIPLSVVQAAHLHLSLLRDAVSFGQW 180  
 DB 121 NQALREDVIRFANTDDALITAINNFTLTSFEIPLSVVQAAHLHLSLLRDAVSFGQW 180  
 QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLNLRGTNRQWARFNQFRDLTLTVLD 240  
 DB 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLNLRGTNRQWARFNQFRDLTLTVLD 240  
 QY 241 IVALPNYDVRYPYQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVAPPHLMDPM 300  
 DB 241 IVALPNYDVRYPYQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVAPPHLMDPM 300  
 QY 301 NSLFTVTAETVRSQTVWGCHLVSSRNATAGNRINPESYGVNPGGAIWIADEDPPEFYRTLS 360  
 DB 301 NSLFTVTAETVRSQTVWGCHLVSSRNATAGNRINPESYGVNPGGAIWIADEDPPEFYRTLS 360  
 QY 361 DPVFRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPPDNSGAPWNDYS 420  
 DB 361 DPVFRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPPDNSGAPWNDYS 420  
 QY 421 HVLNHTVFRWPGEISGDSWRAPMSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480  
 DB 421 HVLNHTVFRWPGEISGDSWRAPMSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480  
 QY 481 VVRGPGFTGDIILRRSTSGGPFATIVNINGQLPQRYARIRYASTNLRIVYTVAGERIF 540  
 DB 481 VVRGPGFTGDIILRRSTSGGPFATIVNINGQLPQRYARIRYASTNLRIVYTVAGERIF 540

QY 541 AGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSFYAGDFFSSGNEVYIDRFELIPV 600  
 DB 541 AGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSFYAGDFFSSGNEVYIDRFELIPV 600  
 QY 601 TATFEAYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVCLSDFECLDEKREL 660  
 DB 601 TATFEAYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVCLSDFECLDEKREL 660  
 QY 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGRGSTDITQRGDDVFKENYVTLGTFD 720  
 DB 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGRGSTDITQRGDDVFKENYVTLGTFD 720  
 QY 721 EGYPTLYQKIDESKLPKPYTRQVLCGYIEDSQDLEIYLIRYNAKHETVNVLTGSLWPLS 780  
 DB 721 EGYPTLYQKIDESKLPKPYTRQVLCGYIEDSQDLEIYLIRYNAKHETVNVLTGSLWPLS 780  
 QY 781 VQSPIKCGEPNRCAPHELEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
 DB 781 VQSPIKCGEPNRCAPHELEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
 QY 841 IPKIKTODGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKEAKES 900  
 DB 841 IPKIKTODGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKEAKES 900  
 QY 901 VDALFYNSOYDQLOADNTIAMIHAADKRVHRIREAYLPVPGVNVDFEELKGRIFT 960  
 DB 901 VDALFYNSOYDQLOADNTIAMIHAADKRVHRIREAYLPVPGVNVDFEELKGRIFT 960  
 QY 961 AFPLYDARNVKNKDNFNGNLSQWNVKGVHDVBEQNNHRSVLYVPEWEAEVQEVRYCPGR 1020  
 DB 961 AFPLYDARNVKNKDNFNGNLSQWNVKGVHDVBEQNNHRSVLYVPEWEAEVQEVRYCPGR 1020  
 QY 1021 GYLRYTAYKEGEGCVTHIENNTDELKFSNCVEEYYPNTVTCNDYTANQOEYGG 1080  
 DB 1021 GYLRYTAYKEGEGCVTHIENNTDELKFSNCVEEYYPNTVTCNDYTANQOEYGG 1080  
 QY 1081 AYTSRNRGYDEYVGSNSPADYASVYEKSYTDGRRDNPCESNRGYGDYTPLPAGYVTK 1140  
 DB 1081 AYTSRNRGYDEYVGSNSPADYASVYEKSYTDGRRDNPCESNRGYGDYTPLPAGYVTK 1140  
 QY 1141 ELEYFPETDKVMEIGETGTFTVDSVELLMEE 1174  
 DB 1141 ELEYFPETDKVMEIGETGTFTVDSVELLMEE 1174

## RESULT 5

AAW76712

ID AAW76712 standard; Protein; 1174 AA.

XX AC AAW76712;

XX AC AAW76712;

XX DT 13-JAN-1999 (first entry)

XX DE B. thuringiensis cryIF/cryIA(b) endotoxin protein.

XX KW Bt toxin; lepidoptera; pest; cryIF; chimeric; core toxin; cryIA(c);

XX KW synergism; plant; primer; endotoxin.

XX OS Bacillus thuringiensis.

XX XX US5827514-A.

XX XX 27-OCT-1998.

XX XX 08-FEB-1996; 96US-0598305.

XX XX 06-DEC-1994; 94US-0349867.

XX XX 08-FEB-1996; 96US-0598305.

XX XX (MYCO ) MYCOGEN CORP.

XX XX Bradfisch GA, Schwab GE, Thompson M;

PI

XX WPI; 1998-593944/50.

XX Composition for biological control of lepidopteran pests -  
 PT comprising cells expressing two chimeric Bacillus thuringiensis  
 PT crystal proteins

XX PS Disclosure; Column 81-88; 75pp; English.

XX CC This sequence represents a Bt endotoxin which is used in a method for  
 CC controlling lepidopteran pests. The method involves the use of cells  
 CC that express the Bacillus thuringiensis delta-endotoxin cryIF chimeric  
 CC core toxin-containing protein and CryIA(c) chimeric core toxin-containing  
 CC protein in a combination that have synergistically enhanced activity,  
 CC against e.g. corn earworm (Heliothis zea).

XX SQ Sequence 1174 AA;

Query Match 100.0%; Score 6244; DB 19; Length 1174;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIQNCQVPYNCLNNEVEILNEERSTGRPLDLSLTRELLSEFVGVGVAFLFD 60

DB 1 MENNIQNCQVPYNCLNNEVEILNEERSTGRPLDLSLTRELLSEFVGVGVAFLFD 60

QY 61 LIWGFITPDSWSLFIQIEQLIEQRIETLERNRAITTLRGLADSYEIIYI EALREWEANPN 120

DB 61 LIWGFITPDSWSLFIQIEQLIEQRIETLERNRAITTLRGLADSYEIIYI EALREWEANPN 120

QY 121 NAQLRDVRIRFANTDDALITAINNFTLSFEIPLSVYVQAAANLHLSLLRDVSVGQGW 180

DB 121 NAQLRDVRIRFANTDDALITAINNFTLSFEIPLSVYVQAAANLHLSLLRDVSVGQGW 180

QY 181 GLDIATVNNHNYRLNLHRYTKHCLDTYNOGLENRGTNTROWARFNQFRDLTLTVLD 240

DB 181 GLDIATVNNHNYRLNLHRYTKHCLDTYNOGLENRGTNTROWARFNQFRDLTLTVLD 240

QY 241 IVAFPNYDVRTYPIOTSSQLTREIYTSVIEDSPYSANIPNGFNRAEFGVRPHLMDFM 300

DB 241 IVAFPNYDVRTYPIOTSSQLTREIYTSVIEDSPYSANIPNGFNRAEFGVRPHLMDFM 300

QY 301 NSLFTVAETVRSQTVMGHLYSSRNAGNINFPSPGVFNPGGAIWLADEDPPTFTLS 360

DB 301 NSLFTVAETVRSQTVMGHLYSSRNAGNINFPSPGVFNPGGAIWLADEDPPTFTLS 360

QY 361 DPVVRGGFGNPHYVLGLGVAFQQTGTNHTFRNSGTIDSLDEIPPDQNSGAPNDYS 420

DB 361 DPVVRGGFGNPHYVLGLGVAFQQTGTNHTFRNSGTIDSLDEIPPDQNSGAPNDYS 420

QY 421 HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480

DB 421 HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480

QY 481 VVRGPGTGGDILRRITSGGPFAYTIIVNINGQLPQRYRARIYASTTNRLIYVTVAGERIF 540

DB 481 VVRGPGTGGDILRRITSGGPFAYTIIVNINGQLPQRYRARIYASTTNRLIYVTVAGERIF 540

QY 541 AGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSFYAGDFFSSGNEVYIDRFELIPV 600

DB 541 AGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSFYAGDFFSSGNEVYIDRFELIPV 600

QY 601 TATFEAYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVCLSDFECLDEKREL 660

DB 601 TATFEAYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVCLSDFECLDEKREL 660

QY 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGRGSTDITQRGDDVFKENYVTLGTFD 720

DB 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGRGSTDITQRGDDVFKENYVTLGTFD 720

QY 721 EGYPTLYQKIDESKLPKPYTRQVLCGYIEDSQDLEIYLIRYNAKHETVNVLTGSLWPLS 780

DB 721 EGYPTLYQKIDESKLPKPYTRQVLCGYIEDSQDLEIYLIRYNAKHETVNVLTGSLWPLS 780

781 VQSPIKCGEPCNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVGCTDLNEDLDVWV 840  
 781 VQSPIKCGEPCNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVGCTDLNEDLDVWV 840  
 841 IFKIKTQGHARLGNLEFLEKPLVGEALARKVRAEKWKRDREKLELETNIVYKEAKES 900  
 841 IFKIKTQGHARLGNLEFLEKPLVGEALARKVRAEKWKRDREKLELETNIVYKEAKES 900  
 901 VDLEFVNSQYDQLOADTNIAHAAKRVHRIREAYLPFLSVIPGVNVDIPEELKGRIFT 960  
 901 VDLEFVNSQYDQLOADTNIAHAAKRVHRIREAYLPFLSVIPGVNVDIPEELKGRIFT 960  
 961 AFFLYDARNVTKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWEAEVSOEVRVCPGR 1020  
 961 AFFLYDARNVTKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWEAEVSOEVRVCPGR 1020  
 1021 GYLKRVATYKEGYGEGCVTIHEIENNTDELKFSNCVEVEVPNTVTCNDYTANOEEYGG 1080  
 1021 GYLKRVATYKEGYGEGCVTIHEIENNTDELKFSNCVEVEVPNTVTCNDYTANOEEYGG 1080  
 1081 AYTSNRGYDETYGNSVVPADYASVBEKSYTDGRRDNPCESTRGSGYDYPPLPAGYVTK 1140  
 1081 AYTSNRGYDETYGNSVVPADYASVBEKSYTDGRRDNPCESTRGSGYDYPPLPAGYVTK 1140  
 1141 ELEYFPETDKWIETEGEGTFIVDSVELLME 1174  
 1141 ELEYFPETDKWIETEGEGTFIVDSVELLME 1174

RESULT 6  
 AAY16792  
 ID AAY16792 standard; Protein; 1174 AA.  
 AC AAY16792;  
 DT 27-JUL-1999 (first entry)  
 DE Wild-type B.t cryIF toxin 81IA.  
 KW Plant-optimised gene; pesticidal toxin; CryIF; CryIaC; CryIc; 158C2c;  
 KW 31Gla; CryIaB protoxin; insect control; chimeric.  
 OS Bacillus thuringiensis.  
 PN WO92454581-A2.  
 PD 20-MAY-1999.  
 XX 04-NOV-1998; 98WO-US23457.  
 XX 23-OCT-1998; 98US-0178252.  
 PR 12-NOV-1997; 97US-0065215.  
 PR 02-MAR-1998; 98US-0076445.  
 XX (MYCO ) MYCOGEN CORP.  
 XX Cardineau GA, Narva KE, Stelman SJ;  
 DR WPI: 1999-327409/27.  
 DR N-PSDB; AAX60606.  
 XX Nucleic acids encoding pesticidal proteins, optimized for plant  
 PT expression  
 PT Disclosure; Page 30-34; 67pp; English.  
 PS The invention relates to nucleic acid sequences, optimised for  
 CC expression in plants, that encode: (i) one of the pesticidal toxins  
 CC CryIF, CryIaC, CryIc, 158C2c or 31Gla, or (ii) a portion of the CryIaB  
 CC protoxin. The pesticidal toxins (AAY16790, AAY16792-V16798) are used for  
 CC pest, especially insect control, particularly on plants. The nucleic acid  
 CC sequences are used to produce (truncated or chimeric) toxins, and related

CC fusion genes or proteins, particularly they are used to generate  
 CC transgenic plants that show increased resistance to pests. Compared with  
 CC wild-type Bacillus thuringiensis sequences, the optimised sequences are  
 CC better suited to expression in plants. The present sequence represents  
 CC the amino acid sequence for a wild-type, full-length B.t toxin designated  
 CC 81IA.  
 XX  
 SQ Sequence 1174 AA;  
 Query Match 100.0%; Score 6244; DB 20; Length 1174;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIOQCVPYCNLANPEVEILNEERSTGRPLDLSLTRELLSEFVPGVGVAFLDF 60  
 DB 1 MENNIOQCVPYCNLANPEVEILNEERSTGRPLDLSLTRELLSEFVPGVGVAFLDF 60  
 QY 61 LIWGFITPDSWLSFLIOIEQLIEQRIETLERNAITTLRLGLADSYEIIYIETALREWEANPN 120  
 DB 61 LIWGFITPDSWLSFLIOIEQLIEQRIETLERNAITTLRLGLADSYEIIYIETALREWEANPN 120  
 QY 121 NAOLREDVRIRFANTDDALITAINNFTLSFEIPLSVVQAANHLSLRLDAVSFGQGW 180  
 DB 121 NAOLREDVRIRFANTDDALITAINNFTLSFEIPLSVVQAANHLSLRLDAVSFGQGW 180  
 QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLGTNTQWARFNQFRDLTLTYLD 240  
 DB 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLGTNTQWARFNQFRDLTLTYLD 240  
 QY 241 IVALFPNDYVRTYPIQTSQLTREIYTSVIEDSPYSANIPNGFNRAEFGVPPHLMDFM 300  
 DB 241 IVALFPNDYVRTYPIQTSQLTREIYTSVIEDSPYSANIPNGFNRAEFGVPPHLMDFM 300  
 QY 301 NSLFVTAETVRSQTVWGGHLVSSRNTAGNRINPPSYCVENPGCAIWAIEDDPPFYRTLS 360  
 DB 301 NSLFVTAETVRSQTVWGGHLVSSRNTAGNRINPPSYCVENPGCAIWAIEDDPPFYRTLS 360  
 QY 361 DPVFRGGFGNPHYVLGLRGVAFQQTGNHTRFRNSGTIDSLDEIPPODSCAPNDYS 420  
 DB 361 DPVFRGGFGNPHYVLGLRGVAFQQTGNHTRFRNSGTIDSLDEIPPODSCAPNDYS 420  
 QY 421 HVLNHTVFRWPGGEISGDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLOSQT 480  
 DB 421 HVLNHTVFRWPGGEISGDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLOSQT 480  
 QY 481 VVRGPGFTGDIILRRTSGGPFAYTIYVINGQLPQRYRARIYASTNLRIVTVAGERIF 540  
 DB 481 VVRGPGFTGDIILRRTSGGPFAYTIYVINGQLPQRYRARIYASTNLRIVTVAGERIF 540  
 QY 541 AGOFNKTMDTGDPLTFQSFYSATINTAFTFPMSSQSFYTGADTFSSGNEVYIDREFELPV 600  
 DB 541 AGOFNKTMDTGDPLTFQSFYSATINTAFTFPMSSQSFYTGADTFSSGNEVYIDREFELPV 600  
 QY 601 TATFEAYDLEAQAQKAVNALFTSINGIKTQDVTYHIDQVSNLVDCLDEKREL 660  
 DB 601 TATFEAYDLEAQAQKAVNALFTSINGIKTQDVTYHIDQVSNLVDCLDEKREL 660  
 QY 661 SEVKHAKRLSDERNLLQDPNFKNGINRQLDRGWRGSTDITIQGDDVYFKNVTLPFGTFD 720  
 DB 661 SEVKHAKRLSDERNLLQDPNFKNGINRQLDRGWRGSTDITIQGDDVYFKNVTLPFGTFD 720  
 QY 721 ECTPTLYQKIDESKLPYTRYOLRGYIEDSQDLEYLYLRYNAKHETVNLVLTGSLWPLS 780  
 DB 721 ECTPTLYQKIDESKLPYTRYOLRGYIEDSQDLEYLYLRYNAKHETVNLVLTGSLWPLS 780  
 QY 781 VQSPIKCGEPCNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVGCTDLNEDLDVWV 840  
 DB 781 VQSPIKCGEPCNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVGCTDLNEDLDVWV 840  
 QY 841 IFKIKTQGHARLGNLEFLEKPLVGEALARKVRAEKWKRDREKLELETNIVYKEAKES 900  
 DB 841 IFKIKTQGHARLGNLEFLEKPLVGEALARKVRAEKWKRDREKLELETNIVYKEAKES 900

QY 901 VDALFVNSQVDQLQADNTNIAHAAKRVHRIRIRAYLPESLVIPGVNVDIFEEELKGRIFT 960  
 Db 901 VDALFVNSQVDQLQADNTNIAHAAKRVHRIRIRAYLPESLVIPGVNVDIFEEELKGRIFT 960  
 QY 961 AFPLYDARNVKNGDFNGLSCNWNVGHVDVEQNNHRSVLVVPWEAEVQSVRVCPCR 1020  
 Db 961 AFPLYDARNVKNGDFNGLSCNWNVGHVDVEQNNHRSVLVVPWEAEVQSVRVCPCR 1020  
 QY 1021 GYLIRVTAYKEGEGCVTHIETENTDELKFSNCVEEVEYPNNTVTCNDYTANQBEYGG 1080  
 Db 1021 GYLIRVTAYKEGEGCVTHIETENTDELKFSNCVEEVEYPNNTVTCNDYTANQBEYGG 1080  
 QY 1081 AYTSNRGDEYTGSSNVPADYASVEEKSYPDGRDNPCESNRGYGDYTPLPAGVYTK 1140  
 Db 1081 AYTSNRGDEYTGSSNVPADYASVEEKSYPDGRDNPCESNRGYGDYTPLPAGVYTK 1140  
 QY 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1174  
 Db 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1174

RESULT 7  
 AAU00533  
 ID AAU00533 standard; Protein; 1174 AA.  
 XX AAU00533;  
 AC  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE B. thuringiensis toxin 8IIA (CryIa).  
 XX  
 KW Toxin 8IIA; cryIa; cutworm; pesticide; corn; soybean; canola; cotton;  
 KW Agrotis ipsilon; Agrotis malefida; Porasogrotis gypaetiana; sunflower;  
 KW Xylomyges curialis; Tribe Agrotini; Feltia jaculifera; Euxoa sp.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO200113731-A1.  
 XX  
 PD 01-MAR-2001.  
 XX  
 PF 23-AUG-2000; 2000WO-US23156.  
 XX  
 PR 23-AUG-1999; 99US-0150319.  
 XX  
 PA (MYCO ) MYCOGEN CORP.  
 XX  
 PI Stockhoff BA, Conlan C;  
 XX  
 DR WPI; 2001-211270/21.  
 XX  
 PT Controlling cutworm pests especially black cutworm comprises contacting  
 PT the pest with crystal protein CryIa toxin -  
 XX  
 PS Example 5; Page 44-48; 52pp; English.  
 XX  
 CC The sequence represents the wild-type, full length Bacillus thuringiensis  
 CC toxin 8IIA (CryIa). Full-length, truncated and chimeric CryIa genes and  
 CC proteins can be used for controlling cutworm pests, by contacting the  
 CC pest with a Bacillus thuringiensis toxin comprising a pesticidal portion  
 CC of a CryIa toxin. These genes and proteins are useful for controlling  
 CC cutworm pests such as Agrotis ipsilon, Agrotis malefida, Porasogrotis  
 CC gypaetiana, Xylomyges curialis, members of the Tribe Agrotini, Feltia  
 CC jaculifera, Euxoa messoria, Euxoa scandens, Euxoa auxaliaris, Euxoa  
 CC tersata, Euxoa tessellata, Euxoa ochragaster and Peridroma saucia in  
 CC plants such as corn, sunflower, soybean, canola and cotton. The plants  
 CC are transformed with a polynucleotide encoding a Cry I protein such that  
 CC the transformed plant cells express pesticidal proteins in tissues  
 CC consumed by the target pests.  
 XX  
 SQ Sequence 1174 AA;

Query Match 100.0%; Score 6244; DB 22; Length 1174;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIQOCVPYCNLANPEVEILNEERSTGRPLDLSLTRELLSEFVPGVAFGLFD 60  
 Db 1 MENNIQOCVPYCNLANPEVEILNEERSTGRPLDLSLTRELLSEFVPGVAFGLFD 60  
 QY 61 LINGFTIPSDWSLFLQIEQLIQRITETLRNRAITTLRGLADSYEYIIEALREWEANPN 120  
 Db 61 LINGFTIPSDWSLFLQIEQLIQRITETLRNRAITTLRGLADSYEYIIEALREWEANPN 120  
 QY 121 NAQLREDVRIRFANTDDALITANNFTLTSEFPLISVYVQAAHLHLRLDVAVSFGQW 180  
 Db 121 NAQLREDVRIRFANTDDALITANNFTLTSEFPLISVYVQAAHLHLRLDVAVSFGQW 180  
 QY 181 GLDIATVNNHYNLNLHRYTKHCLDYNQGLENLRGNTROWARNQFRDLTLVLD 240  
 Db 181 GLDIATVNNHYNLNLHRYTKHCLDYNQGLENLRGNTROWARNQFRDLTLVLD 240  
 QY 241 IVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGENRAEFGVRPPLMDEM 300  
 Db 241 IVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGENRAEFGVRPPLMDEM 300  
 QY 301 NSLFVTAETVRSQTVWGGHLVSSRNAGNINFPSPGVNPGGAIWIADEDPFFYRTLS 360  
 Db 301 NSLFVTAETVRSQTVWGGHLVSSRNAGNINFPSPGVNPGGAIWIADEDPFFYRTLS 360  
 QY 361 DPVFRGGFNGPHYVLGLRGVAFQGTGNHTRTFRNSGTTDSLDEIPPODSNAGPNNDYS 420  
 Db 361 DPVFRGGFNGPHYVLGLRGVAFQGTGNHTRTFRNSGTTDSLDEIPPODSNAGPNNDYS 420  
 QY 421 HVLNHYTFVWPGEISGSDSWRAPMSWTHRSATPTNIDPERITQIPLVKAHTLQSGTT 480  
 Db 421 HVLNHYTFVWPGEISGSDSWRAPMSWTHRSATPTNIDPERITQIPLVKAHTLQSGTT 480  
 QY 481 VVRGPFTGGDILRRTSGGPFATYIVNINQOLPORRARIYASTNLRIYTVVAGERIF 540  
 Db 481 VVRGPFTGGDILRRTSGGPFATYIVNINQOLPORRARIYASTNLRIYTVVAGERIF 540  
 QY 541 AGQFNKTMGTDPPLTFQSPSYATINTAFTPPMSQSSFTVGADTFSSGNEYIYIDREFELIPV 600  
 Db 541 AGQFNKTMGTDPPLTFQSPSYATINTAFTPPMSQSSFTVGADTFSSGNEYIYIDREFELIPV 600  
 QY 601 TATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDHIDQVSNLVCLSDPECLDEKREL 660  
 Db 601 TATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDHIDQVSNLVCLSDPECLDEKREL 660  
 QY 661 SEKVHAKRLSDERNLLQDPNFKGINRQDLDRGWSGTDITIQRGDDVFKENYVTLPGTFD 720  
 Db 661 SEKVHAKRLSDERNLLQDPNFKGINRQDLDRGWSGTDITIQRGDDVFKENYVTLPGTFD 720  
 QY 721 ECVPTLYOKIDSKLKPTRYQLRGYIEDSQDLEYTLIRYNAKHETVNVLTGCSLWPLS 780  
 Db 721 ECVPTLYOKIDSKLKPTRYQLRGYIEDSQDLEYTLIRYNAKHETVNVLTGCSLWPLS 780  
 QY 781 VQSPIKCEPNKCAPHLENNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840  
 Db 781 VQSPIKCEPNKCAPHLENNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840  
 QY 841 IPKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLELEFNIVYKAKES 900  
 Db 841 IPKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLELEFNIVYKAKES 900  
 QY 901 VDALFVNSQVDQLQADNTNIAHAAKRVHRIRIRAYLPESLVIPGVNVDIFEEELKGRIFT 960  
 Db 901 VDALFVNSQVDQLQADNTNIAHAAKRVHRIRIRAYLPESLVIPGVNVDIFEEELKGRIFT 960  
 QY 961 AFPLYDARNVKNGDFNGLSCNWNVGHVDVEQNNHRSVLVVPWEAEVQSVRVCPCR 1020  
 Db 961 AFPLYDARNVKNGDFNGLSCNWNVGHVDVEQNNHRSVLVVPWEAEVQSVRVCPCR 1020  
 QY 1021 GYLIRVTAYKEGEGCVTHIETENTDELKFSNCVEEVEYPNNTVTCNDYTANQBEYGG 1080

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|||||
Db 1021 GYILRVTAKEGCGGCTT|HEIENNTDELAFSNCVEEYVPNTVTCNDYTANQEEYGG 1080
|||||
QY 1081 AYTSNRGYDETYGNSVPADYASVYEKSYTDGRRDNPCESTRNGYCDYTPPLPAGYVTK 1140
|||||
Db 1081 AYTSNRGYDETYGNSVPADYASVYEKSYTDGRRDNPCESTRNGYCDYTPPLPAGYVTK 1140
|||||
QY 1141 ELEYFETDKVWIEIGETEGTFIVDSVLELLMEE 1174
|||||
Db 1141 ELEYFETDKVWIEIGETEGTFIVDSVLELLMEE 1174
|||||

RESULT 8
AAR84737
ID AAR84737 standard; Protein: 1184 AA.
AC AAR84737:
XX
XX
DT 26-JUN-1996 (first entry)
XX
DE Native cryIF toxin.
XX
KW CryIF toxin; delta endotoxin; crystal protein; chimeric toxin;
KW insecticide; pesticide; Pseudomonas fluorescens;
KW biological control agent; transgenic plant; insect resistance;
KW disease resistance; crop improvement; protein engineering.
XX
OS Bacillus thuringiensis.
XX
PN W09530753-A1.
XX
PD 16-NOV-1995.
XX
PF 05-MAY-1995; 95WO-US05431.
XX
PR 06-MAY-1994; 94US-0239476.
XX
PA (MYCO ) MYCOGEN CORP.
XX
PI Schwab GE, Thompson M;
XX
DR WPI; 1995-404120/51.
XX
XX
PT Nucleic acid encoding chimeric Bacillus thuringiensis
PT delta-endotoxin - providing increased expression in Pseudomonas,
PT esp. for control of lepidoptera pests.
XX
PS Disclosure; Page 61-65; 91pp; English.
XX
XX
CC The sequence represents the cryIF native toxin. The coding
CC sequences are engineered for construction of chimeric genes
CC encoding chimeric toxins, which are expressed in Pseudomonas
CC fluorescens better than native delta endotoxins. Host cells
CC expressing the chimeric gene and producing chimeric toxin may
CC be used in insecticide compositions. Where the host cells are
CC plant cells, the gene confers insect resistance to the
CC transformed plant.
XX
SQ Sequence 1184 AA;
Query Match 100.0%; Score 6244; DB 16; Length 1184;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIQCVPNCLNNPEVILNEERSTGRPLDLSLTRFLLSERFVPGVGFGLFD 60
|||||
Db 11 MENNIQCVPNCLNNPEVILNEERSTGRPLDLSLTRFLLSERFVPGVGFGLFD 70
|||||
QY 61 LINGFTIPSDWSLFLLOIQLEQRIETLERNRAITTLGLADSYEIEALREWEANPN 120
|||||
Db 71 LINGFTIPSDWSLFLLOIQLEQRIETLERNRAITTLGLADSYEIEALREWEANPN 130
|||||
QY 121 NAQLREDVRIRFANTDDALITAINNFTLTSFPEILLSVYVQAANLHLSLLRDVAFSGQGW 180
|||||

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|||||
Db 131 NAQLREDVRIRFANTDDALITAINNFTLTSFPEILLSVYVQAANLHLSLLRDVAFSGQGW 190
|||||
QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDYNQGLENLGTNTQWARFNQFREDLTLTVLD 240
|||||
Db 191 GLDIATVNNHYNRLINLIHRYTKHCLDYNQGLENLGTNTQWARFNQFREDLTLTVLD 250
|||||
QY 241 IVALFENYDVRYPYIQTSSQLTREIYTSVIEDSPYSANIPNGFNRAEFGVPPHLMDFM 300
|||||
Db 251 IVALFENYDVRYPYIQTSSQLTREIYTSVIEDSPYSANIPNGFNRAEFGVPPHLMDFM 310
|||||
QY 301 NSLFTVTAETVRVSTQVWGHLVSSRNTAGNINFPSPYGVFENPGCAIWIADDEDPFYRTLS 360
|||||
Db 311 NSLFTVTAETVRVSTQVWGHLVSSRNTAGNINFPSPYGVFENPGCAIWIADDEDPFYRTLS 370
|||||
QY 361 DPVVRGFGFNHYVLGRGVAFOQTGTHRTFRNSGTIDSLDEIPQDNGAPWNDYS 420
|||||
Db 371 DPVVRGFGFNHYVLGRGVAFOQTGTHRTFRNSGTIDSLDEIPQDNGAPWNDYS 430
|||||
QY 421 HVLNHYTEVRWPGEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480
|||||
Db 431 HVLNHYTEVRWPGEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 490
|||||
QY 481 VVRGPGTGGDILRRTSGGPFAYTIIVNINGQLPQRYRARIYASTNLRILYVTVAGERIF 540
|||||
Db 491 VVRGPGTGGDILRRTSGGPFAYTIIVNINGQLPQRYRARIYASTNLRILYVTVAGERIF 550
|||||
QY 541 AGOFNKMTDGTDLTFSFSYATINTAFTFPMSSQSFYTGADTFSSGNEVYIDRLELIPV 600
|||||
Db 551 AGOFNKMTDGTDLTFSFSYATINTAFTFPMSSQSFYTGADTFSSGNEVYIDRLELIPV 610
|||||
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDQVSNLVDCLSDEFCLDEKREL 660
|||||
Db 611 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDQVSNLVDCLSDEFCLDEKREL 670
|||||
QY 661 SEVKUAKRLSDERNLLQDPNFKGINRQDLDRGWSGTDITIQRGDDVFKENVTLPGETD 720
|||||
Db 671 SEVKUAKRLSDERNLLQDPNFKGINRQDLDRGWSGTDITIQRGDDVFKENVTLPGETD 730
|||||
QY 721 ECRYPTLYOKIDESKLPYTRYOLRGYIEDSODLEYILIRYNAKHETVNLVGTSLWPLS 780
|||||
Db 731 ECRYPTLYOKIDESKLPYTRYOLRGYIEDSODLEYILIRYNAKHETVNLVGTSLWPLS 790
|||||
QY 781 VQSPIRKCGEPNRCAPHLENNPDLDCSCRDEKCAHSHHFSLDIDVGCTDLNEDLDVWV 840
|||||
Db 791 VQSPIRKCGEPNRCAPHLENNPDLDCSCRDEKCAHSHHFSLDIDVGCTDLNEDLDVWV 850
|||||
QY 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKEKLELTNIVYKEAKES 900
|||||
Db 851 IFKIKTQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKEKLELTNIVYKEAKES 910
|||||
QY 901 VDALFVNSQYDQLQADTNIAIHAADKRVHRIREAYLPELSVIPGVNVDIFEELGRIFT 960
|||||
Db 911 VDALFVNSQYDQLQADTNIAIHAADKRVHRIREAYLPELSVIPGVNVDIFEELGRIFT 970
|||||
QY 961 AFLYDARNVINKGDFNGLSCHNVKGVHDVEQNHRHSVLVVPWEAEVSQVRVCPGR 1020
|||||
Db 971 AFLYDARNVINKGDFNGLSCHNVKGVHDVEQNHRHSVLVVPWEAEVSQVRVCPGR 1030
|||||
QY 1021 GYILRVTAKEGCGGCTT|HEIENNTDELAFSNCVEEYVPNTVTCNDYTANQEEYGG 1080
|||||
Db 1031 GYILRVTAKEGCGGCTT|HEIENNTDELAFSNCVEEYVPNTVTCNDYTANQEEYGG 1090
|||||
QY 1081 AYTSNRNGYDETYGNSVPADYASVYEKSYTDGRRDNPCESTRNGYCDYTPPLPAGYVTK 1140
|||||
Db 1091 AYTSNRNGYDETYGNSVPADYASVYEKSYTDGRRDNPCESTRNGYCDYTPPLPAGYVTK 1150
|||||
QY 1141 ELEYFETDKVWIEIGETEGTFIVDSVLELLMEE 1174
|||||
Db 1151 ELEYFETDKVWIEIGETEGTFIVDSVLELLMEE 1184
|||||

RESULT 9

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AAR84735  
 ID AAR84735 standard; Protein: 1174 AA.  
 AC AAR84735;  
 XX 23-JUN-1996 (first entry)  
 XX CryIF toxin with limited codon rework.  
 XX Delta endotoxin; crystal protein; chimeric toxin; codon rework;  
 KW insecticide; pesticide; Pseudomonas fluorescens;  
 KW biological control agent; transgenic plant; insect resistance;  
 KW disease resistance; crop improvement; protein engineering.  
 XX Bacillus thuringiensis.  
 OS  
 XX  
 XX W09530753-A1.  
 XX  
 XX 16-NOV-1995.  
 XX  
 XX 05-MAY-1995; 95WO-US05431.  
 XX  
 XX 06-MAY-1994; 94US-0239476.  
 XX  
 XX (MYCO ) MYCOGEN CORP.  
 XX  
 XX Schwab GE, Thompson M;  
 PI  
 XX  
 XX WPI: 1995-404120/51.  
 DR N-PSDB; AAT05270.  
 XX  
 XX Nucleic acid encoding chimeric Bacillus thuringiensis  
 PT delta-endotoxin - providing increased expression in Pseudomonas,  
 PT esp. for control of lepidoptera pests.  
 XX  
 XX Example 5; Page 47-50; 91pp; English.  
 PS  
 XX The sequence represents the CryIF toxin sequence with codon rework.  
 CC DNA encoding this sequence can be used in the construction of  
 CC chimeric toxins, which are expressed in Pseudomonas fluorescens  
 CC better than native delta endotoxins. Host cells expressing the  
 CC chimeric gene and producing chimeric toxin may be used in insecticide  
 CC compositions. Where the host cells are plant cells, the gene confers  
 CC insect resistance to the transformed plant.  
 XX  
 XX Sequence 1174 AA;  
 SQ  
 Query Match 99.9%; Score 6238; DB 16; Length 1174;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MENNIONQVPCVNCNPNVEILNEERSTGRPLDLSLRFLLSEFVPGVAFGLFD 60  
 DB 1 MENNIONQVPCVNCNPNVEILNEERSTGRPLDLSLRFLLSEFVPGVAFGLFD 60  
 QY 61 LWGFTTPSDWSLFLQIEQLIEQRIETLERNRAITLRLGLADSYEIEALRWEANPN 120  
 DB 61 LWGFTTPSDWSLFLQIEQLIEQRIETLERNRAITLRLGLADSYEIEALRWEANPN 120  
 QY 121 NAQLREDVIRFANTDAILTAINFTLTSFEIPLLSVYVQANLHLLRDVAVSFGOGW 180  
 DB 121 NAQLREDVIRFANTDAILTAINFTLTSFEIPLLSVYVQANLHLLRDVAVSFGOGW 180  
 QY 181 GLDIATVNNHYNFLNLIHRYTKHCLDYNQGLNLRGTNTROWARFNQFRDLTLTVLD 240  
 DB 181 GLDIATVNNHYNFLNLIHRYTKHCLDYNQGLNLRGTNTROWARFNQFRDLTLTVLD 240  
 QY 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPYSANIPNGFNRAEFGVRPPLMDFM 300  
 DB 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPYSANIPNGFNRAEFGVRPPLMDFM 300  
 QY 301 NSLFTVTAETVRSQTVWGGHLVSSRNVTAGNRINFPSPYGVNPGCAIWIADDEPRPYRTLS 360  
 DB 301 NSLFTVTAETVRSQTVWGGHLVSSRNVTAGNRINFPSPYGVNPGCAIWIADDEPRPYRTLS 360

DB 301 NSLFTVTAETVRSQTVWGGHLVSSRNVTAGNRINFPSPYGVNPGCAIWIADDEPRPYRTLS 360  
 QY 361 DPVFRGGFNGPHYVVLGRGVAFOQTGTNHTRTFRNSGTIDSLDEIPFDNSGAPWNDYS 420  
 DB 361 DPVFRGGFNGPHYVVLGRGVAFOQTGTNHTRTFRNSGTIDSLDEIPFDNSGAPWNDYS 420  
 QY 421 HVLNHTVFRWPGFGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLOSITT 480  
 DB 421 HVLNHTVFRWPGFGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLOSITT 480  
 QY 481 VVRGPGFTGSDILRRFSGGPFATVINGQLPQRYRARIYASTINRIYVTVAGERIF 540  
 DB 481 VVRGPGFTGSDILRRFSGGPFATVINGQLPQRYRARIYASTINRIYVTVAGERIF 540  
 QY 541 AGQFNKMTDGTPLTFQSFYSYATINTAFTFPMQSQSFTVGADTFSSGNEVYIDRPELIPV 600  
 DB 541 AGQFNKMTDGTPLTFQSFYSYATINTAFTFPMQSQSFTVGADTFSSGNEVYIDRPELIPV 600  
 QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTVDYTHIDQVSNLYDCLSDSECLDEKREL 660  
 DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTVDYTHIDQVSNLYDCLSDSECLDEKREL 660  
 QY 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQGDDVFKEVNTLPGTFD 720  
 DB 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQGDDVFKEVNTLPGTFD 720  
 QY 721 EGYPTLYQKIDESKLPKPYTRYOLRGYIEDSQDLEYLIYRYNAKHETVNVLTGSLWPLS 780  
 DB 721 EGYPTLYQKIDESKLPKPYTRYOLRGYIEDSQDLEYLIYRYNAKHETVNVLTGSLWPLS 780  
 QY 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
 DB 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
 QY 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKWKREKLELETNIVYKAKES 900  
 DB 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKWKREKLELETNIVYKAKES 900  
 QY 901 VDALFVNSQYDQLOADTNIAHIAADKRVHRIREAYLPELSVIPGVNVDIFELKGRIFT 960  
 DB 901 VDALFVNSQYDQLOADTNIAHIAADKRVHRIREAYLPELSVIPGVNVDIFELKGRIFT 960  
 QY 961 AFFLYDARNYKNGDFNGLSCNWNKGVHDVEQNNHRSVLVYVPEWEAEVQSVRYCPGR 1020  
 DB 961 AFFLYDARNYKNGDFNGLSCNWNKGVHDVEQNNHRSVLVYVPEWEAEVQSVRYCPGR 1020  
 QY 1021 GYLRTVTAEGYEGGCVTTHEIENNTDELKFSNCVVEEYVNNVTTCNDYTANQEEYGG 1080  
 DB 1021 GYLRTVTAEGYEGGCVTTHEIENNTDELKFSNCVVEEYVNNVTTCNDYTANQEEYGG 1080  
 QY 1081 AYTSRNGYDETYGSSSVFADYASVVEEKSYSYDGRDNPCESNRGYGYDTPLPAGYVTK 1140  
 DB 1081 AYTSRNGYDETYGSSSVFADYASVVEEKSYSYDGRDNPCESNRGYGYDTPLPAGYVTK 1140  
 QY 1141 ELEYFPTDKWIEIGETGTFIVDSVELLMEE 1174  
 DB 1141 ELEYFPTDKWIEIGETGTFIVDSVELLMEE 1174

RESULT 10  
 AAR94914  
 ID AAR94914 standard; Protein: 1174 AA.  
 XX  
 AC AAR94914;  
 XX  
 DT 18-AUG-1996 (first entry)  
 XX  
 DE CryIF toxin encoded by pMYC2243.  
 XX  
 KW CryIF; crystal protein; chimeric toxin; protoxin; pMYC2243;  
 KW delta-endotoxin; chimeric gene; fusion protein;  
 KW Pseudomonas fluorescens; CryIA(b); CryIA(c); synerg; Lepidoptera;  
 KW insect; biological control agent; transgenic plant;

insect resistance; crop improvement.

Bacillus thuringiensis.

Key Location/Qualifiers

Peptide 590..601

Peptide /note= "Core toxin-prototoxin junction marker (AAR94909);"

Peptide 1061..1068

Peptide /note= "Marker (AAR94910) for start of critical

Peptide hypervariable region in protoxin"

US5508264-A.

16-APR-1996.

06-DEC-1994; 94US-0349867.

06-DEC-1994; 94US-0349867.

(MYCO ) MYCOGEN CORP.

Bradfish GA, Schwab GE, Thompson M;

WPI; 1996-208745/21.

N-PSDB; AAT18722.

Compsn. for controlling lepidopteran pests - comprises CryIF and

CryIA(c) chimeric core toxin-contg. proteins.

Example 5; Column 55-62; 59pp; English.

This sequence represents a Bacillus thuringiensis CryIF delta-  
endotoxin. A gene from pMC2047 has been subjected to splice  
overlap extension to alter codons in a limited region in the cryIF  
fragment to favor G or C in the wobble position, to improve  
expression in Pseudomonas spp. The resulting cryIF clone is  
pMC2243. The cryIF fragment may be fused with cryIA(b) and/or  
cryIA(c) fragments to give fusion proteins by recombinant DNA  
methods. The core toxin sequence ends with peptide AAR94909,  
which marks the start of the protoxin sequence, and the preferred  
heterologous region is the hypervariable fragment beyond peptide  
AAR94910. The resulting chimeric genes may be cloned in a  
Pseudomonas fluorescens lactose-inducible strain to produce  
chimeric toxins. The toxins, when combined in synergy, have  
unexpectedly enhanced toxicity to lepidopteran pests. P.  
fluorescens or B. thuringiensis cells expressing the genes may be  
used as insect biological control agents, or transgenic plants  
expressing the genes may become resistant to insect attack.

Query Match 99.9%; Score 6237; DB 17; Length 1174;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNQOCVPYCNLNNPEVEILNEERSTGRPLDLSLFRLLSEFVPGVGAFGLFD 60  
DB 1 MENNQOCVPYCNLNNPEVEILNEERSTGRPLDLSLFRLLSEFVPGVGAFGLFD 60

QY 61 LIWGFITPSDWSLFLQIQEQLTEQLERNAITTLRGLADSYEIVYALREWEANPN 120  
DB 61 LIWGFITPSDWSLFLQIQEQLTEQLERNAITTLRGLADSYEIVYALREWEANPN 120

QY 121 NAQLREDVRIRFANTDDALITAINNFTLSFEIPLSYVQAANLHLSLLRDVAVSFGOGW 180  
DB 121 NAQLREDVRIRFANTDDALITAINNFTLSFEIPLSYVQAANLHLSLLRDVAVSFGOGW 180

QY 181 GLDIATVNNHYNRLINLHRYTKHCLDITYNQGLENLRTNQWAFRPNQFRDLTLTVLD 240  
DB 181 GLDIATVNNHYNRLINLHRYTKHCLDITYNQGLENLRTNQWAFRPNQFRDLTLTVLD 240

QY 241 IVALFPNYDVRTYPIQTSQLTREIYTSVIEDSPVSNIPNGFNRAEFGVPRPHLMDFM 300  
DB 241 IVALFPNYDVRTYPIQTSQLTREIYTSVIEDSPVSNIPNGFNRAEFGVPRPHLMDFM 300

DB 241 IVALFPNYDVRTYPIQTSQLTREIYTSVIEDSPVSNIPNGFNRAEFGVPRPHLMDFM 300

QY 301 NSLFVTAETVRSOTVMGGHLVSSRNTAGNRINFPSPYGVFNPGGAIIWADEDEPRFVRLS 360  
DB 301 NSLFVTAETVRSOTVMGGHLVSSRNTAGNRINFPSPYGVFNPGGAIIWADEDEPRFVRLS 360

QY 361 DPVFGGNGFNHYVLGLRGVAFQQTGTHRTFRNSGTIDSLDEIPPODNGAPWNDYS 420  
DB 361 DPVFGGNGFNHYVLGLRGVAFQQTGTHRTFRNSGTIDSLDEIPPODNGAPWNDYS 420

QY 421 HVLNHYTEVRWPGCEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTILOSQT 480  
DB 421 HVLNHYTEVRWPGCEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTILOSQT 480

QY 481 VVRGPGTGGDILRRTSGGPFAYTIIVNINGQLPQRVRIYASTNLIYVTVAGERIF 540  
DB 481 VVRGPGTGGDILRRTSGGPFAYTIIVNINGQLPQRVRIYASTNLIYVTVAGERIF 540

QY 541 AGOFNKMTDGTDLTQSFYSYATINTAFTPMSQSSFTVGADTFSSGNEVYIDRPELIV 600  
DB 541 AGOFNKMTDGTDLTQSFYSYATINTAFTPMSQSSFTVGADTFSSGNEVYIDRPELIV 600

QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTQVTDYHIDQVSNLVCLSDFCLEKREL 660  
DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTQVTDYHIDQVSNLVCLSDFCLEKREL 660

QY 661 SEKVHAKRLSDERNLLQDPNFKGINRQDRGWSGTDITIQGDDVFKENYVTLPGTFD 720  
DB 661 SEKVHAKRLSDERNLLQDPNFKGINRQDRGWSGTDITIQGDDVFKENYVTLPGTFD 720

QY 721 ECPYTYLYQKIDESKLPYTRYOLRGYIEDSQDLEYILIRYNAKHETVNVLTGSLWPLS 780  
DB 721 ECPYTYLYQKIDESKLPYTRYOLRGYIEDSQDLEYILIRYNAKHETVNVLTGSLWPLS 780

QY 781 VQSPIKRCGEPNRCAPHELNWPLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840  
DB 781 VQSPIKRCGEPNRCAPHELNWPLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840

QY 841 IFKIKTQDCHARLGNLEFLEEKPLVGENLARVKAEEKKEDKREKLELETINIVYKEAKES 900  
DB 841 IFKIKTQDCHARLGNLEFLEEKPLVGENLARVKAEEKKEDKREKLELETINIVYKEAKES 900

QY 901 VDALFVNSOYDQLQADNTNIAHAAKRVHRIEAYLPELSVIPGVNVDIFEELKGRIFT 960  
DB 901 VDALFVNSOYDQLQADNTNIAHAAKRVHRIEAYLPELSVIPGVNVDIFEELKGRIFT 960

QY 961 AFLYDARNVIKNGDFNNGLSCHWVGHVDYEQNHRSVLYVPEWEAEVQSQVRYCPGR 1020  
DB 961 AFLYDARNVIKNGDFNNGLSCHWVGHVDYEQNHRSVLYVPEWEAEVQSQVRYCPGR 1020

QY 1021 GYLIRVTAYKEGYGEGCVTTHEIENNTDELKFSNCVDEEYVNNVTTCNDYTANQBEYGG 1080  
DB 1021 GYLIRVTAYKEGYGEGCVTTHEIENNTDELKFSNCVDEEYVNNVTTCNDYTANQBEYGG 1080

QY 1081 AYTSSRNGYDETYGSSNSVPADYASVYEKSYTDGRRDNPCESNRGYGYDTPLPAGYVTK 1140  
DB 1081 AYTSSRNGYDETYGSSNSVPADYASVYEKSYTDGRRDNPCESNRGYGYDTPLPAGYVTK 1140

QY 1141 ELEVEPETDKVWIEIGETGTFIVDSVELLMEE 1174  
DB 1141 ELEVEPETDKVWIEIGETGTFIVDSVELLMEE 1174

RESULT 11  
AAR94916  
ID AAR94916 standard; Protein; 1174 AA.  
XX AAR94916;  
XX AC  
XX DT 18-AUG-1996 (first entry)  
XX XX  
XX Native CryIF/CryIA(b) toxin.

KW CryIF; CryIA(b): crystal protein; chimeric toxin;  
 KW protoxin; delta-endotoxin; fusion protein; CryIA(C);  
 KW Pseudomonas fluorescens; synergy; Lepidoptera; insect;  
 KW biological control agent; transgenic plant; insect resistance;  
 KW crop improvement.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 590...601  
 FT /note= "Core toxin-prototoxin junction marker (AAR94909)"  
 FT 1061..1068  
 FT /note= "Marker (AAR94910) for start of critical  
 FT hypervariable region in protoxin"  
 XX  
 PN US5508264-A.  
 XX  
 PD 16-APR-1996.  
 XX  
 PF 06-DEC-1994; 94US-0349867.  
 XX  
 PR 06-DEC-1994; 94US-0349867.  
 XX  
 PA (MYCO ) MYCOGEN CORP.  
 XX  
 PI Bradfisch GA, Schwab GE, Thompson M;  
 XX  
 DR WPT; 1996-208745/21.  
 XX  
 PT Compsn. for controlling lepidopteran pests - comprises CryIF and  
 PT CryIA(c) chimeric core toxin-contg. proteins.  
 XX  
 PS Disclosure; Column 79-86; 59pp; English.  
 CC This sequence represents a Bacillus thuringiensis delta-endotoxin  
 CC native CryIF/CryIA(b) toxin sequence. The core toxin sequence ends  
 CC with peptide AAR94909, which marks the start of the protoxin  
 CC sequence, and the critical hypervariable fragment beyond peptide  
 CC AAR94910 may be used for insertion of heterologous fragments to give  
 CC chimeric toxins with altered activity by recombinant DNA methods.  
 CC The resulting chimeric genes may be cloned in a Pseudomonas  
 CC fluorescens lactose-inducible strain. The chimeric toxins, when  
 CC combined in synergy, have unexpectedly enhanced toxicity to  
 CC lepidopteran pests. P. fluorescens or B. thuringiensis cells  
 CC expressing the chimeric genes may be used as insect biological  
 CC control agents, or transgenic plants expressing the genes may  
 CC become resistant to insect attack.  
 XX  
 SQ Sequence 1174 AA;

Query Match 99.9%; Score 6236; DB 17; Length 1174;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNTONOCVPYNCLNNEVEILNEERSTGRPLDLSLTLSEFVPGVGAFLGD 60  
 DB 1 MENNTONOCVPYNCLNNEVEILNEERSTGRPLDLSLTLSEFVPGVGAFLGD 60  
 QY 61 LHWGPTSDWSLSFLQLEQLIEQRIETLERNRAITTLRLGLADSYEITYEALREWEANPN 120  
 DB 61 LHWGPTSDWSLSFLQLEQLIEQRIETLERNRAITTLRLGLADSYEITYEALREWEANPN 120  
 QY 121 NAOLEDVRIREFANTDDALITAINFTLTSFPIPLSVVQAAHLHLSLRDAVSFGOGW 180  
 DB 121 NAOLEDVRIREFANTDDALITAINFTLTSFPIPLSVVQAAHLHLSLRDAVSFGOGW 180  
 QY 181 GLDIATVNNHYNRLINLHRYTKHCLDIYNOGLNRLRGNTNQWARFNQFRDLTLTLVD 240  
 DB 181 GLDIATVNNHYNRLINLHRYTKHCLDIYNOGLNRLRGNTNQWARFNQFRDLTLTLVD 240  
 QY 241 IVALFPNDVTRTYPIQTSQTLREITYTSSVIEDSPVSANIPNGFRAEFGVPRPHLMDFM 300  
 DB 241 IVALFPNDVTRTYPIQTSQTLREITYTSSVIEDSPVSANIPNGFRAEFGVPRPHLMDFM 300

QY 301 NSLFVTAETVRSQTVWGHVLSRNTAGRIINFPSPSYGVNPGGAIWIADDPFPFRTLS 360  
 DB 301 NSLFVTAETVRSQTVWGHVLSRNTAGRIINFPSPSYGVNPGGAIWIADDPFPFRTLS 360  
 QY 361 DPVFRGGFGNPHYVLGLRGVAFQQTGTNFTFRNSGTIDSLEIPPODNGSAPNDYS 420  
 DB 361 DPVFRGGFGNPHYVLGLRGVAFQQTGTNFTFRNSGTIDSLEIPPODNGSAPNDYS 420  
 QY 421 HVLNHTVFRVPEIGSGDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480  
 DB 421 HVLNHTVFRVPEIGSGDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480  
 QY 481 VVRGPGFTGGDILRLRTSGGPFAYTIVNINGQLPQRYRARIRYASTNLRIYTVAGERIF 540  
 DB 481 VVRGPGFTGGDILRLRTSGGPFAYTIVNINGQLPQRYRARIRYASTNLRIYTVAGERIF 540  
 QY 541 AGQFNKTMGTGDLTFOQSFYSATINTAFTFPMQSSFTVGADTFSSGNEWYIDRPELIIV 600  
 DB 541 AGQFNKTMGTGDLTFOQSFYSATINTAFTFPMQSSFTVGADTFSSGNEWYIDRPELIIV 600  
 QY 601 TATFEAYDLERAQAVNALFTSIQIGIKTDVTDYHIDQVSNLVDCLDSEFCDEKREL 660  
 DB 601 TATFEAYDLERAQAVNALFTSIQIGIKTDVTDYHIDQVSNLVDCLDSEFCDEKREL 660  
 QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDRGRWGSTDITIQGGDDVFKENVTPLGTED 720  
 DB 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDRGRWGSTDITIQGGDDVFKENVTPLGTED 720  
 QY 721 EGYPTLYQKIDESKLPYTRYOLRGYIEDSDLEILYIRYNAKHETVNVLTGSLWPLIS 780  
 DB 721 EGYPTLYQKIDESKLPYTRYOLRGYIEDSDLEILYIRYNAKHETVNVLTGSLWPLIS 780  
 QY 781 VQSPIRKCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
 DB 781 VQSPIRKCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
 QY 841 IFKIKTDGSHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKRELELETNIVYKAKES 900  
 DB 841 IFKIKTDGSHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKRELELETNIVYKAKES 900  
 QY 901 VDALFVNSOYDQLOADNTIAMHAADKRVHRIREAYLPESLVPVGVNDFIFELKGRIFT 960  
 DB 901 VDALFVNSOYDQLOADNTIAMHAADKRVHRIREAYLPESLVPVGVNDFIFELKGRIFT 960  
 QY 961 AFPLDARNVIRKNGDFNGLSCWNVKHVDVEEQNNHRSVLVYVPEWEAEVSQVRCPCR 1020  
 DB 961 AFPLDARNVIRKNGDFNGLSCWNVKHVDVEEQNNHRSVLVYVPEWEAEVSQVRCPCR 1020  
 QY 1021 GYLIRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEVEYVNTVTCNDYTANQOEYGG 1080  
 DB 1021 GYLIRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEVEYVNTVTCNDYTANQOEYGG 1080  
 QY 1081 AYTSNRGYDETYGSNSVPADYASYIEEKSYTDGRRDNPCESNRGYGDTPLPAGYVTK 1140  
 DB 1081 AYTSNRGYDETYGSNSVPADYASYIEEKSYTDGRRDNPCESNRGYGDTPLPAGYVTK 1140  
 QY 1141 ELEYFPETDKVWIEIGETEGTTFIVDSVELLMEE 1174  
 DB 1141 ELEYFPETDKVWIEIGETEGTTFIVDSVELLMEE 1174

RESULT 12  
 AAR84732  
 ID AAR84732 standard; Protein; 1174 AA.  
 XX  
 AC AAR84732;  
 XX  
 DT 27-MAY-1996 (first entry)  
 XX  
 DE CryIF/436 chimeric toxin.  
 XX  
 KW Delta endotoxin; crystal protein; chimeric toxin; insecticide;

KW pesticide; Pseudomonas fluorescens; biological control agent;  
 KW transgenic plant; insect resistance; disease resistance;  
 KW crop improvement; protein engineering.  
 XX  
 OS Bacillus thuringiensis.

Key Location/Qualifiers

FT Misc-difference 619 /note= "E to A substitution"

FT Misc-difference 624 /note= "S to I substitution"

FT Misc-difference 646 /note= "E to T substitution"

FT Misc-difference 658 /note= "K to R substitution"

FT Misc-difference 680 /note= "P to S substitution"

FT Misc-difference 684 /note= "G to D substitution"

FT Misc-difference 689 /note= "L to P substitution"

FT Misc-difference 694 /note= "R to G substitution"

FT Misc-difference 698 /note= "D to G substitution"

FT Misc-difference 716 /note= "L to S substitution"

FT Misc-difference 782 /note= "P to Q substitution"

FT Misc-difference 912 /note= "R to Q substitution"

FT W09530753-A1.

PN 16-NOV-1995.

XX 05-MAY-1995; 95WO-US05431.

XX 06-MAY-1994; 94US-0239476.

XX (MYCO ) MYCOGEN CORP.

XX Schwab GE, Thompson M;

XX WPI; 1995-404120/51.

XX N-PSDB; AAT05250.

XX Nucleic acid encoding chimeric Bacillus thuringiensis

XX delta-endotoxin - providing increased expression in Pseudomonas,

XX esp. for control of lepidoptera pests.

XX Claim 10; Page 58-61; 91pp; English.

XX The sequence represents the cryIF/436 chimeric toxin encoded by

XX plasmid pMYC2254. The chimeric toxin is expressed in Pseudomonas

XX fluorescens better than native delta endotoxins. Host cells

XX expressing the chimeric gene and producing chimeric toxin may be

XX used in insecticide compositions. Where the host cells are plant

XX cells, the gene confers insect resistance to the transformed

XX plant.

XX Sequence 1174 AA;

XX Query Match 96.9%; Score 6049; DB 16; Length 1174;

XX Best Local Similarity 97.4%; Pred. No. 0;

XX Matches 1143; Conservative 5; Mismatches 26; Indels 0; Gaps 0;

QY 1 MENNIONQCVNCLNPNVEILNEERSTGRPLDLSLSTRFLLSSEFPVGVGVAFLGFD 50

DB 1 MENNIONQCVNCLNPNVEILNEERSTGRPLDLSLSTRFLLSSEFPVGVGVAFLGFD 60

QY 61 LIWGFITPDSWLSFLIQIEQLIEQRIETLERNRAITTLRGLADSYEITYEALREWEANPN 120

•

DB 61 LIWGFITPDSWLSFLIQIEQLIEQRIETLERNRAITTLRGLADSYEITYEALREWEANPN 120  
 QY 121 NAQREDVRIRFANTDDALITAINNETLTLSFEIPLLSVYQAAANLHLSLRDVSFGQGW 180  
 DB 121 NAQREDVRIRFANTDDALITAINNETLTLSFEIPLLSVYQAAANLHLSLRDVSFGQGW 180  
 QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLENLRGNTROWARFNFRDLTLTVLD 240  
 DB 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLENLRGNTROWARFNFRDLTLTVLD 240  
 QY 241 IVALFPNDVRYPIQTSOLTRIEYTSVIEDSPYSANIPNGFNRAEFGVRPHLDMFM 300  
 DB 241 IVALFPNDVRYPIQTSOLTRIEYTSVIEDSPYSANIPNGFNRAEFGVRPHLDMFM 300  
 QY 301 NSLFTVTAETVRSQTVWGGHLVSSRNATAGRNIPFSGVFNPGGAIWIADDPFPFYRTLS 360  
 DB 301 NSLFTVTAETVRSQTVWGGHLVSSRNATAGRNIPFSGVFNPGGAIWIADDPFPFYRTLS 360  
 QY 361 DPVVRGGFGNHYVLGLRGVAFQQTGTHRTFRNSGTIDSLEIPPODNGAPWNDYS 420  
 DB 361 DPVVRGGFGNHYVLGLRGVAFQQTGTHRTFRNSGTIDSLEIPPODNGAPWNDYS 420  
 QY 421 HVLNHYTFVRWPGCEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLOSGET 480  
 DB 421 HVLNHYTFVRWPGCEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLOSGET 480  
 QY 481 VVRGPGTGGDILRRTSGGPFAYTIIVNINGQLPQRYRARIYASTTNLRIYTVAGERIF 540  
 DB 481 VVRGPGTGGDILRRTSGGPFAYTIIVNINGQLPQRYRARIYASTTNLRIYTVAGERIF 540  
 QY 541 AGQFNKMTDGPPLTFQSFYSYATINTAFTFMSQSSTFVGADTFSSGNEVYIDRFELIPV 600  
 DB 541 AGQFNKMTDGPPLTFQSFYSYATINTAFTFMSQSSTFVGADTFSSGNEVYIDRFELIPV 600  
 QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDVHDQVSNLVCLSDEFCCLDEKREL 660  
 DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDVHDQVSNLVCLSDEFCCLDEKREL 660  
 QY 661 SEKVHAKRLSDERNLLODPNFKGINRQLDRGRWGSTDITIQRGDDVFKENYVTLPGTFD 720  
 DB 661 SEKVHAKRLSDERNLLODPNFKGINRQLDRGRWGSTDITIQRGDDVFKENYVTLPGTFD 720  
 QY 721 ECPYLYIQKIDESKLPYTRYQLRGYIEDSODLEIYLIRYNAKHETVNLGTGSLWPLS 780  
 DB 721 ECPYLYIQKIDESKLPYTRYQLRGYIEDSODLEIYLIRYNAKHETVNLGTGSLWPLS 780  
 QY 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCITDNLNEDLVWV 840  
 DB 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCITDNLNEDLVWV 840  
 QY 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARYKRAEKKWRDKREKLELETNTIYVKEAKES 900  
 DB 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARYKRAEKKWRDKREKLELETNTIYVKEAKES 900  
 QY 901 VDALLFVNSQYDQLOADNTIAMTHAADKRVHRTREAYLPVLPVGNVDIFELKGRIFT 960  
 DB 901 VDALLFVNSQYDQLOADNTIAMTHAADKRVHRTREAYLPVLPVGNVDIFELKGRIFT 960  
 QY 961 AFPLDYDARNVKNQDFNGLSCWNVKGHVDEEONHRSVLVVPWEAEVSOEVRVCPGR 1020  
 DB 961 AFPLDYDARNVKNQDFNGLSCWNVKGHVDEEONHRSVLVVPWEAEVSOEVRVCPGR 1020  
 QY 1021 GYLIRVATYKGEYGGCVTIHBIENNTDELKFSNCVEEVEYNNVTNCNDYTANOEEYGG 1080  
 DB 1021 GYLIRVATYKGEYGGCVTIHBIENNTDELKFSNCVEEVEYNNVTNCNDYTANOEEYGG 1080  
 QY 1081 ATYSNRNGYDETYGNSNSVPADYASVYEEKSYTDGRRONPCSNRGYGDYTPLPAGYVTK 1140  
 DB 1081 ATYSNRNGYDETYGNSNSVPADYASVYEEKSYTDGRRONPCSNRGYGDYTPLPAGYVTK 1140  
 QY 1141 ELEYFPETDKWVIEGTETGTFIVDSVELLMEE 1174  
 DB 1141 ELEYFPETDKWVIEGTETGTFIVDSVELLMEE 1174

RESULT 13	
AAR94908	
ID	AAR94908 standard; Protein; 1174 AA.
XX	
XX	AAR94908;
XX	
DT	18-AUG-1996 (first entry)
DE	CryIF/436 chimeric toxin encoded by pMYC2254.
XX	
KW	CryIF: CryIA(C); CryIA(b): crystal protein; chimeric toxin;
KW	protoxin; pMYC2244; delta-endotoxin; fusion protein;
KW	Pseudomonas fluorescens; synergy; Lepidoptera; insect;
KW	biological control agent; transgenic plant; insect resistance;
KW	crop improvement.
XX	
OS	Bacillus thuringiensis.
XX	
XX	Key Location/Qualifiers
FT	Region 1..601
FT	/note= "CryIF toxin region"
FT	Peptide 590..601
FT	/note= "Core toxin-protoxin junction marker (AAR94909)";
FT	Region 602..1148
FT	/note= "CryIA(c)/CryIA(b) 436 protoxin region"
FT	Peptide 1061..1068
FT	/note= "Marker (AAR94910) for start of critical
FT	hypervariable region in protoxin"
XX	
PN	U55508264-A.
XX	
XX	16-APR-1996.
XX	
XX	06-DEC-1994; 94US-0349867.
XX	
PR	06-DEC-1994; 94US-0349867.
XX	
PA	(MYCO ) MYCOGEN CORP.
XX	
PI	Bradfish GA, Schwab GE, Thompson M;
XX	
DR	WPI: 1996-208745/21.
XX	
XX	N-PSDB; AAT18702.
PT	
XX	Compos. for controlling lepidopteran pests - comprises CryIF and
XX	CryIA(C) chimeric core toxin-contg. proteins.
PS	Claim 7; Column 73-80; 59pp; English.
XX	
CC	This sequence represents a Bacillus thuringiensis chimeric
CC	CryIF/436 delta-endotoxin. The sequence is constructed by
CC	substitution of a CryIA(c)-CryIA(b) 436 (AAR94911) fragment for a
CC	CryIA(b) fragment encoded by pMYC2523 (AAR94907). The 436 protoxin
CC	sequence consists of CryIA(c) sequence except at the very
CC	C-terminus. The product contains CryIF up to the toxin-protoxin
CC	junction, followed by a CryIA(c) protoxin sequence with a small
CC	C-terminal fragment of CryIA(b). The core toxin sequence ends
CC	with peptide AAR94909, which marks the start of the protoxin
CC	sequence, and the preferred heterologous region is the
CC	hypervariable fragment beyond peptide AAR94910. The resulting
CC	chimeric gene may be cloned in a pseudomonas fluorescens
CC	lactose-inducible strain to produce a chimeric toxin. The toxin,
CC	when combined with another chimeric toxin in synergy, has
CC	unexpectedly enhanced toxicity to lepidopteran pests. P.
CC	fluorescens or B. thuringiensis cells expressing the gene may be
CC	used as an insect biological control agent, or a transgenic plant
CC	expressing the gene may become resistant to insect attack.
XX	
SQ	Sequence 1174 AA;

Query Match 96.9%; Score 6049; DB 17; Length 1174;

[illegible]

Db 1021 GYLLRVAYKEGYGEGCVTHIEIENNTDELKFSNCVEEVEYPNNVTICNDYATATQEEYEG 1080  
 QY 1081 AYTSRNGYDEYGSNSVADYASVVEEKSYTDGRRDNPCESSNGYGYDTPPLPAGYVTK 1140  
 Db 1081 TYTSRNGYDAYSNSVADYASVVEEKAYTDGRRDNPCESSNGYGYDTPPLPAGYVTK 1140  
 QY 1141 ELEYPETDKWIEIGETEGTFIVDSVELLMEE 1174  
 Db 1141 ELEYPETDKWIEIGETEGTFIVDSVELLMEE 1174

RESULT 14  
 AAW76710  
 ID AAW76710 standard; Protein; 1174 AA.  
 XX  
 AC AAW76710;  
 XX  
 DT 13-JAN-1999 (first entry)  
 DE  
 XX Plasmid pMYC2254 cryIF/436 chimeric toxin protein fragment.  
 KW Bt toxin; lepidoptera; pest; cryIF; chimeric; core toxin; cryIA(c);  
 KW synergism; plant; primer; endotoxin.  
 XX Synthetic.  
 OS  
 XX US5827514-A.  
 PN  
 XX 27-OCT-1998.  
 PD  
 XX 08-FEB-1996; 96US-0598305.  
 PF  
 XX 06-DEC-1994; 94US-0349867.  
 PR 08-FEB-1996; 96US-0598305.  
 XX  
 XX (MYCO ) MYCOGEN CORP.  
 PA  
 XX  
 XX Bradfish GA, Schwab GE, Thompson M;  
 PI  
 XX WPI; 1998-593944/50.  
 DR N-PSDB; AAV62083.  
 DR  
 XX Composition for biological control of lepidopteran pests -  
 PT comprising cells expressing two chimeric *Bacillus thuringiensis*  
 PT crystal proteins  
 PT  
 PS Claim 9; Column 75-82; 75pp; English.  
 XX  
 CC This sequence represents a Bt endotoxin which is used in a method for  
 CC controlling lepidopteran pests. The method involves the use of cells  
 CC that express the *Bacillus thuringiensis* delta-endotoxin cryIF chimeric  
 CC core toxin-containing protein and cryIA(c) chimeric core toxin-containing  
 CC protein in a combination that have synergistically enhanced activity,  
 CC against e.g. corn earworm (*Heliothis zea*).  
 XX  
 SQ Sequence 1174 AA;

Query Match 96.9%; Score 6049; DB 19; Length 1174;  
 Best Local Similarity 97.4%; Pred. No. 0;  
 Matches 1143; Conservative 5; Mismatches 26; Indels 0; Gaps 0;

QY 1 MENNIQCVPYCNLNNPEYIENRSTGRPLDLSLSTRFLLSFVPGVGVAFLFD 60  
 Db 1 MENNIQCVPYCNLNNPEYIENRSTGRPLDLSLSTRFLLSFVPGVGVAFLFD 60  
 QY 61 LINGFTPPDSWLSFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120  
 Db 61 LINGFTPPDSWLSFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120  
 QY 121 NAQLREDVIRFANTDDALITANNNTLTSTFETPLISVYVQAAANLHLSLRDAVSFGQW 180  
 Db 121 NAQLREDVIRFANTDDALITANNNTLTSTFETPLISVYVQAAANLHLSLRDAVSFGQW 180

RESULT 15  
 AAW76716  
 ID AAW76716 standard; Protein; 1175 AA.  
 XX

QY 181 GLDIATVNNHYNRLNLHRYTKKCLDITYNOGLENLRGCTNTQWARFNQFRDLTLTVLD 240  
 Db 181 GLDIATVNNHYNRLNLHRYTKKCLDITYNOGLENLRGCTNTQWARFNQFRDLTLTVLD 240  
 QY 241 IVALFPNDVDTYPIQTSSQLTREIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300  
 Db 241 IVALFPNDVDTYPIQTSSQLTREIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300  
 QY 301 NSLFVTAETVRSQTVWGGHLVSSRNTAGNINFFSYGVFNPGGAIWIADDEPRFYRTL 360  
 Db 301 NSLFVTAETVRSQTVWGGHLVSSRNTAGNINFFSYGVFNPGGAIWIADDEPRFYRTL 360  
 QY 361 DPVEVRGFGNPHYVGLRGVAFQOTGTNHTRTFRNSGTIDSLDEIPPODNSGAPWNDYS 420  
 Db 361 DPVEVRGFGNPHYVGLRGVAFQOTGTNHTRTFRNSGTIDSLDEIPPODNSGAPWNDYS 420  
 QY 421 HVLNHTVFRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITOPLVKAHTLQSGTT 480  
 Db 421 HVLNHTVFRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITOPLVKAHTLQSGTT 480  
 QY 481 VVRPGTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYASTTNLRIYTVVAGERIF 540  
 Db 481 VVRPGTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYASTTNLRIYTVVAGERIF 540  
 QY 541 AGQFNKTMDTGDLTFOSESYATINTAFTPMSSOSSTVGADTFSSGNEVYIDREFELIPV 600  
 Db 541 AGQFNKTMDTGDLTFOSESYATINTAFTPMSSOSSTVGADTFSSGNEVYIDREFELIPV 600  
 QY 601 TATPEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSBDFCLDEKREL 660  
 Db 601 TATPEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDVSNLVYLSDFECLDEKREL 660  
 QY 661 SEVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDTITQRGDDVFKENYVLTPTFD 720  
 Db 661 SEVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTITQGGDDVFKENYVLTPTFD 720  
 QY 721 EGYPTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYNAKHETVNVLTGSLAPLS 780  
 Db 721 EGYPTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYNAKHETVNVLTGSLAPLS 780  
 QY 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHFLSDIDVGCCTDLNEDLDVWV 840  
 Db 781 AQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHFLSDIDVGCCTDLNEDLDVWV 840  
 QY 841 IFKIKTODGHARLGNLEFLEEKPLVGEALARKAERKWRDKREKLEETNIVYKEAKES 900  
 Db 841 IFKIKTODGHARLGNLEFLEEKPLVGEALARKAERKWRDKREKLEETNIVYKEAKES 900  
 QY 901 VDALFVNSQDQLOADFNIAHIAADKRVHIREAYLPELSVPGVNDVFEELKGRIFT 960  
 Db 901 VDALFVNSQDQLOADFNIAHIAADKRVHIREAYLPELSVPGVNDVFEELKGRIFT 960  
 QY 961 AFFLYDARNVIKNGDFNGLSCHNVKGVHVDVEEQNNHRSVLVVPWEAEYSQEVRCVPCR 1020  
 Db 961 AFFLYDARNVIKNGDFNGLSCHNVKGVHVDVEEQNNHRSVLVVPWEAEYSQEVRCVPCR 1020  
 QY 1021 GYLIRVAYKEGYGEGCVTHIEIENNTDELKFSNCVEEVEYPNNVTICNDYATATQEEYEG 1080  
 Db 1021 GYLIRVAYKEGYGEGCVTHIEIENNTDELKFSNCVEEVEYPNNVTICNDYATATQEEYEG 1080  
 QY 1081 AYTSRNGYDEYGSNSVADYASVVEEKSYTDGRRDNPCESSNGYGYDTPPLPAGYVTK 1140  
 Db 1081 TYTSRNGYDAYSNSVADYASVVEEKAYTDGRRDNPCESSNGYGYDTPPLPAGYVTK 1140  
 QY 1141 ELEYPETDKWIEIGETEGTFIVDSVELLMEE 1174  
 Db 1141 ELEYPETDKWIEIGETEGTFIVDSVELLMEE 1174

AC AAW76716;  
 XX 13-JAN-1999 (first entry)  
 XX Alternative cryIF/cryIA(b) chimeric endotoxin protein #1.  
 XX Bt toxin; lepidoptera; pest; cryIF; chimeric; core toxin; cryIA(c);  
 KW synergism; plant; primer; endotoxin.  
 XX Synthetic.  
 XX US5827514-A.  
 PN 27-OCT-1998.  
 XX 08-FEB-1996; 96US-0598305.  
 XX 06-DEC-1994; 94US-0349867.  
 PR 08-FEB-1996; 96US-0598305.  
 XX (MYCO ) MYCOGEN CORP.  
 PA Bradfisch GA, Schwab GE, Thompson M;  
 PI WPI; 1998-593944/50.  
 XX Composition for biological control of lepidopteran pests -  
 PT comprising cells expressing two chimeric Bacillus thuringiensis  
 PT crystal proteins  
 XX Claim 10; Column 105-112; 75pp; English.  
 XX This sequence represents a Bt endotoxin which is used in a method for  
 CC controlling lepidopteran pests. The method involves the use of cells  
 CC that express the Bacillus thuringiensis delta-endotoxins cryIF chimeric.  
 CC core toxin-containing protein and CryIA(c) chimeric core toxin-containing  
 CC protein in a combination that have synergistically enhanced activity,  
 CC against e.g. corn earworm (Heliothis zea).  
 XX Sequence 1175 AA;  
 SQ  
 Query Match 96.4%; Score 6018.5; DB 19; Length 1175;  
 Best Local Similarity 96.9%; Pred. No. 0;  
 Matches 1138; Conservative 11; Mismatches 25; Indels 1; Gaps 1;  
 QY 1 MENNIONOCVYNCLNNEVEILNEERSTGRPLDLSLFRLLSERVPGVGAFGLFD 60  
 DB 1 MENNIONOCVYNCLNNEVEILNEERSTGRPLDLSLFRLLSERVPGVGAFGLFD 60  
 QY 61 LIWGFITPSDWSLFLQIEQRIETLERNRAITTLRLGLADSVEIYTEALREWEANPN 120  
 DB 61 LIWGFITPSDWSLFLQIEQRIETLERNRAITTLRLGLADSVEIYTEALREWEANPN 120  
 QY 121 NAQLREDYRIEFANTDDALITAINNFTLTSFEIPLLSVYVQAAHLHLRLRDVAFSGOGW 180  
 DB 121 NAQLREDYRIEFANTDDALITAINNFTLTSFEIPLLSVYVQAAHLHLRLRDVAFSGOGW 180  
 QY 181 GLDIATVNNHYNRLNLRHTKHCIDYNOGLENLRTGNTROWARFNOFRDLTLTVLD 240  
 DB 181 GLDIATVNNHYNRLNLRHTKHCIDYNOGLENLRTGNTROWARFNOFRDLTLTVLD 240  
 QY 241 IVALFPNDYRTPIQTSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300  
 DB 241 IVALFPNDYRTPIQTSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300  
 QY 301 NSLFTVETVRSQTVWGHVLSRNTAGNRINFPYGVNPGCAIWADEDPPTPTILS 360  
 DB 301 NSLFTVETVRSQTVWGHVLSRNTAGNRINFPYGVNPGCAIWADEDPPTPTILS 360  
 QY 361 DPVFRGGFGNPHYVLGLRGVAFQOTGNTHTFRNSGTIDSLDEIPPODNSGAPWNDYS 420  
 DB 361 DPVFRGGFGNPHYVLGLRGVAFQOTGNTHTFRNSGTIDSLDEIPPODNSGAPWNDYS 420

QY 421 HVLNHNFTVRWPGBEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLOSGET 480  
 DB 421 HVLNHNFTVRWPGBEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLOSGET 480  
 QY 481 VVRGPGFTGGDILRRTSGGPFAYTIVNINQOLPORRYARIRYASTTNLRIRYVTVAGERIF 540  
 DB 481 VVRGPGFTGGDILRRTSGGPFAYTIVNINQOLPORRYARIRYASTTNLRIRYVTVAGERIF 540  
 QY 541 AGQFNKTMDTGDLTFSQSYATINTAFTFPMSSOSTFVGADTFSSNEVEYIDRFELIPV 600  
 DB 541 AGQFNKTMDTGDLTFSQSYATINTAFTFPMSSOSTFVGADTFSSNEVEYIDRFELIPV 600  
 QY 601 TATFEAEYDLERAQAVNALFTSINQIGIKTDVYDIDQVSNLYDCLSDFCDEKREL 660  
 DB 601 TATFEAEYDLERAQAVNALFTSINQIGIKTDVYDIDQVSNLYDCLSDFCDEKREL 660  
 QY 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGWSGTITITQRGDDVFKENVTLPGTFD 720  
 DB 661 SEKVHAKRLSDERNLLQDPNFKGINRQLDRGWSGTITITQRGDDVFKENVTLPGTFD 720  
 QY 721 EGYPTLYQKIDESKLPYTRYQLRGYIEDSDQLEIYLIRYNAKHETVNVLTGSLNPLS 780  
 DB 721 EGYPTLYQKIDESKLPYTRYQLRGYIEDSDQLEIYLIRYNAKHETVNVLTGSLNPLS 780  
 QY 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGCEKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
 DB 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGCEKCAHSHHFSLDIDVGCTDLNEDLDVWV 840  
 QY 841 IFKIKTDGSHARLGNLEFLEEK - PLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKE 899  
 DB 841 IFKIKTDGSHARLGNLEFLEEK - PLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKE 899  
 QY 900 SVDALFVNSQYDQLQADTNIAHIAADKRVHRIRREAYLPESLVPVGNVDIFEELKGRIF 959  
 DB 900 SVDALFVNSQYDQLQADTNIAHIAADKRVHRIRREAYLPESLVPVGNVDIFEELKGRIF 959  
 QY 960 TAFELYDARNVKNKGNGLSCNNVKGHDVDEONHRSVLVPEWEAEVSOEVRVCPG 1019  
 DB 960 TAFELYDARNVKNKGNGLSCNNVKGHDVDEONHRSVLVPEWEAEVSOEVRVCPG 1019  
 QY 1020 RGYTLRVTAKEGYGEGCVTITHEIENNTDELKFSNCVEEYPPNNTVTCNDYTANQEEYG 1079  
 DB 1020 RGYTLRVTAKEGYGEGCVTITHEIENNTDELKFSNCVEEYPPNNTVTCNDYTANQEEYG 1079  
 QY 1080 GAYTSRNRGYDETYGNSVSPADYASVYEEKSYTDGRDRDNPCESNRGYDYTLPAGVYT 1139  
 DB 1080 GAYTSRNRGYDETYGNSVSPADYASVYEEKSYTDGRDRDNPCESNRGYDYTLPAGVYT 1139  
 QY 1140 KELEYFPETDKWIEIGETEGTFIVDSVELLME 1174  
 DB 1141 KELEYFPETDKWIEIGETEGTFIVDSVELLME 1175

Search completed: November 27, 2002, 18:38:03

Job time : 87 secs